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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta is described. Also described are single exon nucleic acid probes expressed in the placenta and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file pto_PLACENTA.txt, created 24
25 January 2001, having 26,548,337 bytes. The Sequence
Listing contained in said file on said disc is incorporated
herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

placenta and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins — known or suspected — about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences — that is, those accessible through isolation of mRNA — are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches – and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species – there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that
25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al.,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence.
Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

 Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the
20 predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

25 Recently, techniques have been developed that permit direct sampling of placenta earlier in pregnancy. There is a need for methods and apparatus that permit analysis of placenta samples for the prediction and diagnosis of diseases caused by genetic defect,
30 particularly those with polygenic etiology.

Summary of the Invention

35 The present invention solves these and other

problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the
5 expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified
10 within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon
15 microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta, comprising a plurality
20 of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 13,232 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at
25 least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

30 In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.
35 Preferably, each of said plurality of probes is amplifiable

using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

5 Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 26,232 or a complimentary sequence, or a portion of such a sequence.

10 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

15 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
20 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
25 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single
30 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
35 nylon may preferably, be positively-charged. Other suitable

substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 5 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable 10 set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or 15 more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome- 20 derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of 25 SEQ ID Nos. 13,233 - 26,232, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 13,232.

Accordingly, in a third aspect of the invention, 30 there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 13,232 or a complementary sequence or a fragment thereof 35 wherein said probe hybridizes at high stringency to a

nucleic acid expressed in the human placenta.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.:
5 13,233 - 26,232 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human
10 placenta which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,233 - 38,837 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed
15 in the human placenta.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the
20 single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon
25 nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably,
30 no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

35 In another embodiment of either the third or

fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human placenta, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human placenta; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

5 wherein said detectably labeled nucleic acids are derived from mRNA from the placenta of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon
10 microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,
15 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in
20 a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types
25 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 26,232 wherein said sequence encodes a peptide.

30 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOs: 13,233 - 26,232, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
35 encoded by a sequence comprising a sequence set out in any

of SEQ ID NOS.: 1 -13,232 .

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ
5 ID NOS.: 26,233 - 38,837.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 26,233 - 38,837, or fragment thereof.

10 In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for
15 electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

20

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each
25 of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called
30 in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books
35 Division (2000) (ISBN: 1881299376). As so defined, the

term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a
5 natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a
10 portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a
15 combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF
20 present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another
25 of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit
30 specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

35 As used herein with respect to the visual display

of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

10

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color

hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed
5 in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by
10 microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for
15 scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the
20 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

25 FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

30

Methods and Apparatus for Predicting, Confirming,
Annotating, and Displaying Functional Regions From Genomic
Sequence Data

35 FIG. 1 is a flow chart illustrating in broad

outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly

include several divisions thereof, including the
htgs(draft), NT (nucleotide, command line), and NR
(nonredundant) divisions. GenBank is produced by the
National Institutes of Health and is maintained by the
5 National Center for Biotechnology Information (NCBI).
Databases of genomic sequence from species other than
human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*
briggsii, *Drosophila*, zebra fish, and other higher
eukaryotic organisms will also prove useful as genomic
10 sequence database 100.

Genomic sequence obtained by query of genomic
sequence database 100 is then input into one or more
processes 200 for identification of regions therein that
are predicted to have a biological function as specified by
15 the user. Such functions include, but are not limited to,
encoding protein, regulating transcription, regulating
message transport after transcription into mRNA, regulating
message splicing after transcription into mRNA, of
regulating message degradation after transcription into
20 mRNA, and the like. Other functions include directing
somatic recombination events, contributing to chromosomal
stability or movement, contributing to allelic exclusion or
X chromosome inactivation, and the like.

The particular genomic sequence to be input into
25 process 200 will depend upon the function for which
relevant sequence is to be identified as well as upon the
approach chosen for such identification. Process step 200
can be iterated to identify different functions within a
given genomic region. In such case, the input often will
30 be different for the several iterations.

Sequences predicted to have the requisite
function by process 200 are then input into process 300,
where a subset of the input sequences suitable for
experimental confirmation is identified. Experimental
35 confirmation can involve physical and/or bioinformatic

assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational

substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or
5 interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of
10 functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20
15 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis
20 approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast,
25 corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

30 The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic
35 sequence, the query will accordingly require that the

sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been

described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to

report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query
5 criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable
10 for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to,
15 or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and
20 subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual
25 sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable,
30 including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known
35 restriction sites. As another example, vector sequence can

be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25,

where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For

the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%;
5 and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling,
10 consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such
15 iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored
20 in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further
25 described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27
30 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three
35 of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process
5 can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison
10 can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the
15 multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process
20 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to
25 identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon
30 consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene
35 expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible
5 secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving
10 hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such
15 sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process
20 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in
25 process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the
30 sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression
35 of putative genes identified within genomic sequence. In

particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon
5 nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the
10 polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with
15 minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

20 However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer
25 amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify
30 regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

35 Conversely, somewhat fewer than 10% of ORFs

predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

10 The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

20 Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

30 Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not

exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for
5 amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the
10 organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual,
15 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

20 Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather,
25 the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes
30 not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single
35 exon probe) is disposed in an array upon a support

substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see
5 above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene,
10 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular,
15 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

20 The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination
25 thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or
30 can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

35 As is well known in the art, microarrays

typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can
5 readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create
10 a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.
15 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using
20 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on
25 nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.
30 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads
35 provides in aggregate a higher density of nucleic acid

probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high
5 throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will
10 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one
15 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

20 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created
25 by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or
30 indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*, or from the *de novo* construction of "problem specific"
35 libraries targeted at a particular biological question,

R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure
5 expression only of those genes found in EST libraries,
shown herein to represent only a fraction of expressed
genes. Furthermore, such libraries - and thus microarrays
based thereupon - are biased by the tissue or cell type of
message origin, by the expression levels of the respective
10 genes within the tissues, and by the ability of the message
successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the
methods of the present invention enable sequences that do
not appear in EST or other expression databases to be
15 determined - subsequently arrayed for expression
measurements could not, therefore, have been represented as
probes on an EST microarray. And as further demonstrated
in the examples, *infra*, the remaining population of genes
identified from genomic sequence by the methods of the
20 present invention - that is, the one third of sequences
that had previously been accessioned in EST or other
expression databases - are biased toward genes with higher
expression levels.

Representation of a message in an EST and/or cDNA
25 library depends upon the successful reverse transcription,
optionally but typically with subsequent successful
cloning, of the message. This introduces substantial bias
into the population of probes available for arraying in EST
microarrays.

30 In contrast, neither reverse transcription nor
cloning is required to produce the probes arrayed on the
genome-derived single exon microarrays of the present
invention. And although the ultimate deposition of a probe
on the genome-derived single exon microarray of the present
35 invention depends upon a successful amplification from

genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse
5 transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias,
10 than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric
15 stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention
20 lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present
25 invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the
30 specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically
35 include a fair amount of vector sequence, more so when the

probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the

genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without
5 such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such
10 microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present
15 invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual
20 probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be
25 designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often
30 include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized
35 probes. For human genes, the near-complete sequence of

human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

5 In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70,
10 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single
15 exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression
20 patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such
25 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention
30 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon
35 microarrays of the present invention include sequence drawn

from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and
5 thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic
10 synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to
15 achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

20 In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present
25 invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved
30 for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention
35 typically are, but need not necessarily be, bound

noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm

expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased

commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of
5 nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As
10 further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

15 After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are
20 related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain
25 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for
30 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived
35 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate
5 can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits
10 addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-
15 derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3'
20 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

25 Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

30 In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered
35 set of amplifiable probes is packaged separately from the

genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences,

SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query - including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively

described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given
5 the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left
10 border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

15 As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides
20 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other
25 pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.
30 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or
35 fulcrum point about which a chosen range of sequence is

anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or

approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

- 5 For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

- 10 Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

- Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 25 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

- As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, 30 field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

- Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 35 can include as few as one such series of rectangles and as

many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show
5 predictions of a plurality of different functions.
However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis,
10 such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the
15 portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional
20 inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an
25 increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

30 Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84
35 identifies the sequence included within the probe

immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of

rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity
5 has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links
10 directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be
15 resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical
20 assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of
25 rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of
30 hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to
35 depict expression less than control, corresponding to the

spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 13,232 of these ORFs in placenta.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in placenta is currently available for use in measuring the level of its ORF's expression in placenta.

Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been

interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

Classically, such antenatal diagnosis was
5 effected during second trimester by metaphase karyotyping of fetal cells that had shed spontaneously into amniotic fluid.

More recently, techniques have been developed that permit direct sampling of placenta earlier in
10 pregnancy.

One technique in current clinical practice is chorionic villus sampling, which can be used to detect gene defects or polymorphisms in cells from the developing fetus, usually between 10 and 12 weeks of pregnancy. In
15 chorionic villus sampling, a small sample of chorionic villi, which are tiny projections that make up part of the placenta, a fetal-derived tissue, is removed through the mother's cervix or the abdominal wall. Placental chromosomal DNA is then isolated from the chorionic villus
20 cells and analyzed to detect a small number of known genetic defects. Such defects range from gross karyotypic changes, such as triploidy, to discrete point mutations known to cause diseases having significant morbidity or mortality.

25 Although only a few diseases are at present diagnosed by antenatal analysis of human placenta, a far higher number of human diseases and disorders have been catalogued in which dysfunction or misregulation of one or more genes contributes to the disease phenotype. At one
30 end of the spectrum of genetic diseases are those, such as sickle cell trait, in which a single point mutation is responsible for the disease phenotype. At the other end of the spectrum lie disorders such as Down syndrome wherein the presence of a supernumerary chromosome manifests itself
35 in variety of phenotypic defects that vary in severity

among affected individuals. For most, possibly all genetic diseases, the precise phenotypic manifestation and its severity is a function of a complex interaction between the definable genetic lesion and the action of many other genes
5 and environmental factors.

Although the incidence of many genetic diseases is low, a sufficient number of such genetic diseases affect a sufficiently large population that they impact the national health economy. For example, cystic fibrosis,
10 caused by mutations in a gene encoding a chloride ion channel and resulting in lung and other disorders, occurs at a rate of about 1 in 3000 births among Caucasians and costs over \$1 billion annually for direct medical treatment in the U.S. alone. Furthermore, it is increasingly thought
15 that for many diseases where no clear-cut genetic lesion appears responsible, possession by individuals of particular gene alleles naturally occurring within certain populations places such individuals at increased risk for developing those diseases. Examples include heart disease,
20 neurogenerative disorders, diabetes, cancer and autoimmune disorders. For yet other diseases, especially cancer, the etiology is truly polygenic in that defects in multiple genes must coincide in the same individual or even the same cell for the disease to develop and/or progress.

25 A large number of human genetic diseases and disorders are known, as are the gene or genes implicated in the etiology of the disease. Although in some cases single gene defects are known to be responsible for the etiology of a genetic disease, it is believed that for most or all
30 such diseases, penetrance of the disease is affected by interaction with other genes. For other diseases or disorders, is believed that their mechanism is explained by the interaction of multiple genes, or by mutations or other defects in multiple genes. Such diseases and disorders may
35 be detected in placenta.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for antenatal diagnosis of human genetic disorders. With each of the single exon probes described herein shown to be
5 expressed at detectable levels in human placenta, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, antenatal diagnosis can be based
10 upon the quantitative relatedness of a placental gene expression profile to one or more reference expression profiles known to be characteristic of a given disease, or to specific grades or stages thereof.

In one embodiment, the gene expression profile is
15 generated by hybridizing nucleic acids obtained directly or indirectly from placenta, typically through chorionic villus sampling, to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from
20 individuals with known disease.

Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

25 In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits presence and/or predisposition to disease to be assessed through the
30 massively parallel determination of altered copy number, deletion, or mutation of exons known to be expressed in human placenta. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated
35 gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art – see Ausubel et al. and Maniatis et al. – each probe reports the level of
5 expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the placenta has been demonstrated are useful for both measurement in the placenta and for survey of expression in
10 other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which
15 are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was
20 measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten
25 tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have
30 significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon
35 microarrays, in turn, are useful devices for measuring and

for surveying gene expression in the human.

Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell

Carcinoma Using Combination of cDNA Subtraction and
Microarray Analysis," *Oncogene* 19(12):1519-28 (2000);
Whitney et al., "Analysis of Gene Expression in Multiple
Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.*
5 46(3):425-8 (1999)), in drug discovery screens (see, for
example, Scherf et al., "A Gene Expression Database for the
Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44
(2000)) and in diagnosis to determine appropriate treatment
strategies (see, for example, Sgroi et al., "In vivo Gene
10 Expression Profile Analysis of Human Breast Cancer
Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of
pharmacological drug candidates upon cells, each probe
provides specific useful data. In particular, it should be
15 appreciated that even those probes that show no change in
expression are as informative as those that do change,
serving, in essence, as negative controls.

For example, where gene expression analysis is
used to assess toxicity of chemical agents on cells, the
20 failure of the agent to change a gene's expression level is
evidence that the drug likely does not affect the pathway
of which the gene's expressed protein is a part.
Analogously, where gene expression analysis is used to
assess side effects of pharmacological agents - whether in
25 lead compound discovery or in subsequent screening of lead
compound derivatives - the inability of the agent to alter
a gene's expression level is evidence that the drug does
not affect the pathway of which the gene's expressed
protein is a part.

30 WO 99/58720 provides methods for quantifying the
relatedness of a first and second gene expression profile
and for ordering the relatedness of a plurality of gene
expression profiles. The methods so described permit
useful information to be extracted from a greater
35 percentage of the individual gene expression measurements

from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold *et al.*, *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999);

5 Schena *et al.*

The invention particularly provides genome-derived single-exon probes known to be expressed in placenta. The individual single exon probes can be provided in the form of substantially isolated and purified
10 nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA
15 complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as
20 complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

25 Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity
30 suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and
35 WO 00/15779. As is well understood, where the probes are

to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

5 Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or
10 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged
15 therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting,
20 in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a
25 genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF.
30 Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase
35 hybridization, however - that is, for use in a

hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,233 - 26,232, respectively, for probe SEQ ID NOS. 1 - 13,232. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,233 - 26,232 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high

stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have

sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is

obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human placenta.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human placenta. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group

consisting of SEQ ID NOS.: 1 - 13,232.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,232 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 13,233 - 26,232, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 13,232 can be used, or that portion thereof in SEQ ID NOS. 13,233 - 26,232 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA;

Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 13,233 - 26,232. Such amino acid sequences are set out in SEQ ID NOS: 26,233 - 38,837. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

30 EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

Bioinformatics Results

35 All human BAC sequences in fewer than 10 pieces

that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

5 After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets:
10 GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic
15 DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION
20 yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three
25 programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs
30 ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single
35 gene if fewer than 7 exons were found within the 25 kb

window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto,

CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR
5 amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon)
10 length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median
15 size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

20 Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of
25 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were
30 sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR
35 and sequencing results. The reasons for this are unclear,

but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material
5 flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was
10 similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-
15 described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally
20 included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt
25 GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1 e^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe
30 sequences showed some homology to a known EST or mRNA (BLAST E values from 1 e^{-5} to 1 e^{-99}). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

35 All of the probe sequences (as amplified) were

then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single

Exon Microarrays

The two genome-derived single exon microarrays
5 prepared according to Example 1 were hybridized in a series
of simultaneous two-color fluorescence experiments to (1)
Cy3-labeled cDNA synthesized from message drawn
individually from each of brain, heart, liver, fetal liver,
placenta, lung, bone marrow, HeLa, BT 474, or HBL 100
10 cells, and (2) Cy5-labeled cDNA prepared from message
pooled from all ten tissues and cell types, as a control in
each of the measurements. Hybridization and scanning were
carried out using standard protocols and Molecular Dynamics
equipment.

15 Briefly, mRNA samples were bought from commercial
sources (Clontech, Palo Alto, CA and Amersham Pharmacia
Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were
incorporated during separate reverse transcriptions of 1 µg
of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer
20 and 2 µg random 9mer primers as follows. After heating to
70°C, the RNA:primer mixture was snap cooled on ice. After
snap cooling on ice, added to the RNA to the stated final
concentration was: 1X Superscript II buffer, 0.01 M DTT,
100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM
25 Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II
enzyme. The reaction was incubated for 2 hours at 42°C.
After 2 hours, the first strand cDNA was isolated by adding
1 U Ribonuclease H, and incubating for 30 minutes at 37°C.
The reaction was then purified using a Qiagen PCR cleanup
30 column, increasing the number of ethanol washes to 5.
Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured
for dye incorporation. Volumes of both Cy3 and Cy5 cDNA
corresponding to 50 pmoles of each dye were then dried in a
35 Speedvac, resuspended in 30 µl hybridization solution

containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_ot1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all

tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective

tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; 5 HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose 10 expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, 15 fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

20

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those 25 genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") 30 upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 35 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present

in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

30

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain

Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates

				activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097

(1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to
5 rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being
10 absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the
15 highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20
20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,
25 AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in
30 the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 α (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
35 chromosome RNA-binding motif (Chai et al., *Genomics*

49(2):283-89 (1998))(AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature
 5 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process.
 10 The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average
 15 expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ± 0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±
Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

10 EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION

identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be
5 from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show
10 identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes.
15 Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very
20 good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following
25 colors indicate a known gene (top to bottom):
red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and
30 12 did not sequence verify.

EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring
35 Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique
5 exons in the human genome that could be shown to be expressed at significant levels in placenta tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon
10 microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the
15 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,232 single exon probes, each fragment corresponding to an extension product from one of
20 the two amplification primers.)

The structures of the 13,232 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,232. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not
25 included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,233 - 26,232, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than
30 one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant
35 expression is based on a statistical confidence that the

signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give
5 a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the
10 population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining
15 control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations)
20 are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean +
25 (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any
30 signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human placenta and thus
35 presents the subset of probes that was recognized to be

useful for measuring expression of their cognate genes in human placenta tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,233 - 26,232 was individually
5 used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were
10 scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted
15 in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective
20 probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be
25 expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the
30 name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide
35 sequences. These are set out as PEPTIDE SEQ ID NOS.: The

peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs
5 are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the
10 exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all
15 of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion
20 of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the
25 protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as
30 the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ - which is probative evidence that the query sequence has previously
35 been shown to be expressed - the top hit is highly unlikely

exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even
5 the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent
10 a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 13,232) and probe exon (SEQ ID NOs.: 13,233 - 26,232, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

15 (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST
20 query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

25 (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

30 EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human Placenta

Table 4 (550 pages) presents expression, homology, and
35 functional information for the genome-derived single exon

probes that are expressed significantly in human placenta.

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
463	13658	26695	5				
912	14087	27152	9.68				
1070	14236		3.01				
1330	14487	27555	10.9				
1845	14787	27882	1.92				
1666	14818	27901	4.94				
1764	14913	28008	1.03				
1788	14937	28030	1.67				
1784	14943	28036	8.53				
1939	15082	28183	1.57				
2034	15175	28285	2.66				
2234	15368	28497	3.39				
2363	15484	28616	2.53				
3255	16429	29447	3.75				
3537	16702	29713	1.48				
3504	16768	29783	10.5				
3651	16814		0.84				
3747	16908	29912	0.98				
4057	17213		0.94				
4314	17457	30445	1.55				
4377	17520	30500	6.88				
4396	17539	30519	0.87				
4398	17539	30520	0.87				
4457	17587		1.69				
4512	17651	30639	0.61				
4958	18088	31084	1.86				
5002	18131		0.6				
5157	18279	31244	5.14				
5168	18290	31255	1.24				
5371	18574	31442	1.78				
5371	18574	31443	1.76				
5538	18735		4.12				
5714	18907		7.26				
5786	18735		3.31				

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Table 4
Single Exon Probes Expressed in Placenta

Probe Seq ID NO:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5858	19048	32354	4.22				
6146	25820	32668	1.61				
6174	19350	32698	1.92				
6540	19708		1.01				
6679	19838	33226	1.25				
6679	19838	33227	1.25				
7275	20358	33812	1.42				
7275	20358	33813	1.42				
7568	20641	34117	1.18				
7568	20641	34118	1.18				
8251	21333	34851	1.44				
8682	21762	35286	1.14				
9081	22140	35884	0.76				
9081	22140	35885	0.76				
9734	22799	36373	3.82				
9968	23007	36902	0.56				
10088	23124	36725	1.51				
10228	23264	36853	0.88				
10643	23677	37286	0.74				
10643	23677	37287	0.74				
10922	24005		2.32				
11260	24346		1.76				
11348	24410	38063	2.79				
11641	24721	38414	1.73				
11749	23835	37561	1.36				
11749	23835	37562	1.36				
11792	24782		2.09				
12057	25038	38746	1.56				
12623	25419		2.06				
12667	25628	31980	1.5				
6177	19353	32700	16.82	9.9E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 16, 17 and 18
8195	21277	34800	1.5	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9944	22963	36575	0.48	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
9944	22963	36576	0.48	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7139	20274	33714	0.82	9.6E+00	AF085630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7139	20274	33715	0.82	9.6E+00	AF085630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10336	23070	37279	0.93	9.6E+00	AF242432.1	NT	Mus musculus Nalp3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalp1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
10336	23070	37280	0.93	9.6E+00	AF242432.1	NT	Mus musculus Nalp3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalp1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
2731	15849	28959	0.97	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M) envelope glycoprotein (E) polyprotein mRNA, partial cds
2731	15849	28960	0.97	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M) envelope glycoprotein (E) polyprotein mRNA, partial cds
2930	18198	29182	3.08	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
8290	21372	34893	1.08	9.3E+00	AF130690.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
9204	22282	35822	3.03	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
7625	20685	34171	0.6	9.2E+00	Q81767	SWISSPROT	3 BETA-HYDROXYSTEROID DEHYDROGENASE TYPE IV (3BETA-HSD IV) (3-BETA-HYDROXY-DELTA(5)-STEROID DEHYDROGENASE) (3-BETA-HYDROXY-5-ENE STEROID DEHYDROGENASE) (PROGESTERONE REDUCTASE)
5411	18613	31586	2.59	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5411	18613	31587	2.59	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9630	22885		1	9.0E+00	P09241	SWISSPROT	RHODOPSIN
6100	19336	32681	5.15	8.9E+00	BE971806.1	EST_HUMAN	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
6570	19875	33044	2.03	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
6570	19875	33045	2.03	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
453	13649	26885	1.79	8.4E+00	5031804	NT	Homo sapiens Insulin receptor substrate 1 (IRS1) mRNA
9654	21097	34811	2.09	8.1E+00	AJ131719.1	NT	Zae mays mRNA for legumain-like protease (sec2a)
11443	24504		1.96	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8345	21428		0.98	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7501	20576		1.85	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8556	21637	35174	1.42	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8556	21637	35175	1.42	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5921	19108	32421	3.6	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285506 5'
8953	22032	35573	3	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
8953	22032	35574	3	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3042	16218	29238	3.41	7.2E+00	L12051.1	NT	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
3042	16218	29239	3.41	7.2E+00	L12051.1	NT	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
7174	20307	33750	1.07	7.2E+00	BE170090.1	EST_HUMAN	LOC10613-200300-031-a07 HT10613 Homo sapiens cDNA
7299	20381	33838	1.22	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7299	20381	33839	1.22	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9798	22838		9.23	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11688	24745	38437	2.44	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
10187	23224	36818	2.76	7.0E+00	P48810	SWISSPROT	ARGININE KINASE (AK)
11528	24584	38261	1.52	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
8478	21559	35093	3.17	6.9E+00	P35879	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10589	23594	37200	1.12	6.8E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10579	23614	37219	0.6	6.9E+00	P34226	SWISSPROT	SKT5 PROTEIN
8092	21174	34688	1.64	6.8E+00	W03412.1	EST_HUMAN	za07c11.1 Scars melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:291860 5'
8092	21174	34689	1.64	6.8E+00	W03412.1	EST_HUMAN	za07c11.1 Scars melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:291860 5'
9333	22409		1.62	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VPs AND VP8]
10413	23448	37053	3.6	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
5398	18600		0.65	6.6E+00	Q39028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
6675	19834	33223	0.86	6.6E+00	BF672121.1	EST_HUMAN	602152573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283427 5'
9234	26226		0.55	6.6E+00	P51825	SWISSPROT	AF-4 PROTEIN (FEL PROTEIN)
10279	23314	36912	2.14	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10279	23314	36913	2.14	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10843	23876	37496	0.47	6.6E+00	H29330.1	EST_HUMAN	ym80f06.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:52737 3'
11393	24454		1.48	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C6C3.05C
9382	22457	36020	7	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP62; COAT PROTEIN GP36]
10512	23647	37158	0.52	6.5E+00	BE866001.1	EST_HUMAN	601078435F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3960989 5'
9943	22982	36574	1.34	6.2E+00	AY010901.1	NT	Schizophyllum commune unknown mRNA
10787	23820	37444	0.7	6.2E+00	6754621	NT	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA
7181	20313	33756	1.6	6.0E+00	BE780163.1	EST_HUMAN	601468031F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3871303 5'
10021	23059	36855	0.49	6.0E+00	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (617)
10732	23765	37373	0.82	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10732	23765	37374	0.82	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
6850	19809	33197	7.14	5.9E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11933	24919		3.02	5.9E+00	BE958530.1	EST_HUMAN	601645278F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930451 5'
3613	16777		1.15	5.8E+00	7661557	NT	Homo sapiens DESCI1 protein (DESCI1), mRNA
7312	20394	33855	0.74	5.7E+00	AF302048.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7312	20394	33856	0.74	5.7E+00	AF302048.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7742	20803		1.34	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLII)
11289	24355	37996	2.03	5.6E+00	AB027305.1	NT	Cyprinus carpio mRNA for lysozyme C, complete cds
11289	24355	37997	2.03	5.6E+00	AB027305.1	NT	Cyprinus carpio mRNA for lysozyme C, complete cds
11765	23951	37581	2.52	5.6E+00	Q55278	SWISSPROT	LYCOPENE BETA CYCLASE
6381	19550	32906	0.74	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
9982	23021		0.56	5.5E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
11018	24097		1.46	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11763	23949	37578	2.32	5.5E+00	P11990	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
7069	20122	33536	1.11	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7484	20559	33537	1.11	5.4E+00	Q99435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
8013	21063	34575	0.74	5.4E+00	P50391	SWISSPROT	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4-R) (PANCREATIC POLYPEPTIDE RECEPTOR 1) (PP1)
8054	21137		1.62	5.4E+00	Q91082	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C;
8998	22078	35618	0.93	5.4E+00	P40379	SWISSPROT	LIPOVITELLIN LV-2J
8998	22078	35618	0.93	5.4E+00	P40379	SWISSPROT	REPI PROTEIN
10242	23277	36870	1.45	5.4E+00	Q17094	SWISSPROT	REPI PROTEIN
10242	23277	36871	1.45	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4906	18036	31024	1.47	5.3E+00	L43126.1	NT	RHODOPSIN
6617	19777		0.7	5.3E+00	P41779	SWISSPROT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
8270	21352		3.39	5.3E+00	P54098	SWISSPROT	HOMEOBOX PROTEIN CEH-20
9184	22262		0.72	5.3E+00	AB034990.1	NT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
11928	24914	38616	1.51	5.3E+00	Q27905	SWISSPROT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
5590	18775		1.16	5.2E+00	BE184840.1	EST_HUMAN	PROBABLE ANTIBACTERIAL PEPTIDE POLYPEPTIDE PRECURSOR
10583	23618		0.98	5.2E+00	AF248070.1	NT	QV4-HT0691-270400-186-f09 HT0691 Homo sapiens cDNA
11470	24529		1.93	5.2E+00	Q10136	SWISSPROT	Drosophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds
9102	22240	35784	0.94	5.1E+00	O16005	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME I
10030	23058	36667	1.33	5.1E+00	P09182	SWISSPROT	RHODOPSIN
6415	19584	32946	0.74	5.0E+00	BF310443.1	EST_HUMAN	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
10397	23432		0.7	5.0E+00	BF308591.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
							601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10645	23679	37289	2.89	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds
11568	24824	38304	7.24	5.0E+00	Z63850.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162
10437	23472						Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4172	17322		0.76	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
8348	21429	34953	12.39	4.8E+00	AF185255.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
8738	21817		0.6	4.8E+00	BF367909.1	EST_HUMAN	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
300	13517	26550	4.92	4.8E+00	AW750087.1	EST_HUMAN	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
301	13517	26550	3.04	4.7E+00	BF240552.1	EST_HUMAN	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
3347	16520	29534	1.85	4.7E+00	BF240552.1	EST_HUMAN	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7962	21012	34522	1.02	4.7E+00	AL163280.2	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9397	22471	36036	0.59	4.6E+00	U97569.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9397	22471	36037	1.1	4.6E+00	BE646437.1	EST_HUMAN	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10800	23635		1.1	4.6E+00	BE646437.1	EST_HUMAN	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7947	20897		0.63	4.6E+00	AF240786.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11904	24892	38593	0.7	4.5E+00	AF126177.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12058	25039	38747	1.87	4.5E+00	AE001044.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
3105	16281	29286	1.53	4.5E+00	BF688941.1	EST_HUMAN	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
3105	16281	29286	0.84	4.4E+00	BF530893.1	EST_HUMAN	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6331	16502		0.84	4.4E+00	BF530893.1	EST_HUMAN	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6245	19419		1.58	4.4E+00	X13414.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7596	20866	34142	0.77	4.3E+00	AF058679.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7792	20848	34341	2.53	4.3E+00	Y13402.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11101	24174	37809	0.68	4.3E+00	AE001222.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5634	18828		14.74	4.3E+00	AF240786.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5711	18904	32199	4.1	4.2E+00	P16444	SWISSPROT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5880	19070		1.07	4.2E+00	P51826	SWISSPROT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6911	20223	33657	0.71	4.2E+00	O27830	SWISSPROT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
			1.67	4.2E+00	P13983	SWISSPROT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6911	20226	33658	1.67	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9160	22238	35783	5.3	4.2E+00	A1809013.1	EST_HUMAN	wf67g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:230692 3'
10122	23160	36759	1.03	4.2E+00	P31368	SWISSPROT	NUBBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
10352	23387		0.47	4.2E+00	P40896	SWISSPROT	HEXOSE TRANSPORTER HXT8
7261	20344	33796	0.98	4.1E+00	BE253668.1	EST_HUMAN	601110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'
7839	20894	34396	7.86	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
7960	21010		0.64	4.1E+00	AB041523.1	NT	Patinopecten yessoensis mRNA for calcineurin A, complete cds
7963	21013	34523	3.8	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
7963	21013	34524	3.8	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8101	21183	34703	2.88	4.1E+00	U57803.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
8740	22805	36381	0.61	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9873	22913	36498	2.25	4.1E+00	BF692425.1	EST_HUMAN	60247938F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'
10370	23405		0.55	4.1E+00	AJ235273.1	NT	Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4
							CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27)
10514	23549		0.52	4.1E+00	P46414	SWISSPROT	(P27KIP1)
11124	24196		2.15	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVL1
11214	24283		12.25	4.1E+00	BE865880.1	EST_HUMAN	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909051 5'
3635	16799		0.72	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5575	20130	33546	0.93	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
5575	20130	33547	0.93	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7077	20130	33546	0.99	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7077	20130	33547	0.99	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7339	20419	33881	1	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
9074	22153	35697	0.49	4.0E+00	Q14157	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0144
10148	23186	36783	0.65	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS)
10368	23403	37014	0.6	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
10464	23499	37111	0.45	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10464	23499	37112	0.45	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11762	23948	37577	1.59	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
							GENOME POLYPEPTIDE [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS2C, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11843	24832	38524	2.98	4.0E+00	P07564	SWISSPROT	

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11843	24832	38525	2.98	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5))
12133	25113	38817	1.34	4.0E+00	P35811	SWISSPROT	ERYTHROCYTE ADDUCIN ALPHA SUBUNIT
3531	16755	29770	5	3.9E+00	X64518.1	NT	N. tabacum chitinase gene 50 for class I chitinase C
4441	17681		0.87	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5775	18967	32270	2.82	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
5775	18967	32271	2.92	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
6772	19927	33322	0.93	3.9E+00	AF298209.1	NT	Dicotyledon discoidium non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6829	19982	33389	0.7	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7013	20149	33570	4.43	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDS-RPSF INTERGENIC REGION
7519	20562	34068	4.25	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
8512	21593	35128	2.44	3.9E+00	X65865.1	NT	X.laevis mRNA for M4 muscarinic receptor
11674	23902	37524	2.77	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2693	15813		1.53	3.8E+00	AE001592.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6520	19885	33057	1.05	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN M.J0385
8827	21707	35244	1.12	3.8E+00	D44725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
9999	23037		0.6	3.8E+00	AJ300661.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7864
12120	25100		11.65	3.8E+00	9631294	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
4129	17282	30277	12.79	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7316	20398		0.83	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
9379	22454	36017	1.04	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11715	24755	38450	2.11	3.7E+00	BF689278.1	EST_HUMAN	602120551F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4277748 5'
11715	24755	38451	2.11	3.7E+00	BF689279.1	EST_HUMAN	602120551F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4277748 5'
12280	25196		1.87	3.7E+00	AB013746.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
600	13795	28814	3.76	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
5369	18572	31440	0.78	3.6E+00	BF316316.1	EST_HUMAN	601901866F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4131016 5'
8749	21828	35364	0.86	3.6E+00	D12367.1	EST_HUMAN	HUM0007B08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8749	21828	35365	0.86	3.6E+00	D12367.1	EST_HUMAN	HUM0007B08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8847	21926	35464	3.67	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PAO1, section 8 of 529 of the complete genome

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8847	21928	35465	3.67	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
9864	22804	36488	0.51	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
9864	22804	36489	0.51	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
11093	24167		3.21	3.6E+00	M96795.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
3319	16492	29509	1.04	3.5E+00	AF221538.1	NT	Escherichia coli glycerophosphate dehydrogenase (gpd) gene, partial cds; and the translation start site has been verified (gpe), the translation start site has been verified (gpe), and repressor protein (gpr) genes, complete cds
6123	19302		1	3.5E+00	L42898.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
6341	19511	32888	0.93	3.5E+00	R19745.1	EST_HUMAN	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
8881	21761		0.96	3.5E+00	P24557	SWISSPROT	940d08.1 Soares infant brain IN1B Homod sapiens cDNA clone IMAGE:34940 5'
9232	22310	35851	0.99	3.5E+00	AA190998.1	EST_HUMAN	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
9232	22310	35851	0.99	3.5E+00	AA190998.1	EST_HUMAN	z88b04.s1 Stratagene Hela cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element
9694	22743	36313	0.99	3.5E+00	AA190998.1	EST_HUMAN	z88b04.s1 Stratagene Hela cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element
10739	23772	37383	0.58	3.5E+00	AJ133723.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53
1542	14694	27773	3.81	3.4E+00	AF264577.1	NT	Bos taurus mRNA for Ran-binding protein 2, partial
2644	15767	28892	1.07	3.4E+00	AL163278.2	NT	Brassica napus RPB5d mRNA, complete cds
7518	20591	34065	2.33	3.4E+00	P04052	SWISSPROT	Homo sapiens chromosome 21 segment HS21C078
7880	20932	34437	0.76	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8876	21955		0.77	3.4E+00	U66406.1	NT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
9274	22350	35901	0.77	3.4E+00	AJ229042.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNU1) gene, complete cds
9312	22388	35939	0.54	3.4E+00	AJ250567.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
10471	23506	37119	3.35	3.4E+00	AF013167.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
11822	24811	38506	2.06	3.4E+00	L77570.1	NT	Saccharomyces cerevisiae MFS1 gene, complete cds
6193	19369	32719	0.97	3.3E+00	Q09669	SWISSPROT	Homo sapiens DiGeorge syndrome critical region, centromeric end
6193	19369	32720	0.97	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
8077	21159	34676	1.03	3.3E+00	AF111168.2	NT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
10881	23715	37321	1.04	3.3E+00	AF001511.1	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10881	23715	37322	1.04	3.3E+00	AF001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
513	13707	26735	1.79	3.2E+00	X96422.1	NT	Bacillus halodurans genomic DNA, section 5/14
							D. rerio zp-50 POU gene

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4136	13707	26735	0.78	3.2E+00	X98422.1	NT	D. rerio zp-50 POU gene
4850	17983	30971		3.2E+00		NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5686	18880	32170	0.95	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5686	18880	32171	1.16	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5719	18912	32207	2.49	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5719	18912	32208	2.49	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6436	19603	32966	1.91	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6436	19603	32967	1.91	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7781	20837	34330	0.86	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7852	21002	34513	2.41	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7852	21002	34514	2.41	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
9230	22808		5.26	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
9730	22795	36569	1.31	3.2E+00	M96383.1	NT	S. cerevisiae threonine deaminase (LTV) gene, complete cds
10345	23380	36991	2.06	3.2E+00	AB016081.2	NT	Oryza latipes OIGC6 gene for guaranyl cyclase C, complete cds
12219	25169		2.95	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5998	19181	32503	2.29	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.6 KD PROTEIN C33E2.02 IN CHROMOSOME 1
7547	20619	34085	0.91	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)
7904	20956		1.09	3.1E+00	AF303225.1	NT	Bacillus alcalophilus pectate lyase (palE) gene, complete cds
8279	21361	34880	0.51	3.1E+00	P40985	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4
8801	21880	35417	5.14	3.1E+00	P49894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE 1 5'DEIODINASE) (DIO1) (TYPE 1 DI) (5DI)
8801	21880	35418	5.14	3.1E+00	P49894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE 1 5'DEIODINASE) (DIO1) (TYPE 1 DI) (5DI)
9459	22575		3.7	3.1E+00	Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9528	22591	36162	0.56	3.1E+00	Q01149	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
10100	23138	36739	0.76	3.1E+00	7524759	NT	Chlorella vulgaris chloroplast, complete genome
10193	23230		0.56	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL 56.3 KD PROTEIN F5209.5 IN CHROMOSOME III
10543	23578	37187	4.09	3.1E+00	P49365	SWISSPROT	DEOXYTHYMPINE SYNTHASE (DHS)
11751	23937		2.45	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11771	24763		2.49	3.1E+00	S56860.1	NT	retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]
13019	25670		1.17	3.1E+00	U77668.1	NT	Brassica rapa pollen coat protein homolog (BAN103) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
2899	16078	26095	0.95	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
5454	18654	31633	1.29	3.0E+00	X53096.1	NT	S aureus genes encoding Sau861 DNA methyltransferase and Sau861 restriction endonuclease
6886	19844	33234	0.82	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6886	19844	33235	0.82	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7306	20388		11.21	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (SCH61)
7346	20426		0.7	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
9108	22187		1.62	3.0E+00	X67838.1	NT	B. rapus DNA for myosinase
10501	23536	37146	0.56	3.0E+00	Q58605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
11259	24328	37967	4.96	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GCF)
11259	24328						RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GCF)
11259	24328	37968	4.96	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GCF)
11885	24873	38570	1.37	3.0E+00	P34194	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
2067	15208	28324	2.69	2.9E+00	AE002225.2	NT	Chlamydia pneumoniae AR38, section 53 of 94 of the complete genome
7049	20102	33519	1.65	2.9E+00	Z38879.1	NT	F. pringlei gdcSP4 gene for P. protein of the glycine cleavage system
7360	20439	33899	4.66	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7360	20439	33900	4.66	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7614	20684	34160	6.19	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
8052	21135	34655	0.57	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8052	21135	34656	0.57	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8289	21371	34892	0.81	2.9E+00	BF344171.1	EST_HUMAN	NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
9438	22512		0.82	2.9E+00	AJ002153.2	NT	602017413F1 NCJ_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4153059 5'
1486	14639	27722	4.77	2.9E+00	AF186398.1	NT	Sagittaria ocellus gene for seminal vesicle secreted protein semenogelin I
1662	14814		3.14	2.9E+00	AL161552.2	NT	Buxus harlandi malvase K (malK) gene, partial cds; chloroplast gene for chloroplast product
7460	20535	34010	5.05	2.9E+00	8393724	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
9813	22853		0.9	2.9E+00	BE665182.1	EST_HUMAN	Mus musculus endomucin (LOC53423), mRNA
10028	20535	34010	1.53	2.9E+00	8393724	NT	601342759F1 NII_L_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
240	13462	26490	13.96	2.7E+00	6679306	NT	Mus musculus endomucin (LOC53423), mRNA
240	13462	26491	13.96	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phw3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5689	18663	32148	1.41	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kingle IV gene, exons 1 and 2
8339	21420		0.74	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
9168	22246		2.16	2.7E+00	AL116459.1	NT	Batrachoseps chirensis strain T4 cDNA library under conditions of nitrogen deprivation
9832	21075	34587	0.61	2.7E+00	AW088191.1	EST_HUMAN	xx88e12.x1 NCI CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:M17733
10718	23751		1.94	2.7E+00	BE083527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4796	17931	30817	5.51	2.6E+00	AF088749.1	NT	CMC-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
5665	18659	32143	2.04	2.6E+00	675560.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5665	18659	32144	2.04	2.6E+00	675560.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5947	19133		2.55	2.6E+00	Y17062.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7727	26220		1.16	2.6E+00	AJ224839.1	NT	Mycobacterium fortuitum furA II gene
7879	20931		11.26	2.6E+00	AF235502.1	NT	Homo sapiens Surf-5 and Surf-6 genes
8249	21331	34847	1.17	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
8249	21331	34848	1.17	2.6E+00	AJ132180.1	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
9658	22698	36481	2.85	2.6E+00	AL161540.2	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
10563	23598		1.91	2.6E+00	9055193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
11281	24347	37984	2.2	2.6E+00	AF143675.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12917	26064		3.3	2.6E+00	11419220	NT	Hemivirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1492	14645	27726	3.03	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1492	14645	27727	3.03	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5934	19120	32431	2.24	2.5E+00	P13485	SWISSPROT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5934	19120	32432	2.24	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6868	19120	32431	1.42	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6868	19120	32432	1.42	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6868	20020	33429	0.77	2.5E+00	D30052.1	NT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
7836	20986	34494	1.19	2.5E+00	AW949198.1	EST_HUMAN	Vibrio cholerae ctxA gene and ctxB gene for cholera toxins, complete cds
7985	21034	34547	0.62	2.5E+00	4502902	NT	QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA
9304	22380	35931	1.55	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
10057	23095	36897	0.71	2.5E+00	BE287758.1	EST_HUMAN	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA
11832	24821		1.39	2.5E+00	P40170	SWISSPROT	Rice DNA for aldolase C-1, complete cds
12216	25167		1.85	2.5E+00	AF289685.1	NT	60117579P1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531080 5'
3078	18254	29276	0.89	2.4E+00	M24282.1	NT	DNAJ PROTEIN
5027	18156	31134	4.93	2.4E+00	4503352	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
						NT	Chicken alpha-3 collagen type VI mRNA, 3' end
						NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA

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6134	10313	32652	4.09	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7538	20811	34085	0.71	2.4E+00	BF687502.1	EST_HUMAN	602120856F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4278012 5'
7538	20811	34086	0.71	2.4E+00	BF687502.1	EST_HUMAN	602120856F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4278012 5'
8334	21416	34941	2.06	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8334	21416	34942	2.06	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8406	21487		2.8	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8852	21631		1.72	2.4E+00	AW876126.1	EST_HUMAN	RC2-PT0004.031289.011-d05 PT0004 Homo sapiens cDNA
9028	22107	35848	8.99	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
10244	23279	36874	2.26	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10244	23279	36875	2.26	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10313	23348	36854	2.31	2.4E+00	X92911.1	NT	H. sapiens CTGF gene and promoter region
10449	23484		7.28	2.4E+00	P09099	SWISSPROT	XYLOSE KINASE (XYLULOXINASE)
10528	23563	37169	1.64	2.4E+00	BE326702.1	EST_HUMAN	h6306.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10528	23563	37170	1.64	2.4E+00	BE326702.1	EST_HUMAN	h6306.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10818	23851	37474	1.06	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN N1RQ
11335	24398	38047	1.36	2.4E+00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: qbpPKD operon and downstream
11640	24720	38413	2.44	2.4E+00	AF158652.2	NT	Fraxia x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1282	14438	27507	9.98	2.3E+00	Z46724.1	NT	G.domesticus artificial single chain antibody gene (L3)
4237	17383		1.41	2.3E+00	AJ401081.1	NT	Bos taurus peritubal cytb gene for cytochrome b
5957	19143		0.91	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYCARBOXYPEPTIDASE
7612	20882	34158	2.76	2.3E+00	6978554	NT	Rattus norvegicus A1Pass, Cat+ transporting, ubiquitous (Atp2a3), mRNA
7771	26221		2.37	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
7988	21008	34518	1.28	2.3E+00	X60265.1	NT	M.mazai drak and drak genes homologues coding for Drak and DnaJ
9310	22386	35938	0.52	2.3E+00	5835317	NT	Polyporus ornatinus mitochondrion, complete genome
9371	22446	36008	1.66	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)
11041	24120	37753	2.72	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
12075	25056	38763	2.14	2.3E+00	BF641987.1	EST_HUMAN	602089121F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4088173 5'
12075	25056	38764	2.14	2.3E+00	BF641987.1	EST_HUMAN	602089121F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4088173 5'
12445	25315	32091	7.41	2.3E+00	BE895237.1	EST_HUMAN	601433673F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3918843 5'
4126	17280	30276	1.08	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4432	17572	30553	4.12	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)

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4432	17572	30554	4.12	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5458	18658	31636	11.22	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5458	18658	31637	11.22	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5575	19160	32478	1.93	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
5575	19160	32479	1.93	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
6187	19363	32711	9.39	2.2E+00	BE250383.1	EST_HUMAN	600343040111 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
6484	19651	33013	2.87	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6730	19886	33278	3.14	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7097	18524		3.4	2.2E+00	AA594574.1	EST_HUMAN	nt5602.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3'
7470	20545	34017	0.83	2.2E+00	AA137027.1	EST_HUMAN	zn19104.11 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:566143 5'
7783	20839	34332	11.91	2.2E+00	AA448012.1	EST_HUMAN	z05g10.1 Soares, total, fetus, Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785634 5'
7866	20920	34427	0.66	2.2E+00	P54918	SWISSPROT	ALANINE RACEMASE
8294	21376	34896	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting complex component of (MOUSE);
8294	21376	34897	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting complex component of (MOUSE);
9542	22607		12.49	2.2E+00	BE741878.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948861 5'
9768	25860		2.12	2.2E+00	Q04705	SWISSPROT	TRANSPOSIN TY1 PROTEIN A
10259	23294	36690	1.12	2.2E+00	A1290373.1	EST_HUMAN	qm69b03.x1 Soares, placenta, 8to9weeks_2NBHP8to9w Homo sapiens cDNA clone IMAGE:1893985 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10259	23294	36691	1.12	2.2E+00	A1290373.1	EST_HUMAN	qm69b03.x1 Soares, placenta, 8to9weeks_2NBHP8to9w Homo sapiens cDNA clone IMAGE:1893985 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10301	23336	36941	3.04	2.2E+00	BF248782.1	EST_HUMAN	similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10673	23707	37315	2.6	2.2E+00	AF183418.1	NT	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
11726	23912	37536	3.3	2.2E+00	P07911	SWISSPROT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
11915	24902	38605	6.04	2.2E+00	P10407	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
583	16016	26795	13.2	2.1E+00	AF132812.2	NT	EARLY E1A 28 KD PROTEIN
3678	16841		1.19	2.1E+00	AW449368.1	EST_HUMAN	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
							UHH-B18-ek1-e-08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'

Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6260	19434		0.97	2.1E+00	P75357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6947	20260	33698	3.51	2.1E+00	O70159	SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7169	20302	33745	0.77	2.1E+00	4503430	NT	Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, and translated products
7191	20056	33466	5.88	2.1E+00	N29575.1	EST_HUMAN	Y08a10.s1 Scars melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654
8694	21774		2.43	2.1E+00	AU123630.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIID (HUMAN);
1223	14383	27444	1.32	2.0E+00	AF180527.1	NT	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000871 5'
1223	14383	27445	1.32	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1366	14520	27595	1.37	2.0E+00	AF204927.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1608	14759		3.09	2.0E+00	P25582	SWISSPROT	Oryctolagus cuniculus Na ⁺ -K ⁺ -ATPase beta 1 subunit mRNA, complete cds
2216	16360	28480	7.2	2.0E+00	Z78279.1	NT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2216	16360	28481	7.2	2.0E+00	Z78279.1	NT	R. norvegicus mRNA for collagen alpha1 type I
4216	17366	30353	1.71	2.0E+00	AW664496.1	EST_HUMAN	h13c05.x1 NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
4216	17366	30354	1.71	2.0E+00	AW664496.1	EST_HUMAN	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7722	20786		0.96	2.0E+00	P07586	SWISSPROT	h13c05.x1 NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
8214	21296	34815	4	2.0E+00	AB008676.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8214	21296	34816	4	2.0E+00	AB008676.1	NT	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE
8214	21296	34817	4	2.0E+00	AB008676.1	NT	GLYCOPROTEINS E1 AND E2]
9122	22201	35743	3.04	2.0E+00	F31500.1	EST_HUMAN	Escherichia coli 0157 DNA, map position at 46 min., complete cds
12615	26022	31670	6.76	2.0E+00	5834843	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
5715	18908	32202	4.28	1.9E+00	6754389	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
5715	18908	32203	4.28	1.9E+00	6754389	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6225	19400	32750	1.2	1.9E+00	BE969695.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117808
6792	19947		0.92	1.9E+00	AW845689.1	EST_HUMAN	Gallus gallus mitochondrion, complete genome
6888	20040		1.91	1.9E+00	Q63627	SWISSPROT	Mus musculus inositol 1,4,5-trisphosphate receptor 1 (ltp1), mRNA
8653	21733	35272	2.21	1.9E+00	P02467	SWISSPROT	Mus musculus inositol 1,4,5-trisphosphate receptor 1 (ltp1), mRNA
8653	21733	35273	2.21	1.9E+00	P02467	SWISSPROT	601676636F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 6'
8659	21638		3.32	1.9E+00	BF360206.1	EST_HUMAN	MRO-C10063-071089-002-g02 C10063 Homo sapiens cDNA
9095	22174		1.86	1.9E+00	O51781	SWISSPROT	CTD-BINDING SRL-LIKE PROTEIN RA4
							COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
							COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
							CM3-MT0114-010900-323-MT0114 Homo sapiens cDNA
							ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9830	22870	36452	0.63	1.8E+00	AA669125.1	EST_HUMAN	at94a04.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element; contains element L1 L1 repetitive element;
10790	23823	37447	0.67	1.8E+00	AF248269.1	NT	Homo sapiens gag-pro-poi precursor protein gene, partial cds
3162	16337	29346	1.69	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3190	16365	29370	2.15	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3190	16365	29371	2.15	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5988	18173		1.63	1.8E+00	P18602	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6230	19405	32755	2.02	1.8E+00	BF311999.1	EST_HUMAN	601987854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6528	19692		1.28	1.8E+00	BF683327.1	EST_HUMAN	602139470F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4298272 5'
6878	20031	33441	1.15	1.8E+00	BF305552.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7204	20069	33479	1.22	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
7411	20489		0.8	1.8E+00	P27127	SWISSPROT	LIPOLYSACCHARIDE 16-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE--(GLUCOSYL)LIPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE)
8308	21390	34913	0.98	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ;
8308	21390	34914	0.98	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ;
8055	22134	35678	2.28	1.8E+00	O43281	SWISSPROT	ENDONUCLEASE
9376	22451	36013	0.78	1.8E+00	R31042.1	EST_HUMAN	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9462	22519	36081	0.82	1.8E+00	AW880004.1	EST_HUMAN	y172a08.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9686	23034	36626	0.47	1.8E+00	P06828	SWISSPROT	QYD-OT0030-070300-148-ad3 OT0030 Homo sapiens cDNA
10054	23092	36694	0.94	1.8E+00	P27050	SWISSPROT	FUSION GLYCOPROTEIN PRECURSOR [CONTAINS: FUSION GLYCOPROTEIN F2; FUSION GLYCOPROTEIN F1]
10490	23525		4.71	1.8E+00	AF111849.1	NT	CHITINASE D PRECURSOR
10777	23810		0.75	1.8E+00	P44325	SWISSPROT	Homo sapiens PRO6630 mRNA, complete cds
12575	25994		4.87	1.8E+00	AF314254.1	NT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12667	25444		6.01	1.8E+00	9506404	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
13005	25987	31854	1.45	1.8E+00	BF212412.1	EST_HUMAN	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA
1132	14297	27352	1.68	1.7E+00	Q60114	SWISSPROT	601813714F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5'
2345	15476	28603	4.9	1.7E+00	AL163280.2	NT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
							Homo sapiens chromosome 21 segment HS21C080

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2445	15573	28702	1.49	1.7E+00	AI141067.1	EST_HUMAN	oz3105.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4581	17718	30701	0.98	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE)(SUCROSE 6-FRUCTOSYL TRANSFERASE)
5730	18923	32216	1.73	1.7E+00	BE063546.1	EST_HUMAN	CXMO-BT0282-171289-127-e05 BT0282 Homo sapiens cDNA
5730	18923	32217	1.73	1.7E+00	BE063546.1	EST_HUMAN	CXMO-BT0282-171289-127-e05 BT0282 Homo sapiens cDNA
6141	19319	32661	3.02	1.7E+00	Q91TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)
6682	19840	33230	0.67	1.7E+00	P36816	SWISSPROT	[PYRUVATE DEHYDROGENASE (LIPOAMIDE)-PHOSPHATASE, MITOCHONDRIAL PRECURSOR (PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDPC)]
7387	20446	33908	1.18	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMDT INTERGENIC REGION
7387	20446	33909	1.18	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMDT INTERGENIC REGION
8038	21121	34841	1.1	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
8222	21304	34825	1.08	1.7E+00	6765715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tal1), mRNA
8252	21334	34852	0.61	1.7E+00	BF530630.1	EST_HUMAN	602071917F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4214659 5'
8739	21818	35352	0.75	1.7E+00	AF245513.1	NT	Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds
8828	21907	35520	1.63	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8901	21980	35519	0.66	1.7E+00	X69063.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
8901	21980	35520	0.66	1.7E+00	X69063.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
9014	22093	35633	1.03	1.7E+00	U19832.1	NT	Rattus norvegicus SA gene, partial cds
9350	25959	35981	2.44	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9350	25959	35982	2.44	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9806	22846		1	1.7E+00	AF161390.1	NT	Homo sapiens HSPC262 mRNA, partial cds
10375	23410		0.54	1.7E+00	AW953681.1	EST_HUMAN	EST366751 MAGE resequences, MAGEC Homo sapiens cDNA
10857	23890	37509	0.47	1.7E+00	BE878280.1	EST_HUMAN	601488170F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890484 5'
10857	23890	37510	0.47	1.7E+00	BE878280.1	EST_HUMAN	601488170F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890484 5'
11896	24884	38582	1.67	1.7E+00	W22424.1	EST_HUMAN	6787 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
12523	25356	32066	1.94	1.7E+00	AI678443.1	EST_HUMAN	tu82407.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.11 MSR1 repetitive element;
2090	15230	28352	19.53	1.6E+00	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2101	15241	28362	4.14	1.6E+00	AF071374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2107	15246	28367	1.28	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
2357	15488		0.97	1.6E+00	X98373.1	NT	B. napue gene encoding endo-polygalacturonase
3026	18202	29225	1.22	1.6E+00	W59426.1	EST_HUMAN	zid25701.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D29806 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3857	17017		1.06	1.6E+00	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4142	17204		6.05	1.6E+00	BF570077.1	EST_HUMAN	602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4472	17612	30590	1.25	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4472	17612	30591	1.25	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5184	18306	31270	0.59	1.6E+00	AF127897.1	NT	Samiti bolivensis olfactory receptor (SBO27) gene, partial cds
5184	18316	31284	2.83	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5184	18316	31285	2.83	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5848	18134	32447	2.38	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class I DA-beta-2'01 gene, 3' end
6035	19218	32840	0.78	1.6E+00	AF006631.1	NT	Homo sapiens transglutaminase type I (TgaseI) gene, promoter region
6599	19759	33147	0.91	1.6E+00	BF380703.1	EST_HUMAN	IL2-UT0073-060900-145-E02 UT0073 Homo sapiens cDNA
6849	20002	33411	1.05	1.6E+00	AW294881.1	EST_HUMAN	UI-HB2-ahr-b-04-0-J1 st NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7394	20472	33638	2.37	1.6E+00	BE5697267.1	EST_HUMAN	RCO-CJ0415-200700-032-c10 C10415 Homo sapiens cDNA
8219	21301		1.3	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8574	21655	35196	3.3	1.6E+00	AJ297131.1	NT	Mus musculus SCL, MAP_17, CYP_a, SCL & CYP_b genes
9101	22180	35724	1.07	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9101	22180	35725	1.07	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9272	22348	35898	0.49	1.6E+00	BE388331.1	EST_HUMAN	601283925F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605847 5'
9659	25857	34815	1.05	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
9659	25857	34816	1.05	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
9786	22826		0.7	1.6E+00	AF043466.1	NT	Thermotoga maritima xylF gene, complete cds
9835	22974	36568	1.49	1.6E+00	T41280.1	EST_HUMAN	ph66_19/TV Outward Atp-pitmed hncDNA library Homo sapiens cDNA clone ph66_19/TV
10388	23423	37029	1.09	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-090200-100-407 LT0016 Homo sapiens cDNA
10388	23423	37030	1.09	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-090200-100-407 LT0016 Homo sapiens cDNA
10582	23587	37195	0.52	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
11010	24089	37726	1.77	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
11082	19218	32540	4.8	1.6E+00	AF005693.1	NT	Homo sapiens transglutaminase type I (TgaseI) gene, promoter region
12006	24991	38695	3.68	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
33	13271	26275	2.95	1.5E+00	U83449.1	NT	Rattus norvegicus jun dimerization protein 2 (dp-2) mRNA, complete cds
241	13463	26492	2.44	1.5E+00	AE002201.2	NT	Chlamydia pneumoniae AR39, section 32 of 84 of the complete genome
636	13821		1.81	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloprotease domain (ADAM) 15 (metagardin) (Adam15), mRNA
2481	15608	28732	1.56	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2584	15709	28828	2.02	1.5E+00	6878350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA

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3208	15608	28732	1.75	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3462	16628	29649	0.77	1.5E+00	AE001945.1	NT	Delnoccocus radiolurans R1 section 82 of 229 of the complete chromosome 1
5846	19036	32342	0.71	1.5E+00	AI655301.1	EST_HUMAN	t12710.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 000237 HKF-1;
5846	19036	32343	0.71	1.5E+00	AI655301.1	EST_HUMAN	t12710.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 000237 HKF-1;
6536	19899	33072	2.43	1.5E+00	R17879.1	EST_HUMAN	yg10e02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
7278	20361		1.68	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7311	20393	33853	16.24	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7311	20393	33854	16.24	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7500	20575	34048	0.61	1.5E+00	AA889259.1	EST_HUMAN	ak25f10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'
7768	20826	34317	0.77	1.5E+00	AI003264.1	EST_HUMAN	an07b11.s1 Streptococcus schizo brain S11 Homo sapiens cDNA clone IMAGE:1684893 3' similar to gb:S95996 SEROTRANSFERRIN PRECURSOR (HUMAN).
8313	21395	34920	0.9	1.5E+00	BE987446.1	EST_HUMAN	601509585F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8367	21448	34971	0.5	1.5E+00	AB040887.1	NT	Homo sapiens mRNA for KIAA1454 protein, partial cds
8846	21925	35463	1.09	1.5E+00	K02138.1	NT	Mouse germline IgM chain gene, mu-delta region
9218	22286		0.48	1.5E+00	AB038516.1	NT	Homo sapiens h3PIb alpha gene for platelet glycoprotein Ib alpha, complete cds
9334	22410	35963	0.61	1.5E+00	BF217818.1	EST_HUMAN	601832662F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096135 5'
9684	22733	36303	0.85	1.5E+00	R81928.1	EST_HUMAN	y03h01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147697 5'
9835	22875	36459	1.6	1.5E+00	AW375697.1	EST_HUMAN	QV3-CT0192-261098-008-d09 CT0192 Homo sapiens cDNA
10064	23102	36705	6.49	1.5E+00	BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
10258	23283		1.85	1.5E+00	BF37944.1	EST_HUMAN	60203577F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183865 5'
10399	23434	37040	2.26	1.5E+00	AA017689.1	EST_HUMAN	ze38g08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
10399	23434	37041	2.26	1.5E+00	AA017689.1	EST_HUMAN	ze38g08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
11684	24683	38373	3.4	1.5E+00	AL134197.1	EST_HUMAN	DKFZp647P243.s1 547 (synonym: hfbt) Homo sapiens cDNA clone DKFZp647P243 3'
11834	24823		7.68	1.5E+00	X07380.1	NT	Maize mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene
11929	24915	38617	1.39	1.5E+00	AI400798.1	EST_HUMAN	ig94409.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2118433 3'
11929	24915	38618	1.39	1.5E+00	AI400798.1	EST_HUMAN	ig94409.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2118433 3'
12615	26095	31662	1.61	1.5E+00	D63490.1	NT	Human mRNA for KIAA0146 gene, partial cds
12765	25508		3.92	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
12888	25599		2.17	1.5E+00	6978492	NT	Rattus norvegicus 5 - Lipoxigenase (Alox5), mRNA
13220	25794	31888	1.31	1.5E+00	BF229835.1	EST_HUMAN	7q28b06.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'
30	13288	26271	2.27	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
30	13288	26272	2.27	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2351	15482		0.97	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds
2411	15541		9.39	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2734	15851	28964	1.7	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2833	15947	29055	3.22	1.4E+00	AF064584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2833	15947	29056	3.22	1.4E+00	AF064584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3414	16563		0.79	1.4E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4370	17513	30493	1.13	1.4E+00	AW900455.1	EST_HUMAN	CMO-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA
4370	17513	30494	1.13	1.4E+00	AW900455.1	EST_HUMAN	CMO-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA
4708	17843		1.51	1.4E+00	BF681547.1	EST_HUMAN	602156687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
5317	18434		0.94	1.4E+00	Q07869	SWISSPROT	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)
5488	18887	31705	1.73	1.4E+00	AW054976.1	EST_HUMAN	wt45g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5645	18839		6.04	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6409	19578	32939	3.07	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6424	28214		3.93	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6542	19705	33078	2.8	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6542	19705	33079	2.8	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6961	20189	33614	0.8	1.4E+00	AW88057.1	EST_HUMAN	CM3-NN0006-300300-132-bt12 NN0006 Homo sapiens cDNA
7438	20515	33988	1.99	1.4E+00	AJ133269.1	NT	Homo sapiens cavedin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7464	20531	34006	1.14	1.4E+00	AW467760.1	EST_HUMAN	he23f05.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918873 3' similar to contains Alu repetitive element;
7514	20588	34062	0.7	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7514	20588	34063	0.7	1.4E+00	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
8530	21611		0.72	1.4E+00	P07693	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8994	22073		5.4	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9295	22371	35920	1.65	1.4E+00	R20459.1	EST_HUMAN	y933f12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
9398	22472	36038	3.83	1.4E+00	BE064687.1	EST_HUMAN	RC1-BT0313-301299-012-05 BT0313 Homo sapiens cDNA
9432	22506	36072	0.65	1.4E+00	AF134844.1	NT	Sceloporus undulatus ornithine transcarbonylase (OTC) mRNA, complete cds
10412	23447	37052	0.88	1.4E+00	BF575545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10457	23492	37102	0.88	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10457	23492	37103	0.88	1.4E+00	BE145374.1	EST_HUMAN	IL6-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10744	23777	37390	0.96	1.4E+00	D63441.1	NT	Pandorina colimariensis chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10744	23777	37391	0.96	1.4E+00	D63441.1	NT	Pandorina colimariensis chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10852	23885	37504	1.15	1.4E+00	Q07283	SWISSPROT	TRICHOHYALIN
11459	24857	38232	4.52	1.4E+00	AB006982.1	NT	Homo sapiens APECD mRNA for AIRE-1, complete cds
11691	24889	38379	3.46	1.4E+00	BE962107.2	EST_HUMAN	80185184R1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3845805 3'
11691	24889	38380	3.46	1.4E+00	BE962107.2	EST_HUMAN	801655184R1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3845805 3'
11711	24751	38444	2.3	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11711	24751	38445	2.3	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12359	26012		2.01	1.4E+00	AL101500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12785	26204		2.89	1.4E+00	11545336	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen sa70-2 (SE70-2), mRNA
694	13776		1.96	1.3E+00	Z73840.1	NT	M. musculo gene encoding 4-Dihydroxyethyl-trisporate dehydrogenase
925	14100	27164	2.79	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 26S rRNA gene, isolate Tibet
1153	14317		23.81	1.3E+00	Y19213.1	NT	Homo sapiens putative psfHbA pseudogene for hair keratin, exons 2 to 7
1325	14482	27549	14.36	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1325	14482	27550	14.36	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1387	14542		0.98	1.3E+00	U61730.2	NT	Gdx lacryme-jobi dihydrodipicolinate synthase (dipa) gene, complete cds
1641	14783		2.35	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2316	15448		2.38	1.3E+00	AB030447.1	NT	Cypripus carpio MRPb and MASPb genes for mannosyl-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2615	15739		1.81	1.3E+00	BE966735.2	EST_HUMAN	801651233R1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3915845 3'
3005	16180	29201	0.86	1.3E+00	67555921	NT	Mus musculus alpha-spectrin 1, erythrocyte (Spm1), mRNA
3686	16849	29857	1.14	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P65), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c2
5631	18825	31900	1	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
5827	19017	32322	0.58	1.3E+00	M27138.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
6142	19320	32662	7.56	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-408 CT0289 Homo sapiens cDNA
6142	19320	32663	7.56	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-408 CT0289 Homo sapiens cDNA
6547	19709	33085	1.14	1.3E+00	M33496.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6890	20042		0.71	1.3E+00	Q00156	SWISSPROT	HYPOTHEICAL GENE 84 PROTEIN
6928	20243		0.58	1.3E+00	P49940	SWISSPROT	SPORE GERMINATION PROTEIN KB
6978	20206	33634	1.04	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7092	20186	33610	1.16	1.3E+00	BE538819.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447065 5'
7249	20332	33779	0.96	1.3E+00	BE243571.1	EST_HUMAN	TCBAP1D0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0959
7616	20886	34162	0.78	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8494	21575	35112	1.78	1.3E+00	AJ009912.1	NT	Sus scrofa plp gene
8642	21722	35259	2.28	1.3E+00	BE963379.2	EST_HUMAN	601687145R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866195 3'
8758	21837	35378	1.05	1.3E+00	BE974290.1	EST_HUMAN	601680260R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8907	21988		1.87	1.3E+00	8910247	NT	Homo sapiens GL004 protein (GL004), mRNA
8990	22069	35609	0.89	1.3E+00	A1927629.1	EST_HUMAN	6065607.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9347	22423	35976	0.61	1.3E+00	H42881.1	EST_HUMAN	y086003.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:183076 3'
9347	22423	35977	0.51	1.3E+00	H42881.1	EST_HUMAN	y086003.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:183076 3'
9715	22780		5.02	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylaseN-sulfotransferase-2 gene, complete cds
9724	22789	36359	2.47	1.3E+00	X72019.1	NT	S.alba phi-1 mRNA for photolyase
9724	22789	36360	2.47	1.3E+00	X72019.1	NT	S.alba phi-1 mRNA for photolyase
9823	22863	36444	1.21	1.3E+00	AF059250.1	NT	Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds
9847	22887		0.47	1.3E+00	AW024390.1	EST_HUMAN	6030303.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2628477 3' similar to gb:M31522 TRANSCRIPTION FACTOR ITF-1 (HUMAN);
9871	22911	36496		1.65	000754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
9952	22991	36584	1.21	1.3E+00	A1927629.1	EST_HUMAN	6065607.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
10031	23069	36668	0.68	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-Invt1 chromosomal inversion junction DNA
10031	23069	36669	0.68	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-Invt1 chromosomal inversion junction DNA
10070	23108	36711	3.93	1.3E+00	BE963379.2	EST_HUMAN	601687145R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866195 3'
10130	23168		0.57	1.3E+00	A1559944.1	EST_HUMAN	6077a12.x1 NCI_CGAP_UJI Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);
10353	23388	36966	0.5	1.3E+00	AF061251.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10353	23388	36967	0.5	1.3E+00	AF061251.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10418	23453	37059	1.68	1.3E+00	AE004392.1	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
10435	23470	37076	1.59	1.3E+00	M29953.1	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10811	23844		0.99	1.3E+00	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10838	23871	37493	0.47	1.3E+00	A1960946.1	EST_HUMAN	6032e10.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2498822 3' similar to SW:TRXB_HUMAN Q16881 THIOREDOXIN REDUCTASE;
10851	23884		0.53	1.3E+00	8923637	NT	Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10854	23887	37506	0.46	1.3E+00	7949159	NT	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10854	23887	37507	0.46	1.3E+00	7949159	NT	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10861	23894	37515	0.45	1.3E+00	H42881.1	EST_HUMAN	yo68c03.s1 Soares breast 3Nbt-Hbt Homo sapiens cDNA clone IMAGE:183076 3'
10861	23894	37516	0.45	1.3E+00	H42881.1	EST_HUMAN	yo68c03.s1 Soares breast 3Nbt-Hbt Homo sapiens cDNA clone IMAGE:183076 3'
10832	24014		4.05	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
11145	24217	37844	2.4	1.3E+00	P26299	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
11169	24240	37872	1.77	1.3E+00	Z18892.2	NT	Mus musculus desmin gene
11619	24670		1.43	1.3E+00	AW274701.1	EST_HUMAN	xp08c03.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2738668 3'
11831	24820	38511	2.73	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11823	24908	38610	2.28	1.3E+00	Z96682.1	NT	Bacillus subtilis genomic DNA 23.9kb fragment
11994	24979		1.35	1.3E+00	L31891.1	NT	Arabidopsis thaliana 3-ketoacyl-acyl carrier protein synthase III (KAS III) mRNA, complete cds
12604	25347		3.81	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12698	25465	32022	2.76	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158452 5'
12707	25899		1.98	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12822	25549		1.53	1.3E+00	AF187035.1	NT	Sturnira illium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
13200	25783		1.34	1.3E+00	U38978.1	NT	Naphthalenesulfonate-degrading bacterium BN6 2,3-dihydroxybiphenyl dioxygenase (bphCII) gene, complete cds
13231	25981		1.63	1.3E+00	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
667	13853	26881	8.73	1.2E+00	AA676246.1	EST_HUMAN	z122d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
846	14024	27082	1.52	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-II)
846	14024	27083	1.52	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
846	14024	27084	1.52	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
901	14076		1.21	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1187	14349	27407	7.6	1.2E+00	AF080245.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1232	14391	27453	1.71	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1232	14391	27454	1.71	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2066	15207	28323	1.02	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3179	16354	28359	1.06	1.2E+00	AB020881.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3234	16408	28421	7.01	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3234	16408	28422	7.01	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3358	16530		3.57	1.2E+00	AF54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3437	16605	28625	0.61	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3804	16964	28687	9.16	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4094	17249	30254	1.87	1.2E+00	BF373570.1	EST_HUMAN	MRO-FT0175-0509800-203-g06_1 FT0175 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4413	16605	28625	1.08	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4504	17731		1.91	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4945	17781	30763	0.94	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4882	17817	30803	2.03	1.2E+00	AF158495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4712	17847		6.6	1.2E+00	Y09200.1	NT	T. plinatum chloroplast rbcL gene, partial
5554	18751	31788	1.13	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5672	18866	32152	2.34	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
5917	19105		0.65	1.2E+00	X81879.1	NT	Calicivirus cDNA for orf1, orf2 and orf3
5995	19180	32502	0.77	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6280	19454	32802	2.45	1.2E+00	X74885.1	NT	D.hyd av1 repeat cluster DNA, fragment D
6342	19512	32869	3.81	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA
6420	19589	32953	1.28	1.2E+00	X80084.1	NT	C. glutamicum pta gene and ackA gene
6420	19589	32854	1.28	1.2E+00	X89084.1	NT	C. glutamicum pta gene and ackA gene
6463	19630	32991	36.06	1.2E+00	AA759254.1	EST_HUMAN	af84g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374.3'
							y93b12.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273599 3' similar to
6566	19728	33105	0.73	1.2E+00	N33295.1	EST_HUMAN	gbIM87935JHUMAAU472 Human carcinoma cell-derived Alu RNA transcript (RNA), gb.J04970
6630	19760	33178	0.62	1.2E+00	P17671	SWISSPROT	ECDYSONE-INDUCIBLE PROTEIN E75-A
6634	19763	33182	1.94	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
7055	20108	33524	1.72	1.2E+00	AB029010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7067	20120	33534	2.81	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
							zc3805.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632001 5' similar to
7180	20312	33755	0.68	1.2E+00	AA167810.1	EST_HUMAN	gbD10522 Human mRNA for 80K-L protein, complete cds (HUMAN);
7403	20481		0.71	1.2E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
7542	25847	34092	1.85	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cda Homo sapiens cDNA clone cdaAFH03 5'
7828	20883	34385	2.91	1.2E+00	X74207.1	NT	L. lactis pyrD and pyrF genes
7997	21047	34560	0.6	1.2E+00	BE787948.1	EST_HUMAN	601481761F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3894270 5'
8767	21846	35387	3.19	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
							ALPHA-ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-GLUCOSEPHOSPHATE
							(TREHALOSE-6-PHOSPHATE SYNTHASE)
8863	21942	35477	0.82	1.2E+00	P38427	SWISSPROT	GLUCOSYLTRANSFERASE
9077	22156		0.7	1.2E+00	7708271	NT	Homo sapiens CGI-30 protein (LOC51611), mRNA
9226	22304	35847	1.81	1.2E+00	AW377210.1	EST_HUMAN	MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA
9440	22514	36078	0.51	1.2E+00	H48599.1	EST_HUMAN	y980a06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202066 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8598	22653	36224	3.79	1.2E+00	Z32850.1	NT	R. communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
8805	22845	36423	2.13	1.2E+00	D11745.1	EST_HUMAN	HJMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
10135	23173	36771	3.6	1.2E+00	X56832.1	NT	H. sapiens ENO3 gene for muscle specific enolase
10332	23567		0.82	1.2E+00	AB009668.1	NT	Homo sapiens kidney gene, exon 1
11432	24493	38158	1.69	1.2E+00	M38686.1	NT	Mus musculus Id gene, exon 1
11627	24707	38400	1.51	1.2E+00	AW817817.1	EST_HUMAN	PMO-ST0264-161199-001-d01 ST0264 Homo sapiens cDNA
11666	24743		7.69	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11744	23930	37556	3.13	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12101	25081	38788	1.68	1.2E+00	M10408.1	NT	Maize mitochondrial F.O.-ATPase proteolipid (subunit 9) gene
12471	25984	31768	17.76	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12491	25339		1.74	1.2E+00	AP001515.1	NT	Bacillus halodurans genomic DNA, section 9/14
13218	25793		2.66	1.2E+00	AA077909.1	EST_HUMAN	7H11A06 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H11A06
476	13671	26703	1.11	1.1E+00	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1802	14951	28045	1.23	1.1E+00	AW965393.1	EST_HUMAN	QVO-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1948	15091	28192	1.21	1.1E+00	AW575899.1	EST_HUMAN	UI-HF-BR0p-ajk-f-02-0-UI.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'
2017	15157		2.74	1.1E+00	AF137273.1	NT	Gallus gallus alpha 1 (V) collagen mRNA, complete cds
3409	16579	29594	8.86	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3409	16579	29595	8.86	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3575	16740	29757	1.02	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3670	16833	29844	0.99	1.1E+00	AI803360.1	EST_HUMAN	w54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW_P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3812	16972	29974	1.16	1.1E+00	AE003886.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3812	16972	29976	1.16	1.1E+00	AE003886.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3920	17079		0.92	1.1E+00	X85374.1	NT	H. parahemolyticus hphIM(A), hphIM(C), hphIR and menB genes
4054	17210	30220	1.03	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4130	17283	30278	0.72	1.1E+00	6755205	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pamb7), mRNA
4331	17474		6.82	1.1E+00	5635331	NT	R. unicomis complete mitochondrial genome
5107	18235	31204	3.45	1.1E+00	U18466.1	NT	African swine fever virus, complete genome
5180	18302	31265	2.06	1.1E+00	X78425.1	NT	E. faecalis ppp5 gene
5422	18623	31599	1.49	1.1E+00	6878530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5731	18924	32218	14.33	1.1E+00	BE960184.1	EST_HUMAN	60165276R1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:3825835 3'
5750	18942	32243	1.32	1.1E+00	AI138582.1	EST_HUMAN	q885c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736280 3'
6217	19392	32740	0.9	1.1E+00	11419739	NT	Homo sapiens solute carrier family 9 (neurotransmitter transporter), member 14 (SLC6A14), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6404	19573	32935	0.59	1.1E+00	AF197851.1	NT	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6637	19700	33073	0.72	1.1E+00	R06037.1	EST_HUMAN	ye8603.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:124924 5'
6856	20009	33419	0.78	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 58 (EP68 gene)
7447	20524	33997	0.58	1.1E+00	X65981.1	NT	Maize mRNA for endase (2-phospho-D-glycerate hydrolase)
7632	20701	34179	0.67	1.1E+00	BF68374.1	EST_HUMAN	602139978F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301322 5'
7659	20726	34201	2.23	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7659	20726	34202	2.23	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7680	20745	34226	8.35	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7754	25853	34305	1.04	1.1E+00	11967960	NT	Mus musculus silent mating type information regulation 2, (S.cerevisiae, homolog)-like (Sir2), mRNA
8325	21407	34934	3.2	1.1E+00	BF693966.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246928 5'
8416	21497	35029	0.91	1.1E+00	AM78339.1	EST_HUMAN	hm39h11.x1.NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160549 3'
8935	22014	35554	0.86	1.1E+00	AB003088.1	NT	Acetabularia caliculus mitochondrial COX-like gene
9015	22094	35634	0.87	1.1E+00	S80750.1	NT	VH-anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial: 376 nt]
9126	22205	35748	0.53	1.1E+00	AI079946.1	EST_HUMAN	oz34f06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 3'
9637	21080	36348	0.75	1.1E+00	BE384876.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9828	22868	36450	0.51	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)
9883	22823		0.81	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9974	23013	36607	1.03	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
10038	23076	36676	1.85	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
10141	23179	36777	4.09	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10202	23239	36829	20.74	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10719	23752	37358	1.21	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10831	23864	37486	0.56	1.1E+00	AI878921.1	EST_HUMAN	au51c11.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2618292 5' similar to gb:D10522
10886	23970	37600	1.97	1.1E+00	11067364	NT	Human mRNA for 80K-L protein, complete cds. (HUMAN); Homo sapiens KIAA0625 gene product (KIAA0626), mRNA
10947	24029		3.14	1.1E+00	AF088942.1	NT	Klebsiella pneumoniae cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11343	24408	38055	3.72	1.1E+00	L16877.1	NT	Homo sapiens cytochrome P450209 (CYP209) gene, 5' flank and exon 1
11361	18489		2.74	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11368	24427	38083	2.93	1.1E+00	AF012852.1	NT	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11369	24427	38084	2.93	1.1E+00	AF012852.1	NT	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11637	24717	38409	3.99	1.1E+00	AI809699.1	EST_HUMAN	w77611.1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
11870	24858	38552	1.38	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
11870	24858	38553	1.38	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
12441	25312	32070	1.82	1.1E+00	P07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12547	25371	32070	3.56	1.1E+00	AF216698.1	NT	Taenia solium immunogenic protein T676 mRNA, partial cds
12689	25680		1.86	1.1E+00	AF224169.1	NT	Dictyostellum discoideum isopentenyl pyrophosphate isomerase (Dipi) mRNA, complete cds
101	13337		1.84	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
116	13347	26374	2.1	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
431	13626		-2.78	1.0E+00	AB021694.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
590	13781	26800	1.44	1.0E+00	AL251650.1	NT	Girardin tigrina mRNA for homeodomain transcription factor (so gene)
694	13877	26910	7.14	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
696	13879		2.29	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1417	16037		1.35	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1795	14944	28037	1.33	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2554	15679	28803	1.11	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2554	15679	28804	1.11	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2621	15744		0.95	1.0E+00	AA628453.1	EST_HUMAN	af26g08.s1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP: C42D8.3 CE04204 ; contains element MER22 MER22 repetitive element ;
2940	16117	29129	4.51	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1)(SR TYPE 1)
2940	16117	29130	4.51	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1)(SR TYPE 1)
3032	16208		0.95	1.0E+00	O14226	SWISSPROT	HYPOPHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME I
3289	16443	29463	1.16	1.0E+00	AA628453.1	EST_HUMAN	af26g08.s1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP: C42D8.3 CE04204 ; contains element MER22 MER22 repetitive element ;
3459	16626		0.73	1.0E+00	AF222781.1	NT	Rattus norvegicus neuromedin U precursor (NmU) gene, exons 5 and 6
3688	13337		0.75	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3772	16933	29939	1.61	1.0E+00	AJ223816.1	NT	Agaricus bisporus mRNA for tyrosinase

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4180	17330	30322	1.12	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4390	17333		0.72	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5396	18598	31568	2.3	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cyclin proteinase
5971	19157	32472	4.38	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5971	19157	32473	4.38	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6077	19259	32588	1.74	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
6241	19415	32763	4.85	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
6248	19422	32768	1.67	1.0E+00	AW452782.1	EST_HUMAN	UI-H-B13-ab-d-09-0-UI.s1 NCI CGAP Sub55 Homo sapiens cDNA clone IMAGE:3068969 3'
6618	19778	33167	2.04	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6671	19830	33219	0.83	1.0E+00	AF104690.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
6787	19923		1.07	1.0E+00	P46508	SWISSPROT	SRB-11 PROTEIN
6796	19950	33349	0.82	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6796	19950	33350	0.82	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6916	20231	33664	1.27	1.0E+00	Y11204.1	NT	V. carteri gene encoding veloxopsin
7288	20371	33826	1.15	1.0E+00	S52770.1	NT	Insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7647	20716		9.68	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7889	20941	34447	1.51	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7903	20955	34482	6.02	1.0E+00	AA775191.1	EST_HUMAN	ac79008.s1 Sitratogene lung (#937270) Homo sapiens cDNA clone IMAGE:868791 3'
8019	21070		0.72	1.0E+00	BF679213.1	EST_HUMAN	602163792F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294727 5'
8148	21230	34749	1.65	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8148	21230	34750	1.65	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8335	18495		1.48	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8545	21626	35163	2.59	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
8545	21626	35164	2.59	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8672	21752		1.07	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8708	21788	35321	0.54	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBPM)
8708	21788	35322	0.54	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBPM)
8735	26858		1.82	1.0E+00	BE147331.1	EST_HUMAN	RC1-H10229-181089-011-606 HT0229 Homo sapiens cDNA
8776	21856	35397	1.15	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes. >
8922	22001	35540	1.8	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33.
9471	22828	36091	1.95	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
9682	22731	36301	1.62	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9682	22731	36302	1.62	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9810	22850	36429	1.81	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GKC Homo sapiens cDNA clone GKCCYA11 5'
9815	22855	36434	1.32	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
9816	22856	36435	1.32	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
10318	23353	36981	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10318	23353	36982	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10408	23443	37050	0.69	1.0E+00	A077920.1	EST_HUMAN	oy15607.s1 Soares_senescent_fibroblasts_NH9F Homo sapiens cDNA clone IMAGE:1685901 3'
10633	23568	37175	3.99	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAW04 5'
10694	23727	37333	19.71	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428908 5'
10694	23727	37334	19.71	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428908 5'
10728	23761	37368	1.22	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
11216	24285	37924	1.37	1.0E+00	S90825.1	NT	PBR1=proline-rich protein (linton 3) [human, Genomic, 888 nt]
11342	24405	38064	1.46	1.0E+00	AA701494.1	EST_HUMAN	zh63b11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435453 3' similar to contains Alu repetitive element; contains element MER38 repetitive element;
11925	24814		1.62	1.0E+00	L47613.1	NT	Picea glauca EMB13 mRNA
12329	25238		5.49	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12676	25451		2.67	1.0E+00	AW876184.1	EST_HUMAN	EST388293 IMAGE sequences, MAGN Homo sapiens cDNA
3693	16855		1.04	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
6752	18944	32246	8.8	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5990	19175	32498	0.83	9.8E-01	Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9461	22518		1.68	9.8E-01	U65667.1	NT	Lycopodium esculentum putative Mt1 copy 1 nematode-resistance gene
9755	22693		2.14	9.8E-01	Q28942	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
536	13729	26763	1.17	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYL-GLUTAMATE SYNTHASE) (AGS) (NAGS)
2370	15501		1.26	9.8E-01	AJ003108.1	NT	Callitrix jacchus UBE1 gene derived retroposon on the Y chromosome
2862	15976		1.29	9.8E-01	AF174644.1	NT	Xenopus laevis rec GTPase mRNA, complete cds
3903	17062	30061	0.67	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3903	17062	30062	0.67	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
7349	20429	33890	4.42	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7349	20429	33891	4.42	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7923	20878	34378	1.14	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3680049 5'
8916	21995	35534	0.94	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3680049 5'
10653	23687		1.02	9.8E-01	AA825565.1	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
11242	24311	37948	1.84	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:1371847 3'
11242	24311	37949	1.84	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
12554	25377		2.43	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7309	20391	33851	2.73	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8701	21781	36314	1.9	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8707	21787	36320	1.54	9.7E-01	M80544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
9039	22118	35861	0.73	9.7E-01	BE799822.1	EST_HUMAN	601592165F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945904 5'
11444	24505		3.56	9.7E-01	BF511209.1	EST_HUMAN	UJH-B14-acc-e-07-0-JL.s1 NC1_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
13208	25789		3.17	9.7E-01	AL114281.1	NT	Bacillus cinereus strain T4 cDNA library under conditions of nitrogen deprivation
4568	17696	30675	0.74	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4588	17696	30678	0.74	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4580	17717	30700	1.28	9.6E-01	AF197925.1	EST_HUMAN	PM2-UM0053-240300-005-F12 UM0053 Homo sapiens cDNA
5872	19062	32369	3.51	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
5872	19062	32370	3.51	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
6866	20038	33447	0.6	9.6E-01	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7512	20586	34059	0.63	9.6E-01	AF197881.1	NT	Helix lucorum presenilin (PS) mRNA, complete cds
8586	21867	28794	1.52	9.6E-01	X95275.1	NT	P. falciparum complete gene map of plastid-like DNA (IR-A)
9092	22131	35875	0.92	9.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rps27 gene, complete cds
11346	24408	38060	1.42	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds
11808	24798	38498	3.91	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11808	24798	38497	3.91	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
12225	25174		1.31	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12915	26061	31656	1.68	9.6E-01	U91423.1	NT	Spizomya liburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2545	15870	28794	1.61	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
3882	17041	30038	2.1	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3882	17041	30039	2.1	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
9202	22280	35819	0.71	9.5E-01	A1190162.1	EST_HUMAN	q457407.x1 Sceres testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9306	22382	35833	1.04	9.5E-01	AW881102.1	EST_HUMAN	RC1-CT0295-241199-011-b02 C10295 Homo sapiens cDNA
11520	24578	38254	1.56	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
11737	23923	37548	1.57	9.5E-01	AW293799.1	EST_HUMAN	UI-H-B12-ahp-403-0-JL.s1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3271	16445		5.72	9.4E-01	AF165990.1	NT	Baronella clarridgeae RNA polymerase beta subunit (rpoB) gene, partial cds
3289	18463		2.17	9.4E-01	AF080595.1	NT	Pimphella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
9066	22145	35692	0.79	9.4E-01	M90724.1	NT	Human Fo-gamma-receptor IIA (FCGR2A) gene, exon 4
12496	25343		1.86	9.4E-01	BE781251.1	EST_HUMAN	601466703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869629 5'
12814	25975		1.4	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1769	14918		1.24	9.3E-01	AF242382.1	NT	Homo sapiens phytoacyl-CoA hydroxylase (PHYH) gene, exon 5
2699	15818	28834	3.62	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4146	17298	30289	0.86	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4146	17298	30290	0.86	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
6709	18902	32197	1.6	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5795	18986	32289	3.48	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
7486	20561		1.08	9.3E-01	AF270846.1	NT	Plasmodium falciparum mature parasite-infected erythrocyte surface antigen (MESA) gene, complete cds
8257	21339	34856	1.99	9.3E-01	AA847040.1	EST_HUMAN	oe09003.s1 NCL CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357
9013	22092		1.1	9.3E-01	AF061851.1	NT	Xenopus laevis CCGH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
9137	22216	35760	0.89	9.3E-01	AL181634.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13039	25883	31981	2.09	9.3E-01	11440298	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA
13049	25888		1.22	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
3311	16484	29505	3.92	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3916184 3'
4989	18128		0.61	9.2E-01	BF129973.1	EST_HUMAN	601817814F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4041363 5'
5835	19025		1.58	9.2E-01	7105410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
6109	19289	32624	4.97	9.2E-01	BF037586.1	EST_HUMAN	601461153F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3864661 5'
6770	19925	33320	0.65	9.2E-01	MG4703.1	NT	N. crassa valyl-tRNA synthetase (cyt-20/un-3) gene
9860	22900	36484	0.98	9.2E-01	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9949	22988	36882	1.31	9.2E-01	6671677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10472	23507	37120	3.6	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10627	23661	37269	1.64	9.2E-01	BF593251.1	EST_HUMAN	7058906.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW.NU6M_TRYBB
10883	23967	37596	1.76	9.2E-01	BE563811.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 ;
12022	25006	38707	1.5	9.2E-01	BF132402.1	EST_HUMAN	601334943F1 NIH_MGC 39 Homo sapiens cDNA clone IMAGE:3688714 5'
							601820312F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4052018 5'
1654	14807	27892	1.52	9.1E-01	T96675.1	EST_HUMAN	ye52f01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains
2193	15328		1.49	9.1E-01	8923056	NT	Alu repetitive element;
							Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3275	16449	29468	1.28	9.1E-01	T28418.1	EST_HUMAN	AB200038R Infant brain, LLNL array of Dr. M. Soares INIB Homo sapiens cDNA clone LLAB200G8 5'
3275	16449	29469	1.28	9.1E-01	T26418.1	EST_HUMAN	AB200038R Infant brain, LLNL array of Dr. M. Soares INIB Homo sapiens cDNA clone LLAB200G8 5'
6295	19469	32824	1.54	9.1E-01	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
6635	19794	33183	3.25	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7760	20810	34300	17.46	9.1E-01	AA086823.1	EST_HUMAN	cb71g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336862 3'
7916	20967	34473	2.81	9.1E-01	U72985.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
10379	23414	37023	0.6	9.1E-01	P38432	SWISSPROT	P80-COLLIN
12595	26054		19.67	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3277	16451	29472	0.8	9.0E-01	7661625	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
3439	16607		0.73	9.0E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
4219	17368	33567	0.68	9.0E-01	8622310	NT	Homo sapiens hypothetical protein FLJ10251 (FLJ10251), mRNA
4493	17638	30620	1.43	9.0E-01	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
5127	18252	31218	13.05	9.0E-01	AF017729.1	NT	Oryzabagus cuniculus Rad51 (RAD51) mRNA, complete cds
7551	20823	34100	0.82	9.0E-01	L42547.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
7579	20651		1.42	9.0E-01	D38621.1	NT	Xenopus laevis gene for aldolase, complete cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9649	22614	35183	0.68	9.0E-01	AF086761.1	NT	Danio rerio aemaphorin Z1a mRNA, complete cds
10035	23073	36873	0.48	9.0E-01	U93702.1	NT	Mycoplasma genitalium section 24 of 51 of the complete genome
12113	25093	38797	1.41	9.0E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
5814	18004	32309	2.5	8.9E-01	AF026199.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
6378	18547	32309	1.28	8.9E-01	X60986.1	NT	Rabbit MHC fragment RLA-DF DNA
6590	25827	33134	0.82	8.9E-01	BF217839.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
6590	25827	33135	0.82	8.9E-01	BF217839.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
8621	21701	35237	0.92	8.9E-01	AF259667.1	NT	Olfonema nana cytochrome-c oxidase subunit I (coxI) gene, partial cds; mitochondrial gene for mitochondrial product
12080	25060	38766	2.72	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
12423	25300	38766	4.02	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AF39, section 21 of 94 of the complete genome
4684	17799	30788	2.11	8.8E-01	O26360	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5489	18688	31706	0.66	8.8E-01	AF310617.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
7701	20768	34250	0.59	8.8E-01	M81182.1	NT	Homo sapiens peroxisomal 70 kD membrane protein mRNA, complete cds
10436	23471	37077	1.07	8.8E-01	7656878	NT	Homo sapiens cell death-inducing DFFA-like effector B (CIDEb), mRNA
11337	24400	38049	2.23	8.8E-01	Z28337.1	NT	M. aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
12092	25072	38779	7.56	8.8E-01	AA808055.1	EST_HUMAN	oc38h11.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1352037 3' similar to contains Alu repetitive element/contains element MER22 repetitive element
12240	26158	38779	2.13	8.8E-01	D30911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
477	13672	26704	2	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2475	15602	28727	0.98	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2938	16115	29127	5.32	8.7E-01	AA595863.1	EST_HUMAN	nm05111.s1 NCL CGAP_P14.1 Homo sapiens cDNA clone IMAGE:1076877
5120	18246		4.12	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa lipodermase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put>
8229	21311	34831	0.66	8.7E-01	AW897335.1	EST_HUMAN	RC4-NN0057-120500-073-c07 NN0057 Homo sapiens cDNA
9130	22209	35752	0.66	8.7E-01	A1239456.1	EST_HUMAN	qh36e06.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9130	22209	35753	0.66	8.7E-01	A1239456.1	EST_HUMAN	qh36e06.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9839	22978	36869	2.07	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PAO1, section 524 of 529 of the complete genome
10511	23546	37156	1.08	8.7E-01	BF570189.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10511	23546	37157	1.08	8.7E-01	BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'
11070	24145	37782	5.87	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
12034	25017	38720	3.32	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
12034	25017	38721	3.32	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
12652	25940		2.8	8.7E-01	AV661898.1	EST_HUMAN	AV661898 GLC Homo sapiens cDNA clone GLCGYG07 3'
487	13681		2.39	8.6E-01	X17012.1	NT	Rat IGFII gene for insulin-like growth factor II
881	14057	27123	3.14	8.6E-01	W69089.1	EST_HUMAN	z44403.r1 Soares_fetal_NbHH19W Homo sapiens cDNA clone IMAGE:343516 5'
2344	15475	28608	1.31	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3710	16871	29875	0.85	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3901	17060	30059	1.31	8.6E-01	U49724.1	NT	Drosophila melanogaster melin (Omerlin) mRNA, complete cds
6019	19202	32521	10.02	8.6E-01	XG0547.1	NT	Chicken lipoprotein lipase gene
6019	19202	32522	10.02	8.6E-01	XG0547.1	NT	Chicken lipoprotein lipase gene
6508	25825	33042	0.7	8.6E-01	S76772.1	NT	polyprotein [Coxsackie B4 virus CB4, host=mouse, E2, originally derived from Edwards CB4 human strain, Genomic RNA Complete, 7397 nt]
6848	20001	33409	1.96	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6848	20001	33410	1.96	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7956	20761		0.84	8.6E-01	AE000591.1	NT	Helicobacter pylori 26695 section 69 of 134 of the complete genome
8112	21194		1.82	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
8232	21314	34834	0.56	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
8887	22927		0.54	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12856	25893		2.11	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2509	15635		1.46	8.5E-01	AJ011924.1	NT	Arabidopsis thaliana (ecotype Columbia) spl2 gene, exons 1-5
6866	20018	33427	1.1	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7694	20759	34243	2.36	8.6E-01	BE542812.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3435305 5'
8180	21262	34784	0.57	8.5E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8613	21693	35230	0.92	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8613	21693	35231	0.92	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8702	21782	35319	0.68	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10358	23593	37198	1.49	8.5E-01	AB006798.1	NT	Cyanidium caldarium gene for SigC, complete cds
10558	23593	37199	1.49	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
12577	26056		5.29	8.5E-01	11416543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
12585	25394		6.39	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4873	18006	30989	0.68	8.4E-01	AF083975.2	NT	Fowl adenovirus 8, complete genome

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5611	25808	31871	2.75	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5811	25808	31872	2.75	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7991	21041	34553	0.57	8.4E-01	AF051142.1	NT	Manesbra brassicae phenolase binding protein 2 precursor (PBP2) mRNA, complete cds
10163	23200		3.42	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
760	13941	26986	2.17	8.3E-01	M82437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3164	16339	29347	3.45	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3912	17071	30069	0.69	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4120	17274	30273	3.17	8.3E-01	Y18177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5933	18585	31454	2.32	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
9870	22910		4	8.3E-01	AI781952.1	EST_HUMAN	nm011212.6 NCI_CGAP_C09 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.11 THR repetitive element:
10316	23351	36958	1.32	8.3E-01	AF098070.1	NT	Drosophila melanogaster L11 homolog mRNA, complete cds
10423	23458	37063	3.9	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10911	23994	37627	2.18	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
10930	24012		1.65	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11584	24637	38317	9.95	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2111	15249	28369	2.72	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2156	15292		1.32	8.2E-01	AF146589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2744	15861		0.95	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
4009	17166	30174	0.68	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0974 protein, partial cds
4247	17393	30381	0.7	8.2E-01	Z72584.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL062w
4247	17393	30382	0.7	8.2E-01	Z72584.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL062w
5217	18338	31311	1.19	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
6781	19336	33332	0.59	8.2E-01	X95283.1	NT	G. gallus mRNA for C-Serratia-1 protein
6781	19338	33333	0.59	8.2E-01	X95283.1	NT	G. gallus mRNA for C-Serratia-1 protein
6913	20228	33661	0.76	8.2E-01	AJ010142.1	NT	Amanita muscaria mRNA for SCII25 protein
7037	20173	33595	3.19	8.2E-01	AW376993.1	EST_HUMAN	OMA4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
7419	25944	33966	4.48	8.2E-01	Z12126.1	NT	S. cerevisiae MET, LEU4, and POL 1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
8639	21719	35256	0.55	8.2E-01	BE283145.1	EST_HUMAN	601144885F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
10231	23266	39856	0.81	8.2E-01	AB014630.1	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
10264	23289	38897	1.51	8.2E-01	AF052659.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10428	23463	37070	0.54	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10428	23463	37071	0.54	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10596	23631	37239	3.78	8.2E-01	Q9J70	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10596	23631	37240	3.78	8.2E-01	Q9J70	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11942	24928	38631	4.72	8.2E-01	L10127.1	NT	Mollusca contigabscum virus type 1 ORF1 and ORF2 DNA
12030	25013	38715	6.12	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
12035	25018	38722	3.97	8.2E-01	H87398.1	EST_HUMAN	yw14d02.1 Soares_placenta_8to9weeks_2NHIP8to9W Homo sapiens cDNA clone IMAGE:252195.5' similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
12607	25408	32046	3.01	8.2E-01	AJ001261.1	NT	Mus musculus mRNA for NIPSNAP2 protein
2817	15931		1.38	8.1E-01	AF181839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3547	16712	29723	2.77	8.1E-01	AF055086.1	NT	Homo sapiens MHC class 1 region
3547	16712	29724	2.77	8.1E-01	AF055086.1	NT	Homo sapiens MHC class 1 region
4730	17866	30847	0.63	8.1E-01	4506290	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2) mRNA
5825	19015	32321	0.63	8.1E-01	Q01727	SWISSPROT	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN RECEPTOR)
6445	19612	32375	0.89	8.1E-01	U16780.1	NT	(MELANOCORTIN-1 RECEPTOR) (MCL-R)
6759	19915	33309	2.17	8.1E-01	Q13491	SWISSPROT	Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds
6759	19915	33310	2.17	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
7681	20746	34227	0.7	8.1E-01	O47477	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
							CYTCHROME B
8095	21177	34693	1.1	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (PicoT) gene, partial cds; putative sodium channel (Nech) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8095	21177	34694	1.1	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (PicoT) gene, partial cds; putative sodium channel (Nech) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8808	21887	35428	0.91	8.1E-01	AF001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8808	21887	35429	0.91	8.1E-01	AF001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
							xc01103.x1 NCI_COAP_Kid11 Homo sapiens cDNA clone IMAGE:2682469.3' similar to SW:LYAR_MOUSE C08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN ; contains MER22.b1-PTRs repetitive element ;
8969	22048	35691	1.14	8.1E-01	AW242647.1	EST_HUMAN	PROBABLE E4 PROTEIN
10330	23365	36974	0.58	8.1E-01	P06425	SWISSPROT	PROBABLE E4 PROTEIN
10623	23667	37267	0.52	8.1E-01	N84541.1	EST_HUMAN	KK9872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872.5' similar to EST(CLONE C-0PE11)
10769	23802		0.54	8.1E-01	AE001226.1	NT	Trepurania pallidum section 42 of 87 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11772	24764	38459	2.62	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11772	24764	38480	2.62	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
12303	25221	32102	2.22	8.1E-01	AE001711.1	NT	Thermoboga maritima section 23 of 136 of the complete genome
181	13404		2.62	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pla gene for phosphate acetyltransferase allele 15
299	13516	26549	10.2	8.0E-01	AJ132772.1	NT	Bos taurus tub and rif genes
2093	15233		1.95	8.0E-01	BF530982.1	EST_HUMAN	602072473F1 NCL CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4215091 5'
3148	16322	28334	1.32	8.0E-01	AF127887.1	NT	Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds
3387	16557	29572	1.29	8.0E-01	AB006103.1	NT	Mus musculus gene for oxiductal glycoprotein, complete cds
4655	17791	30775	6.77	8.0E-01	X83739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5096	18224	31196	1	8.0E-01	7667352	NT	Mus musculus myosin IXb (Myo9b), mRNA
8179	21261		2.68	8.0E-01	AW901489.1	EST_HUMAN	RCO-NN1012-270300-021-h08 NN1012 Homo sapiens cDNA
8722	21802	35338	1.21	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3'
10635	23659		0.48	8.0E-01	BE833326.1	EST_HUMAN	QV3-OT0065-280600-250-c05 OT0065 Homo sapiens cDNA
10827	23860	37483	0.48	8.0E-01	AB045597.1	NT	Gallus gallus PPAR gamma mRNA for peroxisome proliferator-activated receptor, complete cds
11198	24267	37902	1.43	8.0E-01	Q92793	SWISSPROT	CREB-BINDING PROTEIN
486	13681	26697	0.75	7.9E-01	D11476.1	NT	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
733	13915		0.92	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1635	14787		28.32	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1887	14839		1.06	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2337	15488	28603	9.03	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin28, complete cde
2338	15469	28604	4.11	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3805	16769	29784	3.57	7.9E-01	AF228684.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4416	17567		0.87	7.9E-01	BE263612.1	EST_HUMAN	601192033F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3535785 5'
4734	17869	30852	0.84	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4734	17869	30853	0.84	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5210	18331		0.68	7.9E-01	6753763	NT	Mus musculus embigin (Emb), mRNA
5235	18357	31325	0.93	7.9E-01	Z47210.1	NT	Mus musculus enabled homolog (Drosophila) (Enah), mRNA
5236	18367	31328	0.93	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orf5
5283	18402		0.66	7.9E-01	AF139718.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orf5
6475	19842	33003	0.68	7.9E-01	D88145.1	NT	Chrysomya bezziana peritrophin-48 precursor, gene, complete cds
8300	21382	34903	2.68	7.9E-01	X00956.1	NT	Human mRNA for prostacyclin synthase, complete cde
9747	22811	36390	3.24	7.9E-01	U01912.1	NT	P. sativum GR gene
10255	23290	36887	5.43	7.9E-01	P19719	SWISSPROT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
10298	23331	36834	1.17	7.9E-01	AV700860.1	EST_HUMAN	SMALL HYDROPHOBIC PROTEIN
							AV700860 GKC Homo sapiens cDNA clone GKCDRE12 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10729	23762	37369	0.78	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
10845	23878	37498	0.61	7.9E-01	P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
11256	24325		1.75	7.9E-01	7862471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11487	24548	38218	1.94	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
899	14074		1.49	7.8E-01	Z43785.1	EST_HUMAN	HSC70H041 normalized infant brain cDNA Homo sapiens cDNA clone c-1k104
2349	15480	28612	6.99	7.8E-01	AW959587.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4823	17956	30942	0.73	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5149	18271		0.89	7.8E-01	AW753353.1	EST_HUMAN	RC3-C10254-130100-023-c02 C10254 Homo sapiens cDNA
6194	19370	32721	2.26	7.8E-01	AF116566.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds
6348	19518	32876	2.28	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6591	19751	33136	0.84	7.8E-01	AL445068.1	NT	Thermoplasma acidophilum complete genome, segment 4/6
8698	21768	35299	1.13	7.8E-01	BF108927.1	EST_HUMAN	715406.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176 3'
9434	22508	36074	1.53	7.8E-01	Y10159.1	NT	D.discoideum racGAP gene
9633	22598	36170	0.56	7.8E-01	4826873	NT	Homo sapiens nucleoporin 214kD (CAIN) (NUP214), mRNA
10329	23364		1.28	7.8E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12571	26033		1.92	7.8E-01	L28260.1	NT	Arabidopsis thaliana 1-aminol-1-cyclopropanecarboxylate synthase (ACS6) gene, complete cds
146	13371	26403	5.78	7.7E-01	AF184345.1	NT	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
744	19325		1.72	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IiAlpha) and major histocompatibility protein class II beta chain (IiBeta) genes, complete cds;
2776	15892	29003	1.34	7.7E-01	O33915	SWISSPROT	butyrophilin-like (NG9), butyrophilin-li>
3438	16606		0.89	7.7E-01	8393403	NT	CITRATE SYNTHASE
3689	16351	29659	3.86	7.7E-01	AF118085.1	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine polypeptide N-acetylgalactosaminyltransferase 7 (GALNAC-T7) (GALNAC-T7), mRNA
4516	17555	30643	3.38	7.7E-01	AF199488.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4516	17555	30644	3.38	7.7E-01	AF199488.1	NT	Coltunik coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5678	18972	32159	1.39	7.7E-01	P16553	SWISSPROT	Coltunik coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5678	18972	32160	1.39	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6076	19258	32587	1.41	7.7E-01	R08900.1	EST_HUMAN	RAFFINOSE INVERTASE (INVERTASE)
10049	23087	36889	0.68	7.7E-01	AB021134.1	NT	yf24b02.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:127755 3'
12452	25317		7.14	7.7E-01	11497821	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
							Archaeoglobus fulgidus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6224	19399	32748	5.26	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6224	19399	32749	5.26	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6847	19808	33193	0.68	7.6E-01	P37838	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
6900	19509	31501	0.74	7.6E-01	AI253399.1	EST_HUMAN	ac14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
6900	19509	31526	0.74	7.6E-01	AI253399.1	EST_HUMAN	ac14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7196	20061	33472	0.84	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
8255	21337	34855	1.54	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8318	21400	34924	2.38	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
8318	21400	34925	2.38	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
8520	21601	35137	0.53	7.6E-01	Q01098	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8520	21601	35138	0.53	7.6E-01	Q01098	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9167	22245	35789	1.33	7.6E-01	6753577	NT	Mus musculus cytochrome P450_2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
9479	22536	36100	5.24	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9479	22536	36101	5.24	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11639	24719	38411	2.29	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11639	24719	38412	2.29	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
12010	24895		2.78	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
12203	25157		8.21	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
526	13719		1.31	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
597	13787	28807	1.08	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
7690	20755	34240	0.8	7.5E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
12521	25354		5.2	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
1154	14318	27372	1.01	7.4E-01	AI598146.1	EST_HUMAN	h14b09.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element
2419	15548	28676	0.97	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3920	19980	29983	0.97	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4010	17167	30175	0.71	7.4E-01	AF133310.1	NT	Vibrio cholerae phage CTXphi Calcutta-rsR-a (rsR-a) and Calcutta-rsR-b (rsR-b) genes, complete cds
4429	17559	30551	8.12	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8027	21110	34628	1.25	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8027	21110	34629	1.25	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8834	21913	35451	1.01	7.4E-01	BF346266.1	EST_HUMAN	602018456F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154340 5'
8910	21989		1.45	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9298	22374	35925	6.86	7.4E-01	BE747503.1	EST_HUMAN	801573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9357	22432	35990	1.24	7.4E-01	AA187986.1	EST_HUMAN	zp67h01.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCPO_MOUSE P42932 T-COMPLEX PROTEIN 1, THETA SUBUNIT ;
10613	23847	37256	0.7	7.4E-01	11424933	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
12170	25133		3.69	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
12287	25213		1.7	7.4E-01	AF000082.1	EST_HUMAN	tat3h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4083	17238		0.73	7.3E-01	AF000082.1	NT	Aeropyrum pernix genomic DNA, section 5/7
4738	17873	30858	0.8	7.3E-01	AE001186.1	NT	Borrelia burgdorferi (section 62 of 70) of the complete genome
4822	17955	30941	2.38	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
6741	19897	33287	5.5	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6741	19897	33288	5.5	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
7243	25841	33771	0.93	7.3E-01	AJ011418.1	NT	Lycopodium obscurum mRNA for ubiquitin activating enzyme
7617	20687	34163	0.69	7.3E-01	Z14133.1	NT	D.melanogaster Cric mRNA for clathrin heavy chain
7718	20782	34268	7.25	7.3E-01	M26511.1	NT	V.algindylus sucrose (scrB) gene, complete cds
7718	20782	34269	7.25	7.3E-01	M26511.1	NT	V.algindylus sucrose (scrB) gene, complete cds
11714	24754	38448	3.29	7.3E-01	AA678019.1	EST_HUMAN	z25508.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
11714	24754	38449	3.29	7.3E-01	AA678019.1	EST_HUMAN	z25508.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
854	14031		1.86	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
2012	15152	28257	3.43	7.2E-01	X79140.1	NT	N.tabacum NeIF-4A13 mRNA
2532	15657	28781	1.96	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3135	16311	29223	1.27	7.2E-01	AF108100.1	NT	Fowlpox virus, complete genome
3541	16708	29717	2.36	7.2E-01	AF068606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-I) allele, complete cds
3702	16863	29866	1.35	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
3975	17132	30136	1.57	7.2E-01	BF338350.1	EST_HUMAN	602035589F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183222 5'
4173	17323		0.73	7.2E-01	AF108093.1	NT	Homo sapiens IA-2 gene, intron 18

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4982	18022	31007	2.68	7.2E-01	D90314.1	NT	L mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5225	18347	31317	1.07	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
5225	18347	31318	1.07	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
5308	18425	31395	0.85	7.2E-01	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 83
7362	20441	33903	0.59	7.2E-01	U69633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8648	21728	35285	1.31	7.2E-01	AF236081.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
9163	22241		0.54	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD08 5'
10548	23883	37192	2.25	7.2E-01	BF870081.1	EST_HUMAN	602118381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5'
10977	24056	37690	3.26	7.2E-01	U62823.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
12530	18491	31530	1.51	7.2E-01	U02668.1	NT	Dicoryctes viviparus nematode polyprotein antigen precursor (Dva) mRNA, complete cds
12737	25488		4.37	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 87
12784	26075		1.46	7.2E-01	Y10768.1	NT	B. thuringiensis PK1 & cap genes, putative
710	13892	26928	11.37	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha
3130	16308	28320	16.1	7.1E-01	AJ270777.1	NT	Isodent (RyR1), complete cds
4924	17467	30453	3.07	7.1E-01	7305360	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-18
4924	17467	30454	3.07	7.1E-01	7305360	NT	Mus musculus clogelin (Olog), mRNA
6069	19251	32578	1.73	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
6069	19251	32580	1.73	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
7088	20182	33906	6.48	7.1E-01	U36232.1	NT	Drosophila melanogaster α -pyruvyltetrahydropterin synthase (pr) gene, complete cds
8934	22013	35552	1.12	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0667-301299-011-409 BT0667 Homo sapiens cDNA
8934	22013	35553	1.12	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0667-301299-011-409 BT0667 Homo sapiens cDNA
10059	23097	36700	1.6	7.1E-01	BE904406.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
10621	23955	37265	1.1	7.1E-01	MT2861.1	NT	Human T-cell receptor gamma chain J2 gene
12605	25955		2.64	7.1E-01	AA421492.1	EST_HUMAN	zu06h11.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'
1257	14415	27479	0.95	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1257	14415	27480	0.95	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2521	15647	28770	1.29	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares multiple sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2521	15847	28771	1.29	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Scores_multiple_sclerosis_2NhmSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
5199	18291		2.32	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21 C101
6073	19255		0.89	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8673	21654		6.52	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
9517	22582	36150	0.58	7.0E-01	U53888.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mliA, mliR, mliF, and mliD genes, complete cds
9517	22582	36151	0.58	7.0E-01	U53888.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mliA, mliR, mliF, and mliD genes, complete cds
11382	24443	38102	1.47	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
11382	24443	38103	1.47	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
13133	25997	31772	1.47	7.0E-01	9630484	NT	Bacteriophage N15 virion, complete genome
992	14164	27224	6.3	6.9E-01	U69674.1	NT	Candida albicans equalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
992	14164	27225	6.3	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1338	14495	27565	2.91	6.9E-01	AA593530.1	EST_HUMAN	nm28a09.s1 NCI_CGAP_Gast1 Homo sapiens cDNA clone IMAGE:1085176 3'
3291	16465	29484	1.71	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
3531	16696	29707	16.79	6.9E-01	Y17373.1	NT	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2811
5311	18428	31398	97.22	6.9E-01	BE782751.1	EST_HUMAN	601465594F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3888943 5'
5902	19091	32405	0.82	6.9E-01	AB035662.1	NT	Branchiostoma belcheri BbNA3 mRNA for notochord actin, complete cds
6112	19262	32627	0.95	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP530, partial
6500	19696	33029	1.12	6.9E-01	BE298188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
7979	21028	34542	0.58	6.9E-01	AF248863.1	NT	Strongylocentrotus purpuratus myosin V, complete cds
8168	21250	34769	2.94	6.9E-01	AL181573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8168	21250	34770	2.94	6.9E-01	AL181573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9372	22447		0.66	6.9E-01	AF118046.1	NT	Entamoeba dispar caton transporting ATPase (atpase) gene, partial cds
9896	22936	36520	0.56	6.9E-01	AF208319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
9896	22936	36521	0.56	6.9E-01	AF208319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
10619	23453	37263	0.78	6.9E-01	BF242307.1	EST_HUMAN	601880580F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109419 5'
11536	24592	38268	2.11	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11536	24592	38269	2.11	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
12146	25949		3.77	6.9E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFIH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
979	14152	27212	1.84	6.8E-01	AF017784.1	NT	Glialia intestinalis carboxamide kinase gene, complete cds
2739	15856		1.41	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2890	14798	27683	1.43	6.8E-01	AA854475.1	EST_HUMAN	q75a06.e1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to
4694	17829	30815	1.32	6.8E-01	J00762.1	NT	gb:X56411_mai1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4980	18109	31085	0.82	6.8E-01	4758521	NT	Rat(hooded) prolactin gene : exon iii and flanks
8838	22878	36460	1.08	6.8E-01	AB037768.1	NT	Homo sapiens hevln (HEVIN) mRNA
						NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
10567	23602		5.72	6.8E-01	AA687836.1	EST_HUMAN	nv13e07.s1 NCL_GAP_P122 Homo sapiens cDNA clone IMAGE:1220100 3' similar to gb:X13546_rna1
11344	24407	38056	2.4	6.8E-01	AJ276675.1	NT	Human HMG-17 gene for non-Hisbne chromosomal protein (HUMAN);
11344	24407	38057	2.4	6.8E-01	AJ276675.1	NT	Slagospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11376	24437	38096	1.91	6.8E-01	AF038839.1	NT	Slagospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11376	24437	38097	1.91	6.8E-01	AF038839.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11376	24437	38097	1.91	6.8E-01	AF038839.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11579	24633	38312	1.57	6.8E-01	AF104151.1	NT	Anopheles gambiae strain V2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds
						NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11906	24893	38594	1.97	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11906	24893	38595	1.97	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
309	13525	26559	30.38	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
349	13560	26588	25.24	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1961	15104		1.14	6.7E-01	M12132.1	NT	Quail fast skeletal muscle tropomyosin I gene, complete cds
2214	15348	28477	1.98	6.7E-01	AA451894.1	EST_HUMAN	zx12g12.e1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element ;
2235	16058	28498	6.16	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
3060	16238	29256	5.81	6.7E-01	6673580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4575	17712	30896	0.62	6.7E-01	X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase
5626	18820	31894	1.44	6.7E-01	J04836.1	NT	M. barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5626	18820	31895	1.44	6.7E-01	J04836.1	NT	M. barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6083	19265	32894	0.79	6.7E-01	AE001488.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6453	19620	32983	1.3	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6453	19620	32984	1.3	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6754	19610	33304	0.59	6.7E-01	BE966241.2	EST_HUMAN	601650177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
6754	19910	33305	0.59	6.7E-01	BE966241.2	EST_HUMAN	601650177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
7468	20543		3.97	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7495	20570	34042	0.94	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10348	23383		1.01	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
11196	24265	37900	2.06	6.7E-01	BF394649.1	EST_HUMAN	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
11746	23932	37558	2.75	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
11959	24944	38649	2.48	6.7E-01	AA342521.1	EST_HUMAN	EST48065 Fetal spleen Homo sapiens cDNA 3' end
2570	15695	28819	0.97	6.6E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2765	15880	28989	1.13	6.6E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3578	16743	29760	1.16	6.6E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3748	16809	29913	4.58	6.6E-01	Y07669.1	NT	C.albicans random DNA marker, 282bp
4226	17373		2.48	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6462	19629	32890	3.82	6.6E-01	6880577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7272	20355	33508	0.62	6.6E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
7272	20355	33509	0.62	6.6E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
7862	20916	34421	3.7	6.6E-01	AV660506.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLCIGD04 3'
8764	21843	35384	0.58	6.6E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
9865	22905		2.34	6.6E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
10207	23243		0.51	6.6E-01	AU118198.1	EST_HUMAN	AU118198 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5'
640	13825	26848	2.02	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
640	13825	26849	2.02	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3518	16685	29686	5.5	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4148	17300	30292	1.73	6.5E-01	4504632	NT	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA
4397	17540	30521	7.71	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
5174	18296	31258	2.88	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5559	25807	31795	1.86	6.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TFE4)
8865	20017	33426	1.3	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7760	20819	34309	0.74	6.5E-01	X04789.1	NT	Murine Ig-related lambda(50) gene (exon 1) transcribed selectively in pre-B lymphocytes
7848	20901	34404	0.99	6.5E-01	A1769882.1	EST_HUMAN	wc4ba02.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2321842 3'
10042	23080		0.86	6.5E-01	T78904.1	EST_HUMAN	yc21b04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108847 3'
10542	23577	37186	2.53	6.5E-01	AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10869	23954	37583	2.55	6.5E-01	H87583.1	EST_HUMAN	yw17f06.r1 Soares_placenta_8to9weeks_2NBP80c9W Homo sapiens cDNA clone IMAGE:252515 5'
10925	24008	37643	2.98	6.5E-01	AA601287.1	EST_HUMAN	no15c07.s1 NCL_CGAP_Pher1 Homo sapiens cDNA clone IMAGE:1100748 3'
11030	24109		3.38	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
11899	24887	38586	5.43	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12566	25386		8.69	6.5E-01	BE465050.1	EST_HUMAN	hiv74a10.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12640	25889		3.83	6.5E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL097c
282	13481	26513	8.59	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3545	16710	29721	4.42	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3964	17122	30125	1.48	6.4E-01	AB048827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4614	17751	30731	0.74	6.4E-01	Y12488.1	NT	M.musculus whn gene
4614	17761	30732	0.74	6.4E-01	Y12488.1	NT	M.musculus whn gene
8612	21891	36432	1.58	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
10221	23257		0.5	6.4E-01	U1148320.1	NT	Homo sapiens hypothetical protein FLJ10140 (FLJ10140), mRNA
10294	23329	36933	7.31	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10309	23344	36949	1.31	6.4E-01	BF670405.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291126 5'
12693	25461		19.53	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGC09 5'
447	13643	26692	3.76	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-II)
548	13741	26765	1.85	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2230	13364	28493	3.29	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigen resistance locus
2646	15769	28884	3.65	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2646	15769	28885	3.65	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3081	16257		0.83	6.3E-01	Y17275.1	NT	Lycopodium obscurum p69a gene, complete CDS
6189	19365	32713	0.84	6.3E-01	BE093906.1	EST_HUMAN	PMD-BT0757-010500-002-405 BT0757 Homo sapiens cDNA
6733	19889	33281	1.01	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6733	19889	33282	1.01	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8718	21798		3.44	6.3E-01	BE02044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958351 5'
9087	22166	35712	0.79	6.3E-01	S62927.1	NT	glycoprotein Ila (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9421	22495	36062	0.66	6.3E-01	BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102566 5'
9620	22675	36245	3.14	6.3E-01	9827521	NT	Varidla virus, complete genome
9620	22675	36246	3.14	6.3E-01	9827521	NT	Varidla virus, complete genome
10142	23180		0.68	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10641	23675	37285	1.59	6.3E-01	Z73003.1	NT	S.cerevisiae chromosome VII reading frame ORF YGR218w
10747	23780	37393	1	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1685 section 203 of 400 of the complete genome
10781	23814		0.48	6.3E-01	AW795395.1	EST_HUMAN	PM0-UM0018-130500-003-g12 UM0018 Homo sapiens cDNA
11315	24378	38024	1.78	6.3E-01	AA877715.1	EST_HUMAN	m09h06.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 002916 HLAARK :
11620	24671	38359	6.18	6.3E-01	AB04160.1	EST_HUMAN	GM-BT043-090299-046 BT043 Homo sapiens cDNA
11709	24749	38442	1.55	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11888	24876	38573	2.12	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
12086	25066	38772	1.47	6.3E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
12262	26130	31546	15.92	6.3E-01	9910293	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
12358	26257		1.6	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
12582	26029		4.27	6.3E-01	X85528.1	NT	G.limicola pscD gene
5991	19178	32497	2.15	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7684	20731		3.59	6.2E-01	AF022263.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Carr-rs4) mRNA, partial cds
7715	25652	34266	1.16	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea8 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8497	21578	35114	4.67	6.2E-01	H72255.1	EST_HUMAN	ys01508.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:213542 3'
9057	22136	35681	0.7	6.2E-01	AF034411.1	NT	Lyoperisicon esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds, and dehydroquinolate dehydratase/shikimate:NADP oxidoreductase gene, complete cds
9648	21091	34806	1.47	6.2E-01	BE562687.1	EST_HUMAN	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3660010 5'
9710	22759		2.56	6.2E-01	M24481.1	NT	Human pulmonary surfactant-associated protein SP-B (SFT P3) mRNA, complete cds
10283	23318	36619	6.83	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10426	23461	37067	0.63	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10426	23461	37068	0.63	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10756	23789	37405	5.75	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10756	23789	37408	5.75	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEINASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2468	15595		6.27	6.1E-01	6878076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Spac), mRNA
5653	18847	32129	1.33	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 CehVydD (nih-1) alternatively spliced genes, complete cds
7099	20146	33564	3.4	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7099	20145	33565	3.4	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7160	20293	33736	0.67	6.1E-01	AW105653.1	EST_HUMAN	xs50h03.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gb:X12671_mai HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7254	20337	33787	0.69	6.1E-01	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8428	21509	35041	3.47	6.1E-01	AF033535.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8995	22074	35612	1.51	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8995	22074	35613	1.51	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9615	22870	36239	20.44	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9615	22870	36240	20.44	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10047	23085	36883	1.06	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PAO1, section 13 of 529 of the complete genome
10252	23287	36883	0.92	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
10833	23666	37489	0.47	6.1E-01	AF025993.1	NT	Sus scrofa neural cell adhesion molecule (NCAM) gene, 3' UTR and microsatellite repeat region
12033	25016	38718	1.77	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12033	25016	38719	1.77	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
13052	25695		1.16	6.1E-01	X95287.1	NT	M.mazai orfA, orfB, and orfC of archaeal ABC-transporter system
507	13701	26730	1.79	6.0E-01	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
575	13767		4.74	6.0E-01	5802999	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1393	14547	27823	1.83	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH83-53b attachment protein (G) gene, complete cds
3917	17076	30073	0.87	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4305	17448		1.26	6.0E-01	AF058895.1	NT	Homo sapiens Ndc13 (NOTCH3) gene, exons 26, 27, and 28
5395	18597	31567	1.96	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5555	18753	31791	2.5	6.0E-01	AW139713.1	EST_HUMAN	U1-HB1-seb-e-10-Q-U1 st NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
6669	19828	33216	2.74	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6800	19955	33355	0.68	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6955	20268	33705	0.77	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
6955	20268	33706	0.77	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7509	20583	34056	6.49	6.0E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8315	21397	34922	4.15	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8315	21397	34923	4.15	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
10028	23065	36564	1.57	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10480	23515		1.04	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER8 (PEROXIN-3)
10594	23629		0.61	6.0E-01	BE837779.1	EST_HUMAN	RC2-FN0094-190700-017-d08 FN0094 Homo sapiens cDNA
11312	24376	38021	1.38	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11312	24376	38022	1.38	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11846	24835	38529	2.74	6.0E-01	AA20623.1	EST_HUMAN	ff0807.x1 NC1_CGAP_P28 Homo sapiens cDNA clone IMAGE2095621.3
12653	25440	32052	2.08	6.0E-01	11421663	NT	Homo sapiens nuclear factor (erythroid-derived 2) like 3 (NFE2L3), mRNA
12781	25523		1.48	6.0E-01	AA708087.1	EST_HUMAN	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
12953	25968		1.44	6.0E-01	5803136	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
12998	25993	31766	5.46	6.0E-01	9055303	NT	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
13032	25980		8.12	6.0E-01	BE157617.1	EST_HUMAN	Haemophilus influenzae Rd section 18 of 163 of the complete genome
1025	14786	27254	1.09	5.9E-01	U32701.1	NT	Homo sapiens chromosome 21 segment HS21C087
3343	16515	29530	5.23	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
3343	16516	29531	5.23	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
3916	17075	30072	0.62	5.9E-01	U74341.1	NT	Pterodroma neglecta cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
4337	17480		3.95	5.9E-01	AF182756.1	NT	Rattus norvegicus centexin 2 mRNA, partial cds
5289	18407	31374	0.68	5.9E-01	AF026566.1	NT	Ovis aries SRY gene promoter region
6594	19754	33140	1.95	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7416	20494	33962	3.08	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7556	20628		0.63	5.9E-01	X68801.1	NT	G.gallus gene for skeletal alpha-actinin, exon EF2
8188	21270	34795	0.48	5.9E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
8839	21818	35456	0.48	5.9E-01	D12922.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
9743	22807	36385	1.01	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain K/UW/31/Cx major outer membrane protein (omp1) gene, complete cds
10117	23155		0.64	5.9E-01	P06463	SWISSPROT	E6 PROTEIN
10391	23426	37033	1.28	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10908	23991	37624	2.24	5.9E-01	Q9X0I3	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10918	23999	37632	1.71	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
11203	24272	37908	2.76	5.9E-01	AW937175.1	EST_HUMAN	PM1-DT0041-190100-002-H03 DT0041 Homo sapiens cDNA
11469	24528	38201	1.98	5.9E-01	AF064626.1	NT	Mus spretus strain SPRET/EI CD48 antigen (Cd48) gene, partial cds
12302	25220	32101	1.78	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-tyrosin (alpha 1 AT) gene, promoter region
12549	25372		1.92	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for cordline-5-phosphate decarboxylase, complete cds
12789	25533		4.82	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1958	15101	28201	1.26	5.9E-01	P40472	SWISSPROT	SIM1 PROTEIN
4092	17247	30252	1.11	5.9E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4078131 5'
4637	17773	30753	3.59	5.9E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4917	18047		2.22	5.9E-01	AF110846.1	NT	Megascella scalaris sex-lethal homolog (Megsxl) gene, partial cds, alternatively spliced products
5490	18689		1.02	5.9E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 56 of the complete genome
5648	18842	32123	0.81	5.9E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6313	19485	32840	1.69	5.9E-01	D78659.1	EST_HUMAN	HUM500E06B Homo placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-500E06 5'
6442	19609	32872	0.58	5.9E-01	D50601.1	NT	Shigella sonnei DNA for 26 ORFs, complete cds
6952	20265		2.37	5.9E-01	S68091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
8071	21153		2.87	5.9E-01	H41571.1	EST_HUMAN	yr91503.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to
8278	21360	34878	0.86	5.9E-01	A1280051.1	EST_HUMAN	gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8278	21360	34879	0.66	5.9E-01	A1280051.1	EST_HUMAN	qh85d10.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8385	21466	34991	2.71	5.9E-01	P14328	SWISSPROT	qh85d10.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8385	21466	34992	2.71	5.9E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8902	22171	35716	10.4	5.9E-01	AJ270774.1	NT	SPORE COAT PROTEIN SP96
9172	22250	35783	1.23	5.9E-01	Q27368	SWISSPROT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
9173	22251	35794	0.57	5.9E-01	Q20471	SWISSPROT	TRANSCRIPTION FACTOR E2F
9795	22835		0.79	5.9E-01	BF031608.1	EST_HUMAN	PUTATIVE CASEIN KINASE I F46F22 IN CHROMOSOME X
11237	24306	37943	7.26	5.9E-01	AJ243213.1	NT	601567774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
11291	24357		3.35	5.9E-01	BF700092.1	EST_HUMAN	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11407	24468		1.44	5.9E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
3108	16284		0.73	5.7E-01	6755253	NT	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
3295	16469	29488	1.46	5.7E-01	Q9WTJ2	SWISSPROT	Mus musculus plasmatoma variant translocation 1 (Pvt1), mRNA
							PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3593	18757		2.84	5.7E-01	AB033503.1	NT	Populus euramericana peaces-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6485	19652	33014	4.41	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3868590 5'

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6850	20003	33412	0.82	5.7E-01	AA194201.1	EST_HUMAN	z38c06.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:665674 5'
7000	18519	31512	1.15	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7941	20981	34501	1.88	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (PEC REDUCTASE)
8157	21239		0.55	5.7E-01	AJ251835.1	NT	Mus musculus Kcng1, Lrpdc5, Mash2, Tapa-1, Tssc4 and Tssc8 genes, alternative transcripts
10004	23042	36634	1.13	5.7E-01	AL161632.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10004	23042	36635	1.13	5.7E-01	AL161632.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10803	23836	37461	0.91	5.7E-01	BF540662.1	EST_HUMAN	602067712F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4086610 5'
12255	26192		1.29	5.7E-01	BE715051.1	EST_HUMAN	MR3-HT0736-180700-003-a02 HT0736 Homo sapiens cDNA
13025	26675		1.31	5.7E-01	BE989722.2	EST_HUMAN	601654814R1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:3839763 3'
3449	16617	29635	1.1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3449	16617	29636	1.1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3959	17146	30152	0.59	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4354	17497	30476	0.77	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
9003	22082	35625	4.11	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
9003	22082	35626	4.11	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
9575	22717	36285	1.13	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
12153	25123		7.84	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3915457 5'
12272	25204	38362	1.39	5.6E-01	AA489535.1	EST_HUMAN	ng7sg10.s1 NCI CGAP_P16 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element ;
12661	17146	30152	2.38	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12690	25460		2.56	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
13167	25758		3.64	5.6E-01	BF573829.1	EST_HUMAN	602132029F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4271334 5'
1238	14397	27459	6.04	5.5E-01	8363912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2766	15881	28990	9.3	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL
2766	15881	28991	9.3	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL
2965	16161	29178	1.17	5.5E-01	5902085	NT	PROTEIN P30; NUCLEOPROTEIN P10]
3134	16310		1.57	5.5E-01	H46219.1	EST_HUMAN	PROTEIN P30; NUCLEOPROTEIN P10]
3306	16480	29501	2.93	5.5E-01	AF227240.1	NT	Homo sapiens superkiller viral-like activity 2 (S. cerevisiae homolog) hika (SKIV2L), mRNA
3783	16944	29951	1.34	5.5E-01	P48755	SWISSPROT	yo18a10.s1 Soares adult brain N2b5-1B55Y Homo sapiens cDNA clone IMAGE:176266 3'
6249	18370		1	5.5E-01	AF063866.1	NT	Rabbit oral papillomavirus, complete genome
5269	18388	31356	1.01	5.5E-01	U69097.1	NT	FOS-RELATED ANTIGEN-1
							Melanoplus sanguinolpes entomopoxvirus, complete genome
							Bos taurus MHC class II beta-chain BOLA-DIB1 gene, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7405	20483	33950	0.59	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
7405	20483	33951	0.59	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
7439	20516		0.74	5.5E-01	AB015596.1	NT	Carassius auratus gene for gonadotropin II beta subunit, complete cds
8678	21756	35291	0.47	5.5E-01	BE163243.1	EST_HUMAN	QV3-HT0458-170200-090-505 HT0458 Homo sapiens cDNA
9989	23008		0.56	5.5E-01	U88415.1	NT	Crimean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10588	23823	37230	0.83	5.5E-01	T05047.1	EST_HUMAN	EST02935 Fetal brain, Stralagene (calf838206) Homo sapiens cDNA clone HFBCC35
11406	24467	38132	1.64	5.5E-01	BF129507.1	EST_HUMAN	50181107R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3'
147	13372	26404	8.11	5.4E-01	7657268	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
147	13372	26405	8.11	6.4E-01	7657268	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
598	13788	26808	1.01	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
598	13788	26809	1.01	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
1300	14456	27522	2.21	5.4E-01	AW896087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2173	15308		2.8	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 94 of the complete genome
2329	15461	28594	2.82	5.4E-01	AJ276682.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
5774	18988	32269	0.88	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6320	19492	32850	0.93	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
7170	20303	33746	0.77	5.4E-01	BE066692.2	EST_HUMAN	601660276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906030 3'
7480	20566	34035	1.96	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7480	20566	34036	1.96	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7482	20567	34039	1.47	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE : LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
10195	23232		2.69	5.4E-01	BF572536.1	EST_HUMAN	602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
11334	24367	38046	2.68	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11920	24906	38607	2.76	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11920	24906	38608	2.76	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12039	19492	32850	1.3	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
12217	25168		2.41	5.4E-01	AB58398.1	EST_HUMAN	w37g04.x1 NCL_CGAP_UH Homo sapiens cDNA clone IMAGE:2427128 3' similar to gb:M13452 LAMIN A (HUMAN);
529	13722	26748	2.12	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (BF), and complement component C2 (C2) genes;>
2843	15957	29065	8.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2843	15957	29066	8.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3315	16488	28508	3.8	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (SLC) gene, complete cds
4327	17470		1.2	5.3E-01	U39687.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5574	18770	31813	1.55	5.3E-01	AB20921.1	EST_HUMAN	z442h12.y5 Soares ovary tumor NkH0T Homo sapiens cDNA clone IMAGE:740711 5'
5574	18770	31814	1.55	5.3E-01	AB20921.1	EST_HUMAN	z442h12.y5 Soares ovary tumor NkH0T Homo sapiens cDNA clone IMAGE:740711 5'
5671	18866	32150	0.95	5.3E-01	AA193672.1	EST_HUMAN	z42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5671	18865	32151	0.95	5.3E-01	AA193672.1	EST_HUMAN	z42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5762	18954	32257	2.32	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5762	18954	32258	2.32	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9105	22184		1.59	5.3E-01	L01950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast gene for chloroplast product
9156	22234	35779	0.76	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element;
9156	22234	35780	0.76	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element;
10416	23451	37056	0.65	5.3E-01	AB54210.1	EST_HUMAN	w84b02.x1 NCL_CGAP_Mat15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
11857	24845	38542	5.83	5.3E-01	BE566291.1	EST_HUMAN	601339867.F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
12145	25958		1.73	5.3E-01	AA018053.1	EST_HUMAN	cg30cd5.s1 NCL_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611 APOLIPOPROTEIN D PRECURSOR (HUMAN);
839	14017	27072	20.65	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1190	14352	27410	7.57	5.2E-01	Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)
1218	14378	27438	3.05	5.2E-01	AF224492.1	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1935	15078		3.88	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
							Homo sapiens chromosome 21 segment HS21C085

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2213	16347	28476	2.85	5.2E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3189	16364	29369	2.1	5.2E-01	U65942.1	NT	Chlamydia abortus strain S293 POMF90A and POMF90A precursor, genes, complete cds
3309	18483		1.05	5.2E-01	D73443.1	NT	Azobacter vinelandii tcd gene for isocitrate dehydrogenase, complete cds
3491	16658		1.61	5.2E-01	AL116780.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3530	16895	29708	2.01	5.2E-01	AA084165.1	EST_HUMAN	am7705.s1 Strabagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3722	16888		0.77	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
3724	16885	29891	0.87	5.2E-01	U82671.2	NT	Homo sapiens chromosome Xc28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
4729	17984	30848	0.61	5.2E-01		NT	Mus musculus acetylcholine receptor beta (Acrb), mRNA
5770	18982	32263	0.92	5.2E-01	AA284261.1	EST_HUMAN	zc4409.T7 Soares_senescent_fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:325169 3'
9932	25952	36562	0.87	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9932	25962	36563	0.87	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10136	23174	36772	0.49	5.2E-01	AA194518.1	EST_HUMAN	zq05009.r1 Strabagene muscle 937209 Homo sapiens cDNA clone IMAGE:628793 5'
10233	23268	36858	1.32	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
13128	25736		4.83	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
632	13817	26841	2.5	5.1E-01	M58509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
665	13851	26878	4.57	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
665	13851	26879	4.57	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
1684	14836		1.02	5.1E-01	X87985.1	NT	R. norvegicus mRNA for mammalian fusca protein
4188	17338	30331	3.87	5.1E-01	AB59495.1	EST_HUMAN	w339612x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2427263 3'
4303	17448	30432	2.89	5.1E-01	P98380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5179	18301		0.6	5.1E-01	BE091796.1	EST_HUMAN	IL2-BTD731-250400-077-G08 BT0731 Homo sapiens cDNA
6352	19522	32879	1	5.1E-01	BE541088.1	EST_HUMAN	601063606F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
6406	19575		0.9	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAF07 5'
7057	20110	33526	1.35	5.1E-01	R80873.1	EST_HUMAN	y94a09.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:148872 3'
8770	21949	35389	0.84	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
8770	21949	35390	0.84	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
9896	22926	36510	4.65	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
9899	22929	36513	3.95	5.1E-01	W22302.1	EST_HUMAN	6551 Human retina cDNA Tsp509-cleaved sublibrary Homo sapiens cDNA not directional
10363	23398	37009	0.99	5.1E-01	M94579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12368	25874		3.49	5.1E-01	BF030207.1	EST_HUMAN	601566863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12634	25427		1.31	5.1E-01	BF439982.1	EST_HUMAN	nc5110.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element:
2203	15338	28464	1.85	5.0E-01	4885552	NT	Homo sapiens postmitotic segregation increased 2-like 9 (PMS2L9), mRNA
2203	15338	28465	1.65	5.0E-01	4885552	NT	Homo sapiens postmitotic segregation increased 2-like 9 (PMS2L9), mRNA
2211	15345	28472	2.09	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEF), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2211	15345	28473	2.09	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEF), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2231	15365		1.56	5.0E-01	AL161533.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33
3842	17001	30004	0.85	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3934	17093	30091	0.93	5.0E-01	L38483.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3971	17134	30137	2.67	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6782	19937		0.82	5.0E-01	BF576199.1	EST_HUMAN	602132842F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271939 5'
7842	20897	34398	0.84	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7842	20897	34399	0.84	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8727	21807		1.63	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8870	21949	35484	0.66	5.0E-01	BF107948.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9657	21100	34613	2.13	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
9824	22864	36445	1.47	5.0E-01	P35573	SWISSPROT	GLYCAGEN DEBRANCHING ENZYME (GLYCAGEN DEBRANCHER) [INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCAN TRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9824	22864	36446	1.47	5.0E-01	P35573	SWISSPROT	GLYCAGEN DEBRANCHING ENZYME (GLYCAGEN DEBRANCHER) [INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCAN TRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10802	23637		1.23	5.0E-01	BE869218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5'
12307	25225		3.64	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
13093	25713		2.25	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
13109	25724		4.71	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
812	13991	27045	1.83	4.9E-01	BF571462.1	EST_HUMAN	602078949F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4243860 5'
1692	14844	27928	1.08	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1955	15098	28198	1.34	4.9E-01	U40969.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5522	18719	31735	1.17	4.9E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6161	18337	32882	2.67	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6161	18337	32883	2.67	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7610	20680	34156	1.91	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7882	20934	34439	0.86	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
7882	20934	34440	0.86	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
9190	22268		1.96	4.9E-01	BF209781.1	EST_HUMAN	601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'
9389	22464	36028					hc90c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907266 3' similar to TR:O95714
9496	26228		0.96	4.9E-01	AW339805.1	EST_HUMAN	C95714 HERC2.
10524	23559	37166	2.2	4.9E-01	10946863	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
12187	26154		1.05	4.9E-01	AF053980.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
13085	26174		2.61	4.9E-01	AF176912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
13084	25714	31939	4.94	4.9E-01	AA613562.1	EST_HUMAN	nc22e11.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1144652 3'
13181	25768		1.69	4.9E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
			1.27	4.9E-01	11431438	NT	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
4452	17592		0.59	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5624	18818	31892	9.66	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6817	19970	33378	0.89	4.8E-01	U92882.1	NT	Mus musculus slow skeletal muscle troponin T (Ttn1) gene, complete cds
6827	19980		4.18	4.8E-01	AA658878.1	EST_HUMAN	nu85f09.e1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
7469	20544		1.83	4.8E-01	5031650	NT	Homo sapiens reproduction 8 (DRS2288E) mRNA
7845	20900	34403	1.06	4.8E-01	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7938	20988	34497	3.59	4.8E-01	AL161462.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7938	20988	34498	3.59	4.8E-01	AL161462.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
							Y77110.Y5 Soares breast 2NHBst Homo sapiens cDNA clone IMAGE:154785 5' similar to contains element MER6 repetitive element.
8089	21171	34686	1.81	4.8E-01	AI820744.1	EST_HUMAN	
9446	22562		1.05	4.8E-01	BE155148.1	EST_HUMAN	PM1-HT0350-201289-004-604 HT0360 Homo sapiens cDNA
10212	23248		0.55	4.8E-01	BF568633.1	EST_HUMAN	602184267F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
10966	24047		1.9	4.8E-01	X89502.1	NT	S. cerevisiae ORF's from chromosome X
12279	25208		1.56	4.8E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12309	25918		5.78	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
3142	16318		0.59	4.7E-01	AF192387.1	NT	Felis catus feline leukemia virus subgroup C receptor (FLVCR1) mRNA, complete cds
6844	18803	33190	8.07	4.7E-01	BF217173.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
7186	20051	33461	0.84	4.7E-01	AI204374.1	EST_HUMAN	qf72a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8049	21132	34652	0.75	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
8049	21132	34653	0.75	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
9276	22352	35904	0.61	4.7E-01	6981501	NT	Rafus norvegicus Spemline binding protein (Sbp), mRNA
11084	24158		4.37	4.7E-01	AF102673.1	NT	Influenza A virus isolate hk51697 hemagglutinin (HA) gene, partial cds
11340	24403	38052	1.94	4.7E-01	U41069.1	NT	Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 16, and partial cds
11658	24737	38428	1.45	4.7E-01	AW889448.1	EST_HUMAN	RC8-NT0028-240400-011-E08 NT0029 Homo sapiens cDNA
12401	25281		1.84	4.7E-01	BE887763.1	EST_HUMAN	601511333F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3912488 5'
12529	25361		1.25	4.7E-01	AW341561.1	EST_HUMAN	hd11c08.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2909198 3'
3837	16997	29699	1.62	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4245481 5'
3837	16997	30000	1.62	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4245481 5'
5535	18732	31747	0.93	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4128472 5'
5535	18732	31748	0.93	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4128472 5'
5588	18783	31828	3.52	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5588	18783	31829	3.52	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5663	18957	32140	1.84	4.6E-01	BE734781.1	EST_HUMAN	601568755F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3843637 5'
5677	18971	32157	3.62	4.6E-01	A1247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR-O15338 O15338 BUTYROPHILIN.1
5677	18971	32158	3.62	4.6E-01	A1247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR-O15338 O15338 BUTYROPHILIN.1
5685	18879	32159	1.44	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5763	18955		0.85	4.6E-01	AF212124.1	NT	Anolis schwartzi cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5850	19040		0.9	4.6E-01	BE817247.1	EST_HUMAN	PMO-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
6386	19555	32914	0.82	4.6E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of the complete genome
6906	20221	33649	2.39	4.6E-01	U62332.1	NT	Emmericella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6906	20221	33650	2.39	4.6E-01	U62332.1	NT	Emmericella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7379	25843	33920	0.66	4.6E-01	L07320.1	NT	Murine cytomegalovirus ef1 protein gene, complete cds
7906	20658	34464	0.78	4.6E-01	AA493577.1	EST_HUMAN	h04405.s1 NC1_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943363 similar to contains Alu repetitive element; contains element L1 repetitive element
8515	21698	35131	14.55	4.6E-01	BF697399.1	EST_HUMAN	602130953F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4287828 5'
8946	22025	35565	0.54	4.6E-01	AA932237.1	EST_HUMAN	cc76p08.s1 NC1_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8948	22025	35583	0.54	4.8E-01	AA832237.1	EST_HUMAN	cc76b08.s1 NC1_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M88341 ADP- RIBOSYLATION FACTOR 4 (HUMAN);
9501	22557	36120	0.93	4.8E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9501	22557	36121	0.93	4.8E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9866	22906	36490	0.52	4.8E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product;
9866	22906	36491	0.52	4.8E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
10181	23218	36809	1.15	4.8E-01	AI915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
10181	23218	36810	1.15	4.8E-01	AI915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
11238	24307		2.31	4.8E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
11248	24317	37958	5.06	4.8E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11248	24317	37957	5.06	4.8E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11760	23946	37573	4.3	4.8E-01	AF019369.1	NT	Human thiolpurine methyltransferase (TPMT) gene, exon 10 and complete cds
11760	23946	37574	4.3	4.8E-01	AF019369.1	NT	Human thiolpurine methyltransferase (TPMT) gene, exon 10 and complete cds
1960	15103	28203	1.15	4.5E-01	AE001931.1	NT	Dainococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1960	15103	28204	1.15	4.5E-01	AE001931.1	NT	Dainococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2633	16110	29124	4.83	4.5E-01	AA877086.1	EST_HUMAN	455d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3380	16552	29565	0.66	4.5E-01	AW083761.1	EST_HUMAN	xc25c06.x1 NC1_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2585290 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
3380	16552	29566	0.66	4.5E-01	AW083761.1	EST_HUMAN	xc25c06.x1 NC1_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2585290 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
3393	16563	29578	4.46	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3465	16532	29651	1.51	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4139	17291		1.18	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pde) gene, exons 2 through 12
4186	17386	30329	1.02	4.5E-01	AI708908.1	EST_HUMAN	COLLAGEN ALPHA 5(V) CHAIN
4292	18476		4.71	4.5E-01	AW873495.1	EST_HUMAN	as96a09.x1 Barslead_aorta_HPLR36 Homo sapiens cDNA clone IMAGE:2353480 3'
5058	18186	31181	1.18	4.5E-01	BE963445.2	EST_HUMAN	h66g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
5668	18860	32145	1.57	4.5E-01	AW608814.1	EST_HUMAN	601657228R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
6740	19896		1.38	4.5E-01	Q00956	SWISSPROT	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA COAT PROTEIN
7571	20643	34120	0.91	4.5E-01	U37038.1	NT	Rat nuclear proteins B23.1 and B23.2

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7765	20841	34333	2.39	4.5E-01	A1858849.1	EST_HUMAN	w32602.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
8502	21583		1.11	4.5E-01	M32661.1	NT	SWISNF COMPLEX 170 KDA SUBUNIT ; D.melanogaster Shaw2 protein mRNA, complete cds
8598	21679	35217	2.87	4.5E-01	A1848596.1	EST_HUMAN	1250q11.x1 NCL CGAP_Ov055 Homo sapiens cDNA clone IMAGE:2292644 3'
8756	21835	35376	0.85	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
9200	22278	35817	2.36	4.5E-01	11444786	NT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
10145	23183		0.96	4.5E-01	9630816	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
10713	23746	37352	25.59	4.5E-01	M80006.1	EST_HUMAN	Bombyx mori nuclear polyhedrosis virus, complete genome
10713	23746	37353	25.59	4.5E-01	M80006.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
11104	24176	37812	2.52	4.5E-01	AW591271.1	EST_HUMAN	EST02631 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
11225	24294	37835	2.16	4.5E-01	11430799	NT	xc14h01.x1 NCL CGAP_U18 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:JNT8_MOUSE
11530	24586		1.3	4.5E-01	AV719382.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1]
12164	26162		5.58	4.5E-01	BE871461.1	EST_HUMAN	Homo sapiens cadherin 3, P-cadherin (placental) (CDH3), mRNA
12895	25592		1.2	4.5E-01	BF337531.1	EST_HUMAN	AV719382 GLC Homo sapiens cDNA clone GLCCED12 5'
12970	25630		12.42	4.5E-01	11422089	NT	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
2094	15234		1.11	4.5E-01	6680503	NT	602035275F1 NCL CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183280 5'
2462	15589	28715	4.16	4.5E-01	P49765	SWISSPROT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
3390	16560	29575	1.54	4.5E-01	AF058790.1	NT	Mus musculus integral membrane-associated protein 1 (Itmap1), mRNA
3390	16560	29576	1.54	4.5E-01	AF058790.1	NT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3395	16565	29580	2.12	4.5E-01	BF058726.1	EST_HUMAN	Rattus norvegicus SynGAP-b mRNA, complete cds
4349	17492		1.35	4.5E-01	BE378707.1	EST_HUMAN	Rattus norvegicus SynGAP-b mRNA, complete cds
5536	18733	31749	1.31	4.5E-01	P04929	SWISSPROT	791402.Y1 NCL CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
5536	18733	31750	1.31	4.5E-01	P04929	SWISSPROT	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
5805	18995	32300	1.58	4.5E-01	S65019.1	NT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5823	19013	32319	1.81	4.5E-01	AV720408.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
6074	19266	32584	1.12	4.5E-01	AI198413.1	EST_HUMAN	much [fate, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt] AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5'
							q62h11.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6074	19256	32585	1.12	4.4E-01	AI198413.1	EST_HUMAN	q82h11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN :
6370	19639	32899	1.67	4.4E-01	AW080795.1	EST_HUMAN	xe27e08.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:O95154 O95154 AFLATOXIN B1-ALDEHYDE REDUCTASE :
6458	19625		1.05	4.4E-01	AA778132.1	EST_HUMAN	ae85d11.s1 Strategene schizo birth S11 Homo sapiens cDNA clone IMAGE:970965 3' similar to gb:M16038 TYROSINE-PROTEIN KINASE LYN (HUMAN):
7567	20629	34104	1.14	4.4E-01	AE000571.1	NT	Helicobacter pylori 26695 section 49 of 134 of the complete genome
8024	21107		12.3	4.4E-01	Z11679.1	NT	S.tuberosum mRNA for induced stolon tip protein (partial)
8962	22041	35584	1.11	4.4E-01	AA056427.1	EST_HUMAN	z69a03.s1 Strategene colon (#937204) Homo sapiens cDNA clone IMAGE:509836 3' HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds
9352	22427	35985	0.78	4.4E-01	AF112540.1	NT	h105c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to SW_MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 :
9385	22460	36023	0.62	4.4E-01	AW612578.1	EST_HUMAN	ZINC FINGER X-CHROMOSOMAL PROTEIN
9490	22547	36110	1.13	4.4E-01	O62836	SWISSPROT	LYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10167	23204	36798	1.85	4.4E-01	AI268650.1	EST_HUMAN	q639f09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
10168	23205		2.09	4.4E-01	P28922	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10302	23337	36942	4.84	4.4E-01	P35590	SWISSPROT	beta -HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 1 of 2]
10585	23620	37227	1.76	4.4E-01	S76404.1	NT	beta -HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10585	23620	37227	1.76	4.4E-01	S76404.1	NT	ACETYLCHOLINE RECEPTOR PROTEIN, DELTA CHAIN PRECURSOR
10929	23862	37486	0.46	4.4E-01	P02716	SWISSPROT	Terebratulina retusa mitochondrion, complete genome
11522	24578	38256	1.64	4.4E-01		6691408	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12435	25308	32087	4.23	4.4E-01		6677874	Homo sapiens chromosome 21 segment HS21C082
12447	26084		13.47	4.4E-01	AL163282.2	NT	UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG A (HHR23A)
13051	25689		1.41	4.4E-01	P54725	SWISSPROT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
424	13619	26659	2.42	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
424	13619	26660	2.42	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
1933	14785	27871	1.11	4.3E-01	AW868550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
2935	16112		1.34	4.3E-01	AW868550.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3127	16303	28316	0.95	4.3E-01	AW999477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4526	13619	26659	1.27	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4526	13619	26660	1.27	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5071	18199		1.04	4.3E-01	AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5220	18342		0.94	4.3E-01	6635250	NT	Xestia c-nigrum granulovirus, complete genome
5480	18679	31683	0.95	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5480	18679	31694	0.95	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6009	19194	32512	1.31	4.3E-01	BE181665.1	EST_HUMAN	QV1-HT0638-070500-191-c08 HT0638 Homo sapiens cDNA
6027	19210	32530	1.99	4.3E-01	AF179825.1	NT	Salmonella enterica subsp. enterica serovar Enteritidis (SSC186) gene, partial cds
6847	20000	33408	3.1	4.3E-01	AJ001678.1	NT	Coliform coliform japonica tfrG gene
6825	20240	33675	0.67	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
7005	20141		0.77	4.3E-01	Q33367	SWISSPROT	DNA GYRASE SUBUNIT B
7586	20558		1.28	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCJ_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158296 5'
8622	21702		3.15	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-1 (flaC-fla) genes, complete cds
9455	22671	36137	1.02	4.3E-01	Y14604.1	NT	Erwinia amylovora rcsV gene
9928	22968	36556	2.36	4.3E-01	AW630048.1	EST_HUMAN	h174e10.y1 NCJ_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868554 5'
9928	22968	36557	2.36	4.3E-01	AW630048.1	EST_HUMAN	h174e10.y1 NCJ_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868554 5'
10433	23468	37075	0.99	4.3E-01	AW170559.1	EST_HUMAN	TR-000189 000189 MU-ADAPTIN-RELATED PROTEIN 2 ;
11172	20240	33675	2.27	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
13162	25754		1.56	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whiH gene
1389	16036	27618	1.17	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
2002	15143		1.02	4.2E-01	AA761653.1	EST_HUMAN	n224a09.s1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288696 3'
3697	16858	29862	4.1	4.2E-01	AE003947.1	NT	Xyella fastidiosa, section 93 of 229 of the complete genome
3727	16868	29892	1.09	4.2E-01	A1260338.1	EST_HUMAN	q194b01.x1 Soares_NHHMPU_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3803	18477		0.73	4.2E-01	NB1203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07878, Z40493
3984	17141	30146	0.74	4.2E-01	AW835527.1	EST_HUMAN	QV0-L10015-180200-127-h01 LT0015 Homo sapiens cDNA
4819	17952	30837	2.57	4.2E-01	AA594093.1	EST_HUMAN	h199h01.s1 NCJ_CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gbM33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4903	18033	31022	3.8	4.2E-01	R13467.1	EST_HUMAN	y177e01.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5832	19023	32330	1.42	4.2E-01	BF242055.1	EST_HUMAN	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
5901	19090	32404	1.63	4.2E-01	AW854162.1	EST_HUMAN	RC3-CT0254-060400-029-q04 CT0254 Homo sapiens cDNA
6334	19505	32863	0.99	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7090	20184	33608	8.72	4.2E-01	AU168472.1	EST_HUMAN	AU168472 PLAGE2 Homo sapiens cDNA clone PLACE2000470 3'
7090	20184	33609	8.72	4.2E-01	AU168472.1	EST_HUMAN	AU168472 PLAGE2 Homo sapiens cDNA clone PLACE2000470 3'
7151	25839	33727	3.21	4.2E-01	S82504.1	NT	Bcr1=breast cancer gene [rats, WF, spleen, Genomic, 418 nt, segment 2 of 2]
7242	20326	33770	6.61	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7745	20805	34294	0.81	4.2E-01	AL182352.2	NT	Homo sapiens chromosome 21 segment HS21C052
8182	21264	34786	4.01	4.2E-01	AW857448.1	EST_HUMAN	EST369413 IMAGE resequenced, IMAGE Homo sapiens cDNA
8182	21264	34787	4.01	4.2E-01	AW857448.1	EST_HUMAN	EST369413 IMAGE resequenced, IMAGE Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8401	21482	35010	0.72	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit Vlc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
9511	22578	36141	0.51	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
9511	22578	36142	0.51	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
10175	23212		0.81	4.2E-01	AA705007.1	EST_HUMAN	zfp501 s1 Soares fetal liver spleen 1NLS_S1 Homo sapiens cDNA clone IMAGE:462849 3'
10714	23747	37354	1.44	4.2E-01	AW65666.1	EST_HUMAN	MF3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA
11298	24364	38005	1.43	4.2E-01	AB023489.1	NT	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
11879	24678	38368	1.87	4.2E-01	BE966485.2	EST_HUMAN	601600352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
1118	14283	27338	2.11	4.1E-01	AB05481.1	EST_HUMAN	RC-BT091-210199-142 BT091 Homo sapiens cDNA
1127	14292	27347	1.46	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1127	14292	27348	1.46	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1640	14792	27877	1.77	4.1E-01	AB05949.1	EST_HUMAN	PM-BT103-270499-884 BT103 Homo sapiens cDNA
2775	15890	29001	1.46	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
3006	16181	29202	2.12	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3006	16181	29203	2.12	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3375	16547	29561	0.66	4.1E-01	AA906344.1	EST_HUMAN	q94b08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3871	17030	30028	0.73	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGG Homo sapiens cDNA
3871	17030	30029	0.73	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGG Homo sapiens cDNA
4389	17532	30513	3.78	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 IsoG, IsoH, IsoI, IsoJ, IsoK, IsoL, IsoM, IsoN, IsoO, IsoP, IsoQ, IsoR, IsoS, IsoT, IsoU, IsoV, IsoW, IsoX, IsoY, IsoZ, IsoAA, IsoAB, IsoAC, IsoAD, IsoAE, IsoAF, IsoAG, IsoAH, IsoAI, IsoAJ, IsoAK, IsoAL, IsoAM, IsoAN, IsoAO, IsoAP, IsoAQ, IsoAR, IsoAS, IsoAT, IsoAU, IsoAV, IsoAW, IsoAX, IsoAY, IsoAZ, IsoBA, IsoBB, IsoBC, IsoBD, IsoBE, IsoBF, IsoBG, IsoBH, IsoBI, IsoBJ, IsoBK, IsoBL, IsoBM, IsoBN, IsoBO, IsoBP, IsoBQ, IsoBR, IsoBS, IsoBT, IsoBU, IsoBV, IsoBW, IsoBX, IsoBY, IsoBZ, IsoCA, IsoCB, IsoCC, IsoCD, IsoCE, IsoCF, IsoCG, IsoCH, IsoCI, IsoCJ, IsoCK, IsoCL, IsoCM, IsoCN, IsoCO, IsoCP, IsoCQ, IsoCR, IsoCS, IsoCT, IsoCU, IsoCV, IsoCW, IsoCX, IsoCY, IsoCZ, IsoDA, IsoDB, IsoDC, IsoDD, IsoDE, IsoDF, IsoDG, IsoDH, IsoDI, IsoDJ, IsoDK, IsoDL, IsoDM, IsoDN, IsoDO, IsoDP, IsoDQ, IsoDR, IsoDS, IsoDT, IsoDU, IsoDV, IsoDW, IsoDX, IsoDY, IsoDZ, IsoEA, IsoEB, IsoEC, IsoED, IsoEE, IsoEF, IsoEG, IsoEH, IsoEI, IsoEJ, IsoEK, IsoEL, IsoEM, IsoEN, IsoEO, IsoEP, IsoEQ, IsoER, IsoES, IsoET, IsoEU, IsoEV, IsoEW, IsoEX, IsoEY, IsoEZ, IsoFA, IsoFB, IsoFC, IsoFD, IsoFE, IsoFF, IsoFG, IsoFH, IsoFI, IsoFJ, IsoFK, IsoFL, IsoFM, IsoFN, IsoFO, IsoFP, IsoFQ, IsoFR, IsoFS, IsoFT, IsoFU, IsoFV, IsoFW, IsoFX, IsoFY, IsoFZ, IsoGA, IsoGB, IsoGC, IsoGD, IsoGE, IsoGF, IsoGG, IsoGH, IsoGI, IsoGJ, IsoGK, IsoGL, IsoGM, IsoGN, IsoGO, IsoGP, IsoGQ, IsoGR, IsoGS, IsoGT, IsoGU, IsoGV, IsoGW, IsoGX, IsoGY, IsoGZ, IsoHA, IsoHB, IsoHC, IsoHD, IsoHE, IsoHF, IsoHG, IsoHH, IsoHI, IsoHJ, IsoHK, IsoHL, IsoHM, IsoHN, IsoHO, IsoHP, IsoHQ, IsoHR, IsoHS, IsoHT, IsoHU, IsoHV, IsoHW, IsoHX, IsoHY, IsoHZ, IsoIA, IsoIB, IsoIC, IsoID, IsoIE, IsoIF, IsoIG, IsoIH, IsoII, IsoIJ, IsoIK, IsoIL, IsoIM, IsoIN, IsoIO, IsoIP, IsoIQ, IsoIR, IsoIS, IsoIT, IsoIU, IsoIV, IsoIW, IsoIX, IsoIY, IsoIZ, IsoJA, IsoJB, IsoJC, IsoJD, IsoJE, IsoJF, IsoJG, IsoJH, IsoJI, IsoJJ, IsoJK, IsoJL, IsoJM, IsoJN, IsoJO, IsoJP, IsoJQ, IsoJR, IsoJS, IsoJT, IsoJU, IsoJV, IsoJW, IsoJX, IsoJY, IsoJZ, IsoKA, IsoKB, IsoKC, IsoKD, IsoKE, IsoKF, IsoKG, IsoKH, IsoKI, IsoKJ, IsoKL, IsoKM, IsoKN, IsoKO, IsoKP, IsoKQ, IsoKR, IsoKS, IsoKT, IsoKU, IsoKV, IsoKW, IsoKX, IsoKY, IsoKZ, IsoLA, IsoLB, IsoLC, IsoLD, IsoLE, IsoLF, IsoLG, IsoLH, IsoLI, IsoLJ, IsoLK, IsoLL, IsoLM, IsoLN, IsoLO, IsoLP, IsoLQ, IsoLR, IsoLS, IsoLT, IsoLU, IsoLV, IsoLW, IsoLX, IsoLY, IsoLZ, IsoMA, IsoMB, IsoMC, IsoMD, IsoME, IsoMF, IsoMG, IsoMH, IsoMI, IsoMJ, IsoMK, IsoML, IsoMN, IsoMO, IsoMP, IsoMQ, IsoMR, IsoMS, IsoMT, IsoMU, IsoMV, IsoMW, IsoMX, IsoMY, IsoMZ, IsoNA, IsoNB, IsoNC, IsoND, IsoNE, IsoNF, IsoNG, IsoNH, IsoNI, IsoNJ, IsoNK, IsoNL, IsoNM, IsoNO, IsoNP, IsoNQ, IsoNR, IsoNS, IsoNT, IsoNU, IsoNV, IsoNW, IsoNX, IsoNY, IsoNZ, IsoOA, IsoOB, IsoOC, IsoOD, IsoOE, IsoOF, IsoOG, IsoOH, IsoOI, IsoOJ, IsoOK, IsoOL, IsoOM, IsoON, IsoOO, IsoOP, IsoOQ, IsoOR, IsoOS, IsoOT, IsoOU, IsoOV, IsoOW, IsoOX, IsoOY, IsoOZ, IsoPA, IsoPB, IsoPC, IsoPD, IsoPE, IsoPF, IsoPG, IsoPH, IsoPI, IsoPJ, IsoPK, IsoPL, IsoPM, IsoPN, IsoPO, IsoPP, IsoPQ, IsoPR, IsoPS, IsoPT, IsoPU, IsoPV, IsoPW, IsoPX, IsoPY, IsoPZ, IsoQA, IsoQB, IsoQC, IsoQD, IsoQE, IsoQF, IsoQG, IsoQH, IsoQI, IsoQJ, IsoQK, IsoQL, IsoQM, IsoQN, IsoQO, IsoQP, IsoQQ, IsoQR, IsoQS, IsoQT, IsoQU, IsoQV, IsoQW, IsoQX, IsoQY, IsoQZ, IsoRA, IsoRB, IsoRC, IsoRD, IsoRE, IsoRF, IsoRG, IsoRH, IsoRI, IsoRJ, IsoRK, IsoRL, IsoRM, IsoRN, IsoRO, IsoRP, IsoRQ, IsoRR, IsoRS, IsoRT, IsoRU, IsoRV, IsoRW, IsoRX, IsoRY, IsoRZ, IsoSA, IsoSB, IsoSC, IsoSD, IsoSE, IsoSF, IsoSG, IsoSH, IsoSI, IsoSJ, IsoSK, IsoSL, IsoSM, IsoSN, IsoSO, IsoSP, IsoSQ, IsoSR, IsoSS, IsoST, IsoSU, IsoSV, IsoSW, IsoSX, IsoSY, IsoSZ, IsoTA, IsoTB, IsoTC, IsoTD, IsoTE, IsoTF, IsoTG, IsoTH, IsoTI, IsoTJ, IsoTK, IsoTL, IsoTM, IsoTN, IsoTO, IsoTP, IsoTQ, IsoTR, IsoTS, IsoTT, IsoTU, IsoTV, IsoTW, IsoTX, IsoTY, IsoTZ, IsoUA, IsoUB, IsoUC, IsoUD, IsoUE, IsoUF, IsoUG, IsoUH, IsoUI, IsoUJ, IsoUK, IsoUL, IsoUM, IsoUN, IsoUO, IsoUP, IsoUQ, IsoUR, IsoUS, IsoUT, IsoUU, IsoUV, IsoUW, IsoUX, IsoUY, IsoUZ, IsoVA, IsoVB, IsoVC, IsoVD, IsoVE, IsoVF, IsoVG, IsoVH, IsoVI, IsoVJ, IsoVK, IsoVL, IsoVM, IsoVN, IsoVO, IsoVP, IsoVQ, IsoVR, IsoVS, IsoVT, IsoVU, IsoVV, IsoVW, IsoVX, IsoVY, IsoVZ, IsoWA, IsoWB, IsoWC, IsoWD, IsoWE, IsoWF, IsoWG, IsoWH, IsoWI, IsoWJ, IsoWK, IsoWL, IsoWM, IsoWN, IsoWO, IsoWP, IsoWQ, IsoWR, IsoWS, IsoWT, IsoWU, IsoWV, IsoWW, IsoWX, IsoWY, IsoWZ, IsoXA, IsoXB, IsoXC, IsoXD, IsoXE, IsoXF, IsoXG, IsoXH, IsoXI, IsoXJ, IsoXK, IsoXL, IsoXM, IsoXN, IsoXO, IsoXP, IsoXQ, IsoXR, IsoXS, IsoXT, IsoXU, IsoXV, IsoXW, IsoXX, IsoXY, IsoXZ, IsoYA, IsoYB, IsoYC, IsoYD, IsoYE, IsoYF, IsoYG, IsoYH, IsoYI, IsoYJ, IsoYK, IsoYL, IsoYM, IsoYN, IsoYO, IsoYP, IsoYQ, IsoYR, IsoYS, IsoYT, IsoYU, IsoYV, IsoYW, IsoYX, IsoYY, IsoYZ, IsoZA, IsoZB, IsoZC, IsoZD, IsoZE, IsoZF, IsoZG, IsoZH, IsoZI, IsoZJ, IsoZK, IsoZL, IsoZM, IsoZN, IsoZO, IsoZP, IsoZQ, IsoZR, IsoZS, IsoZT, IsoZU, IsoZV, IsoZW, IsoZX, IsoZY, IsoZZ

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11078	24153	37790	40.17	4.1E-01	X58700.1	NT	Zea mays ZMPS2 gene for 19 kDa zein protein
11075	23003	37525	1.88	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL KV1.1 (HUK) (HBK1)
12810	26139		2.33	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
13153	26169		1.24	4.1E-01	AJ131016.1	NT	Homo sapiens SCL gene locus
1084	14229	27286	1.49	4.0E-01	8404658	NT	Lactuca rubella mitochondrion, complete genome
1370	14525	27599	1.21	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1514	14667		5.48	4.0E-01	6579258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2061	18053	28318	1.08	4.0E-01	Z96933.1	NT	Ascolobus immerus masc2 gene
2061	18053	28317	1.08	4.0E-01	Z96933.1	NT	Ascolobus immerus masc2 gene
2886	13369	28402	1.11	4.0E-01	6578490	NT	Mus musculus ubiquitin-protein ligase a3 componen n-recognin (Ubr1), mRNA
3033	16209	29231	1.18	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3033	16209	29232	1.18	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Streptococcus pneumoniae Y1C (y1C), Y1D (y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3786	16947	29655	1.87	4.0E-01	AF068903.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3932	17091	30088	3.21	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3932	17091	30089	3.21	4.0E-01	AJ277511.1	NT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
4938	18088		8.59	4.0E-01	Q31849	SWISSPROT	EST382697 IMAGE resequences, MAGK Homo sapiens cDNA
6031	19214	32535	1.07	4.0E-01	AW970610.1	EST_HUMAN	STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
6568	19730	33108	0.62	4.0E-01	P27285	SWISSPROT	MR4-TN0110-180900-202-902 TN0110 Homo sapiens cDNA
8113	21195	34714	0.51	4.0E-01	BF092834.1	EST_HUMAN	Homo sapiens OCTN2 gene, complete cds
8201	21253	34806	0.73	4.0E-01	AB016625.1	NT	EST260666 Carabellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
9208	22286	35927	1.11	4.0E-01	AA323289.1	EST_HUMAN	601558283F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3828092 5'
11669	24657		1.67	4.0E-01	BF030262.1	EST_HUMAN	Synechocystis sp. PCC 9413 transposase gene, complete cds
12021	25005		2.38	4.0E-01	L76080.1	NT	Homo sapiens chromosome 21 segment HS21C100
12453	25978		2.5	4.0E-01	AL163300.2	NT	S. cerevisiae chromosome X reading frame ORF YJL026w
13027	26116		1.38	4.0E-01	Z49301.1	NT	rab84e05.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3' similar to SW/NTCR_BOVIN O18875 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 1;
13168	26036		1.21	4.0E-01	BF432020.1	EST_HUMAN	S. cerevisiae chromosome X reading frame ORF YJL026w
13222	25907		1.26	4.0E-01	Z49301.1	NT	Garilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
14059	14563	27638	1.94	3.9E-01	AF206618.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2707	15825	28940	3.34	3.9E-01	AB033019.1	NT	H. sapiens B-myb gene
2770	15855	28994	5.03	3.9E-01	X62032.1	NT	

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2770	15885	28995	5.03	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3168	18341	29349	4.24	3.9E-01	AJ225896.1	NT	Sinorhizobium meliloti ejl, syrB2, cys3 genes and orf3
4180	17340	30333	1.48	3.9E-01	BF592611.1	EST_HUMAN	787d01.x1 NCI_CGAP_Brl6 Homo sapiens cDNA clone IMAGE:3339189 3'
5108	18234	31203	1.47	3.9E-01	BE728667.1	EST_HUMAN	601563848F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833689 5'
6055	18237	32562	4.58	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
6410	19578	32940	0.64	3.9E-01	U82885.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8140	21222	34740	0.88	3.9E-01	U79415.1	NT	
9082	22141	35688	0.83	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT0105-170899-004-b08 CT0105 Homo sapiens cDNA
9071	22150		0.82	3.9E-01	BF348634.1	EST_HUMAN	602018944F1 NCI_CGAP_Brl67 Homo sapiens cDNA clone IMAGE:4155322 5'
9435	22509	36075	1.73	3.9E-01	AW186988.1	EST_HUMAN	xn86804.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:094821
9745	22809	36387	1.59	3.9E-01	A1837337.1	EST_HUMAN	Q94821 KIAA0713 PROTEIN ;
10082	23120	36722	2.88	3.9E-01	M19879.1	NT	wp78a02.x1 NCI_CGAP_Brl28 Homo sapiens cDNA clone IMAGE:2467658 3' similar to
10150	23188		0.58	3.9E-01	11465620	NT	SW_RFX5_HUMAN P48382 BINDING REGULATORY FACTOR ;
10369	23404	37016	0.82	3.9E-01	D68722.1	NT	Human clabidin 27 gene, exons 10 and 11, and L1 and Alu repeats
10562	23597	37203	0.61	3.9E-01	BF381856.1	EST_HUMAN	Pophyra purpurea mitochondrion, complete genome
10562	23597	37204	0.51	3.9E-01	BF381856.1	EST_HUMAN	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10836	23869		0.47	3.9E-01	AB037832.1	NT	CM2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
11059	24135		1.37	3.9E-01	AV695974.1	EST_HUMAN	CM2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
12049	25030	38738	1.89	3.9E-01	AV702623.1	EST_HUMAN	Homo sapiens mRNA for KIAA1411 protein, partial cds
12221	26055		4.03	3.9E-01	AF304354.1	NT	AV695974 GKC Homo sapiens cDNA clone GKCBCQ11 5'
12916	26603		1.75	3.9E-01	11433335	NT	AV702623 ADB Homo sapiens cDNA clone ADBDBE06 5'
164	13389		7.58	3.8E-01	7019488	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
618	13711		6.1	3.8E-01	AB029291.1	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
1919	15062		1.38	3.8E-01	AE003870.1	NT	Homo sapiens protein kinase PKXbeta (pkxbeta), mRNA
2637	15760	28874	1.84	3.8E-01	AF214117.1	NT	Mus musculus pom-1 mRNA for pericentriolar material-1, complete cds
2697	16069	28931	5.2	3.8E-01	6678002	NT	Xylella fastidiosa, section 16 of 229 of the complete genome
3088	18242		0.71	3.8E-01	AJ251057.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
3113	16289	29305	1.91	3.8E-01	AF043383.1	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3572	16737	29752	8.7	3.8E-01	AL181618.2	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3628	16762		1.09	3.8E-01	A1807219.1	EST_HUMAN	Pleuronectes americanus aminopeptidase N (ampN) gene, partial cds
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
							wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3643	16792		0.97	3.8E-01	AI807219.1	EST_HUMAN	w38b12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3852	17012	30012	1.07	3.8E-01	BE154080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
4027	17183	30192	0.65	3.8E-01	6754085	NT	Mus musculus general transcription factor II I (Gtf2i), mRNA
5727	18920	32214	1.11	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6469	19636		0.63	3.8E-01	S46825.1	NT	prion protein [mink, Genomic, 2446 nt]
6761	19917	33312	6.74	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271289-049-e02 BT0537 Homo sapiens cDNA
6999	20214	33644	4.39	3.8E-01	AI374601.1	EST_HUMAN	ta54f11.x1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element;
7079	20132	33549	1.38	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7885	20750		4.27	3.8E-01	XG1597.1	NT	M.musculus gene for kallikrein-binding protein
8493	21574	35111	0.54	3.8E-01	M81385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8754	21833	35373	2.04	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8826	21905	35444	1.08	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
9017	22096	35636	1.29	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9761	22699		4.35	3.8E-01	T95413.1	EST_HUMAN	ye43h06.r1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element; contains PTR5 repetitive element;
11034	24113		1.38	3.8E-01	AV755814.1	EST_HUMAN	AV755814 BM Homo sapiens cDNA clone BMFBCE07 5'
11659	24696	36388	1.57	3.8E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
11824	24813		2.87	3.8E-01	BE719219.1	EST_HUMAN	RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
11992	24977	38681	2.5	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
11992	24977	38682	2.5	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
12436	25309		2.61	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12569	26082		2	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12695	25463		1.71	3.8E-01	BE829256.1	EST_HUMAN	QV3-ET0063-190700-271-q05 ET0063 Homo sapiens cDNA
13106	25720		1.48	3.8E-01	U78031.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
13188	25772	31933	1.78	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2551	15678	28789	12.91	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3549	16714	29726	10.67	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3974	17131	30135	1.09	3.7E-01	AA319482.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end
4344	17487	30470	9.09	3.7E-01	AI218707.1	EST_HUMAN	ok39c07.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4440	17580	30559	1.31	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4509	17648	30636	2.91	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 208 of the complete genome

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5280	18399	31368	0.74	3.7E-01	T12298.1	EST_HUMAN	A033R Heart Homo sapiens cDNA clone A033
5280	18399	31369	0.74	3.7E-01	T12298.1	EST_HUMAN	A033R Heart Homo sapiens cDNA clone A033
5883	19072	32380	1.27	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6071	19253	32582	1.25	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS210078
6839	19798	33187	0.7	3.7E-01	M10806.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6660	19819		0.8	3.7E-01	L10353.1	NT	Mus sedocia heptoglobin mRNA, complete cds
7283	20375	33832	3.48	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7965	21015	34527	0.69	3.7E-01	T66802.1	EST_HUMAN	yab5a07.3 Soares fetal liver spleen TNF- α Homo sapiens cDNA clone IMAGE:66324 5'
8524	21605	35143	1.98	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8524	21605	35144	1.96	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8560	21641	35180	0.68	3.7E-01	AA902912.1	EST_HUMAN	ok43b1.1 st NCI_CGAP_La2 Homo sapiens cDNA clone IMAGE:1518701 3'
9402	22476		1.34	3.7E-01	AJ271396.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (PCDO gene)
10373	23408		0.5	3.7E-01	K00691.1	NT	mouse ig gamma alpha membrane exon region
10414	23449	37054	4.21	3.7E-01	A133641.1	EST_HUMAN	q146507.x1 Soares fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:1950997 3'
10783	23816	37437	0.46	3.7E-01	U08381.1	NT	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds
10783	23816	37438	0.46	3.7E-01	U08381.1	NT	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds
11097	24170	37805	1.8	3.7E-01	X05998.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
11285	24351	37989	2.02	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11285	24351	37990	2.02	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11754	23940	37568	2.73	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.31)
12004	24989		1.42	3.7E-01	AA973640.1	EST_HUMAN	004603 st NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569221 3' similar to gb:M77698
12066	25047		3.5	3.7E-01	6677678	NT	TRANSCRIPTIONAL REPRESSOR-PROTEIN YY1 (HUMAN);
12137	25654		1.17	3.7E-01	J04982.1	NT	Mus musculus rethroblastoma 1 (Rb1), mRNA
12314	25229		3.94	3.7E-01	AJ243525.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
12410	25289		1.82	3.7E-01	D86976.1	NT	Chlamydomonas reinhardtii psIIa1 partial cnp1 gene for outer membrane protein 1
12821	25549		2.94	3.7E-01	AL121184.1	EST_HUMAN	Human mRNA for KIAA0223 gene, partial cds
12902	25597	31971	6.99	3.7E-01	Y18000.1	NT	DKFZp782K075.t1 782 (synonym: hmel2) Homo sapiens cDNA clone DKFZp782K075 5'
271	13489	26520	0.77	3.6E-01	AJ009609.1	NT	Homo sapiens NF2 gene
1020	14191		9.07	3.6E-01	U89241.1	NT	Breast cancer mRNA for MAP4K alpha2 protein
1342	14498	27570	3.97	3.6E-01	T80255.1	EST_HUMAN	Human mbp gene, partial cds
1342	14498	27571	3.97	3.6E-01	T80255.1	EST_HUMAN	Human mbp gene, partial cds
1966	15109	28209	6.55	3.6E-01	AW590184.1	EST_HUMAN	y03605.t1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1966	15109	28210	6.55	3.6E-01	AW590184.1	EST_HUMAN	y03605.t1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
							hg3302.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2847419 3'
							hg3302.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2847419 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2007	15147	28253	5.7	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2113	15251		1.15	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2343	15474		2.33	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2453	15590		2.8	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for sc1n
2536	15681	26806	2.66	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-161099-011-q07 ST0171 Homo sapiens cDNA
							PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L- ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2694	15814	28929	1.69	3.6E-01	P24206	SWISSPROT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
2984	16475		8.47	3.6E-01	AF199485.1	NT	H. sapiens serotonins transporter gene, exons 9 and 10
3558	16723	29738	1.98	3.6E-01	X76758.1	NT	H. sapiens serotonins transporter gene, exons 9 and 10
3558	16723	29739	1.98	3.6E-01	X76758.1	NT	H. sapiens serotonins transporter gene, exons 9 and 10
4528	17663	30652	1.2	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4863	17963	30981	0.69	3.6E-01	AJ009608.1	NT	Brassica napus mRNA for MAPK alpha2 protein
5123	18249	31215	3.18	3.6E-01	AW339393.1	EST_HUMAN	h02g04.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5209	18330	31302	0.92	3.6E-01	BE087699.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
5498	18697	31713	0.64	3.6E-01	AJ006565.1	NT	Homo sapiens lipo gene intron 5
							FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6211	19386	32735	0.96	3.6E-01	P16431	SWISSPROT	Homo sapiens PHEX gene
6607	19767	33156	1.63	3.6E-01	Y10196.1	NT	y174a06.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:275987 5'
7298	20380		3.85	3.6E-01	R94090.1	EST_HUMAN	w172c10.x1 Soares thymus_NHFTb Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
7435	20512	33985	1.52	3.6E-01	AW027174.1	EST_HUMAN	O15117 FYN BINDING PROTEIN [1];
8419	21500	35032	0.75	3.6E-01	P98167	SWISSPROT	SCO-SPONDIN
8474	21555	35087	16.45	3.6E-01	AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9179	22257	35799	0.48	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9179	22257	35800	0.48	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9203	22261	35820	3.04	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9203	22261	35821	3.04	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9393	22468	36032	1.23	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9599	22654	36225	1.13	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9599	22654	36228	1.13	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9693	22631		0.58	3.6E-01	X62825.1	NT	C. perfingens plc gene for phospholipase C upstream region containing bent DNA fragment
10067	23105	36708	16.64	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
11187	24256	37891	2.42	3.6E-01	BE602390.1	EST_HUMAN	601676418F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3958897 5'
11370	24431	38088	3.27	3.6E-01	AB004283.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11729	23916	37540	4.44	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
12173	26205		3.16	3.6E-01	Y19210.1	NT	Homo sapiens h-lb5 gene for hair keratin, exons 1 to 9
12281	25187		7.87	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
12420	25297		3.63	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
12828	25552		1.98	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA
13130	26141		1.4	3.6E-01	AW160229.1	EST_HUMAN	x60e11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2879116 3' similar to gb:K00568 TUBULIN ALPHA-1 CHAIN (HUMAN);
13146	25745		1.38	3.6E-01	Z54173.1	NT	Pyrococcus sp. pol gene
214	13437	26467	3.71	3.5E-01	6678933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
695	13878	26911	1.03	3.5E-01	AL161591.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
743	13824	26965	1.53	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
743	13924	26966	1.53	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
801	13881	27033	4.66	3.5E-01	BF129796.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1670	14822	27805	1.28	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2671	16068	28008	1.34	3.5E-01	AA228252.1	EST_HUMAN	zr08e09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
3795	16956		0.73	3.5E-01	BF214391.1	EST_HUMAN	601845470F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076680 5'
4378	17821	30501	2.62	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hxrb5b) gene, complete cds
5048	18176	31153	4.34	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5323	13349	26376	0.6	3.5E-01	AL161596.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
5449	18849	31827	1.1	3.5E-01	Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5449	18849	31828	1.1	3.5E-01	Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5687	18861	32146	1.29	3.5E-01	D42045.1	NT	Human mRNA for KIAA0088 gene, complete cds
6367	19637		1	3.5E-01	AW663916.1	EST_HUMAN	PM4-SN0012-030400-001-a11 SN0012 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6538	19701	33074	0.79	3.5E-01	AA431833.1	EST_HUMAN	zw7903.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR:G1066935
6580	19742	33124	0.69	3.5E-01	U37150.1	NT	G1066935 F10F2.1;
6803	19958	33358	0.9	3.5E-01	O24357	SWISSPROT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
7201	20066		3.38	3.5E-01	X98505.1	NT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7713	20778	34264	0.59	3.5E-01	P47281	SWISSPROT	S.scrofa mRNA for CD31 protein (PECAM-1)
7713	20778	34265	0.59	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8266	21344		2.12	3.5E-01	11448042	NT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8266	21344		0.82	3.5E-01	BF368871.1	EST_HUMAN	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8662	21742		0.77	3.5E-01	AF051561.1	NT	RC4-E70024-260600-014-d07 E70024 Homo sapiens cDNA
9127	22206	35749	1.17	3.5E-01	4507610	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
9937	22976	36567	1.75	3.5E-01	Q02294	SWISSPROT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
10080	23128	36731	4.78	3.5E-01	Z26825.1	NT	VOLTA-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L
10172	23209	36802	1.12	3.5E-01	BE174794.1	EST_HUMAN	TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
10972	24052	37685	2.62	3.5E-01	X61084.1	NT	X.laevi gene for albumin including HPI enhancer
11274	24342	37981	1.97	3.5E-01	AJ243178.1	NT	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
11274	24342	37982	1.97	3.5E-01	AJ243178.1	NT	C.griseus rhodopsin gene for opsin protein
11810	24800	38499	1.33	3.5E-01	U07000.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11802	24880	38577	1.44	3.5E-01	N77597.1	EST_HUMAN	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11990	24965	38667	1.53	3.5E-01	L05145.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
12271	26209		1.51	3.5E-01	AF297488.1	NT	y280h12.1 Soares_multiple_sclerosis_2NblHMSF Homo sapiens cDNA clone IMAGE:280375 5'
12344	25249		6.66	3.5E-01	X64565.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
12507	25348		2.91	3.5E-01	AE001774.1	NT	Schistosoma mansoni strain NMRI chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
12710	25472		1.5	3.5E-01	AE001681.1	NT	B.taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit
13196	26026	31673	3.16	3.5E-01	H80814.1	EST_HUMAN	Thermoboga meritima section 88 of 136 of the complete genome
13196	26026	31674	3.16	3.5E-01	H80814.1	EST_HUMAN	Thermoboga meritima section 3 of 136 of the complete genome
725	13907		1.78	3.4E-01	AJ242956.1	NT	y64f11.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
998	14159	27230	8.2	3.4E-01	Y09798.2	NT	y64f11.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
1000	14171	27232	2.08	3.4E-01	AW380120.1	EST_HUMAN	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
1357	14512	27585	2.35	3.4E-01	Y00554.1	NT	Pseudomonas fluorescens colR, colS genes, orf222 and partial inaA gene
2474	15601	28726	2.54	3.4E-01	D90909.1	NT	QV3-HT0261-241199-019-g10 HT0261 Homo sapiens cDNA
							Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
							Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3065	16241	29261	0.87	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3065	16241	29262	0.87	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3218	16392	29403	1.09	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3230	16404	29416	6.1	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3424	16593	29608	0.78	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3620	16784	29800	4.47	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3890	17049		1.89	3.4E-01	BF449010.1	EST_HUMAN	7n94a01.x1 NCI_CGAP_OV18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15
4163	17313		1.48	3.4E-01	AA584196.1	EST_HUMAN	Q9UJ15.DJ18C9.1 ;
4767	17902	30884	1.79	3.4E-01	BE06912.1	EST_HUMAN	no11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
5066	18194		4.3	3.4E-01	A1240973.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
5802	18992	32295	2.64	3.4E-01	AL161594.2	NT	q95c06.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1857208 3' similar to contains Alu repetitive element;
5932	19118		4.92	3.4E-01	AA085313.1	EST_HUMAN	Arabisopsis thaliana DNA chromosome 4, contig fragment No. 90
6130	19309		2.17	3.4E-01	L02971.1	NT	zn12d11.s1 Stragene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:547221 3'
6154	19330	32676	0.96	3.4E-01	BE748912.1	EST_HUMAN	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6234	19409	32757	1.8	3.4E-01	AW204505.1	EST_HUMAN	601571811T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838828 3'
6364	19534	32893	1.71	3.4E-01	AL120544.1	EST_HUMAN	U1H-B11-act-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6882	20034		1.39	3.4E-01	N95225.1	EST_HUMAN	DKFZp761A249.t1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
7086	20180	33604	1.07	3.4E-01	A1468082.1	EST_HUMAN	zb59a12.s1 Scores_fetal_Jung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'
7205	20070	33480	0.6	3.4E-01	BF678702.1	EST_HUMAN	hm63g05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431
8090	21172		0.48	3.4E-01	AE000493.1	NT	LAMININ RECEPTOR (HUMAN);
8432	21513	35044	0.68	3.4E-01	Y14930.1	NT	602085293F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249365 5'
8684	21764		1.38	3.4E-01	AA337083.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
8760	21839	35380	0.71	3.4E-01	L04690.1	NT	Homo sapiens TCRBV28 gene, allele A4, partial
9053	22132	35576	1.87	3.4E-01	P26013	SWISSPROT	EST41765 Endometrial tumor Homo sapiens cDNA 5' and
9413	22487	36051	4.12	3.4E-01	P26013	SWISSPROT	Orctetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
9413	22487	36052	4.12	3.4E-01	P26013	SWISSPROT	Bovine enterovirus strain K2577, complete genome
9821	22673		0.57	3.4E-01	AB017510.1	NT	INTEGRIN BETA-8 PRECURSOR
9845	21088	34602	4.68	3.4E-01	U19492.1	NT	INTEGRIN BETA-8 PRECURSOR
							Ephratia fluviatilis mRNA for PLC-gamma3, complete cds
							Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9845	21088	34603	4.68	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9897	22937	36522	0.86	3.4E-01	U68763.1	NT	Glycine max putative transcription factor SCOF-1 (scot-1) mRNA, complete cds
10093	23131	36735	2.44	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10895	23728		0.73	3.4E-01	AE004036.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
11267	24336		3.26	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
11307	24372	38014	2.1	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN
11350	24412	38068	1.86	3.4E-01	AF045981.1	NT	Rutillus atcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11561	24616	38295	1.91	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11561	24616	38296	1.91	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11791	24781	38478	1.68	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-gbein/MUC18, complete cds
11817	24806	38502	3.23	3.4E-01	AL161516.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
12078	25058	38765	1.59	3.4E-01	BF061948.1	EST_HUMAN	7k6812.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:3480848 3'
12110	25090	38793	1.65	3.4E-01	Q27646	SWISSPROT	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (IU-NUCLEOSIDE HYDROLASE)
12150	25120		2.03	3.4E-01	U63804.1	NT	(PURINE NUCLEOSIDASE)
12264	25198		1.55	3.4E-01	Z21621.1	NT	Citrus variegation virus putative replicase gene, partial cds
12367	25912		1.16	3.4E-01	AF254351.1	NT	S. cerevisiae RIB5 gene encoding Riboflavin synthase
12489	25338		10.71	3.4E-01	L26339.1	NT	Schizosaccharomyces pombe Cwf8p (cwf8) gene, complete cds
12517	25944		2.38	3.4E-01	BE216652.1	EST_HUMAN	Human autoantigen mRNA, complete cds
12579	26052		1.79	3.4E-01	9898361	NT	hva2h08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
12700	25466	32023	1.38	3.4E-01	AJ297191.1	NT	PTR5 repetitive element;
12954	26160		1.96	3.4E-01	AJ288948.1	NT	Beta vulgaris mitochondrion, complete genome
13055	25891		2.26	3.4E-01	AF019413.1	NT	Mus musculus SIL_MAP_17, CYP_a, SOL & CYP_b genes
15	13253	26253	6.72	3.3E-01	X07990.1	NT	Clostridium cellulolyticum partial spoIVB gene and spoVA gene, strain ATCC 35319
108	13253	26253	3.19	3.3E-01	X07990.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
461	13656	26694	1.41	3.3E-01	AL161545.2	NT	Rhizobium leguminosarum sym plasmid pRL5.1J nodX gene
650	13938	26863	1.97	3.3E-01	7652485	NT	Rhizobium leguminosarum sym plasmid pRL5.1J nodX gene
1227	14397	27450	2.57	3.3E-01	Q12446	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
1335	14492	27562	3.39	3.3E-01	BF568880.1	EST_HUMAN	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
							PROLINE-RICH PROTEIN LAS17
							602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1638	14768	27873	1.26	3.3E-01	6753885	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1674	14828		1.43	3.3E-01	6754477	NT	Mus musculus kappa B and Rss recognition component (Krc), mRNA
1777	14926		1.02	3.3E-01	AA332734.1	EST_HUMAN	EST38722 Embryo, 8 week 1 Homo sapiens cDNA 5' and
2477	15604		6.23	3.3E-01		NT	Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidino-5'- decarboxylase) (UMPS) mRNA
3014	16190	29215	1.61	3.3E-01	AJ251805.1	NT	Bacteriophage phi-YeO3-12 complete genome
3080	16256		1.09	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3121	16297	29311	0.78	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus nitramycin biosynthetic genes
3584	16749	29766	1.04	3.3E-01	AB012922.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3911	17070	30068	2.72	3.3E-01	O84845	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3921	17080	30076	0.82	3.3E-01	P22802	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
4072	17228	30235	1.19	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4108	17262	30262	1.81	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4487	17827		2.37	3.3E-01	D31662.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4812	17945		1.91	3.3E-01	AI539114.1	EST_HUMAN	PEPTIDE TRANSPORTER 1 (HUMAN);
4843	17976	30966	1.02	3.3E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
4960	18089	31065	1.14	3.3E-01	D64003.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 2765703-2868766
5439	18639	31617	2.55	3.3E-01	X89819.1	NT	R. norvegicus mRNA for 3' UTR of ubiquitin-like protein
5439	18639	31618	2.56	3.3E-01	X89819.1	NT	R. norvegicus mRNA for 3' UTR of ubiquitin-like protein
5907	19096	32411	0.68	3.3E-01	BF213873.1	EST_HUMAN	601848090F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4078823 5'
6067	19249	32576	1.37	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3875753 3'
6067	19249	32577	1.37	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3875753 3'
6162	19338	32684	1.29	3.3E-01	P05591	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
6632	20247	33680	0.59	3.3E-01	AB034233.1	NT	Flexibacter litralis gyrB gene for DNA gyrase B subunit, partial cds
6992	20247	33681	0.59	3.3E-01	AB034233.1	NT	Flexibacter litralis gyrB gene for DNA gyrase B subunit, partial cds
7029	20165	33586	4.63	3.3E-01	AI628131.1	EST_HUMAN	ty84101.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7029	20165	33587	4.63	3.3E-01	AI628131.1	EST_HUMAN	ty84101.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7861	21011	34521	1.9	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8759	21838	35379	23.1	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301800 5'
8926	22005	35644	0.73	3.3E-01	BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
9314	22360	35941	0.83	3.3E-01	Q62926	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK 1)
9578	22720	36289	1.16	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA
9578	22720	36289	1.16	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA
9711	22760	36330	2.9	3.3E-01	NG9866.1	EST_HUMAN	za67h01.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297649 3'
9762	22660	36260	2.81	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
10196	23233		2.08	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMG-C) gene, exons 1-3, complete cds
10865	23897	37620	0.74	3.3E-01	AE000631.1	NT	Helicobacter pylori 26895 section 109 of 134 of the complete genome
10960	24041	37676	3.35	3.3E-01	XG3953.1	NT	D.mauritiana Adh gene
10960	24041	37676	3.35	3.3E-01	XG3953.1	NT	D.mauritiana Adh gene
11279	24345		2.1	3.3E-01	BF526499.1	EST_HUMAN	602070802F1 NCI CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4213585 5'
11507	24555	38242	9.35	3.3E-01	BE218351.1	EST_HUMAN	hvs1g02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
11626	24706	38399	3.7	3.3E-01	P47983	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-28) (CBP30)
12018	25002		2.8	3.3E-01	AA806621.1	EST_HUMAN	ob71g02.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
12036	13253	26253	2.33	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
12250	25190	38357	1.85	3.3E-01	6598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
13044	25695		22.03	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (277)
469	13694		2.5	3.2E-01	AF018261.1	NT	Rattus norvegicus E1 domain binding protein Epsin mRNA, complete cds
736	13918		0.76	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1188	14350	27408	23.03	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1311	14457	27535	1.48	3.2E-01	Z50202.1	NT	P.vulgaris arc5-1 gene
1421	14575	27648	6.74	3.2E-01	Q48824	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1663	14815		1	3.2E-01	AF209730.1	NT	Arabidopsis thaliana cultivar Columbia RPP13 (RPP13) gene, complete cds
1815	14964	28057	1.3	3.2E-01	Z36041.1	NT	S.cerevisiae chromosome II reading frame ORF YBR172c
1825	14974	28069	6.42	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGe resequences, MAGD Homo sapiens cDNA
1825	14974	28070	6.42	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGe resequences, MAGD Homo sapiens cDNA
1891	15035	28142	1.25	3.2E-01	AL111655.1	NT	Bcctylis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2227	15381	28490	3.22	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2606	15729		2.83	3.2E-01	7710079	NT	Mus musculus Pbx1knotted 1 homeobox (Pbx1), mRNA
2774	16859	29000	1.23	3.2E-01	AF060668.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3698	16857		0.76	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4081	17217		0.93	3.2E-01	AL181548.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
4514	17653	30841	1.37	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4621	17758	30740	1.35	3.2E-01	Q10268	SWISSPROT	HYPOPHOSPHATASE 1, 7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4860	17993		6.99	3.2E-01	BF693617.1	EST_HUMAN	60208197ZF1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246503 5'
5386	18598	31560	2.93	3.2E-01	BE173964.1	EST_HUMAN	CM0-HT0569-060300-265-f10 HT0569 Homo sapiens cDNA
6078	19260	32589	1.08	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:ferredoxin oxidoreductase and flanking genes
8433	19601	32965	0.73	3.2E-01	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
6729	19866	33277	0.85	3.2E-01	AV718037.1	EST_HUMAN	AV718037 FH7A Homo sapiens cDNA clone FH7AABH01 5'
6872	20024		1.17	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0381 gene, KIAA0381 protein
8040	21123	34843	0.52	3.2E-01	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8385	21446	34989	1.5	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
8481	21642	35072	0.87	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat, map NOS-D12W.alpha1
8582	21843	35182	15.01	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8585	21846	35187	14.52	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8666	21736		1.24	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8698	21778	36310	0.69	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8698	21778	35311	0.69	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8771	21850	35391	1.14	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
8871	21950	35485	0.86	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8871	21950	35486	0.86	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
9287	22344	35895	0.97	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9278	22354		2.54	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9351	22426	35983	0.61	3.2E-01	AF041828.1	NT	Homo sapiens 5-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9351	22426	35984	0.61	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
10198	23235	36824	4.33	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
10402	23437	37044	0.62	3.2E-01	BE326230.1	EST_HUMAN	h69005.X1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181569 3'
10518	23553		3.94	3.2E-01	AB011396.1	NT	Homo sapiens gene for AP-6, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10905	23988	37620	3.05	3.2E-01	T08813.1	EST_HUMAN	EST047022 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFB0221
12289	28083		3.11	3.2E-01	L07288.1	NT	Drosophila melanogaster lamitlin A (Lam-A) mRNA, complete cds
12861	25572		3.26	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12969	25891		2.2	3.2E-01	AF157626.1	NT	Bos taurus inositol 1,4,5-trisphosphate receptor type I mRNA, complete cds
13018	25669		2.07	3.2E-01	L39874.1	NT	Homo sapiens deoxydicylate deaminase gene, complete cds
13089	26129	31545	1.24	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_30 Homo sapiens cDNA clone IMAGE:3616746 5'
						EST_HUMAN	ye80h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN);
2736	15853	28967	3.39	3.1E-01	R18051.1	EST_HUMAN	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2762	16001	28985	3.77	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2762	16001	28986	3.77	3.1E-01	7661971	NT	h44h08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
2820	16098		1.28	3.1E-01	AW620036.1	EST_HUMAN	Mus musculus gene for Ser171r kinase KK (AMIRE), exon 6
3242	16416		3.51	3.1E-01	AB020069.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4016	17173	30181	0.94	3.1E-01	AJ251586.1	NT	Xyella fastidiosa, section 130 of 228 of the complete genome
5077	18205	31177	0.7	3.1E-01	AE003964.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5595	18790	31838	9.24	3.1E-01	AF176111.1	NT	HYPOTHETICAL PROTEIN HI1236
5717	18910	32205	0.7	3.1E-01	P44132	SWISSPROT	S. cerevisiae chromosome XV reading frame ORF YOL141w
5718	18911	32206	0.75	3.1E-01	Z74883.1	NT	Mus musculus mRNA for polycystin
5729	18922		0.83	3.1E-01	Y13278.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
5892	19080	32390	2.65	3.1E-01	AF184122.1	NT	RC3-HN0001-310300-011-504 HN0001 Homo sapiens cDNA
6595	19755	33141	1.3	3.1E-01	AW983548.1	EST_HUMAN	q39401.x1 NCI_CGAP_C68 Homo sapiens cDNA clone IMAGE:1874989 3'
6683	19822	33209	0.96	3.1E-01	A1264458.1	EST_HUMAN	H. sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
6821	19874	33382	0.79	3.1E-01	X71887.1	NT	MR2-CT0222-281099-005-h05 CT0222 Homo sapiens cDNA
6905	20220		0.89	3.1E-01	AW377354.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3840420 5'
7109	25801	31491	2.32	3.1E-01	BE737392.1	EST_HUMAN	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
7858	20911	34416	0.7	3.1E-01	4885390	NT	y44601.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35639 3'
8849	21928	35467	0.84	3.1E-01	R45318.1	EST_HUMAN	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
10108	23144	36742	0.68	3.1E-01	6879322	NT	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10272	23307	36903	1.04	3.1E-01	BF696339.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10272	23307	36904	1.04	3.1E-01	BF696339.1	EST_HUMAN	q161e11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700
10334	23389	36979	1.68	3.1E-01	A1244001.1	EST_HUMAN	HYDROXYMETHYL-GLUTARYL-COA LYASE PRECURSOR (HUMAN);
						EST_HUMAN	y447h08.s1 Stratagene fetal spleen (8937205) Homo sapiens cDNA clone IMAGE:74367 3' similar to similar to gb:M91036_rna22 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
10510	23545		0.98	3.1E-01	T55325.1	EST_HUMAN	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'
11076	24151	37789	1.84	3.1E-01	BF216117.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11474	24633	38203	1.62	3.1E-01	AW074910.1	EST_HUMAN	xs62g09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2571424 3'
11827	24816	38507	2.08	3.1E-01	7662291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
11828	24817	38508	1.67	3.1E-01	R55735.1	EST_HUMAN	yg9b05.11 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:40722 5' similar to contains Alu repetitive element;
12123	25103		1.3	3.1E-01	AF105953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12418	25298		1.22	3.1E-01	AF294308.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12455	25319		1.73	3.1E-01	AF304192.1	NT	Silvestrodon vitreum 40S ribosomal protein S11 mRNA, partial cds
12813	25412		3.73	3.1E-01	AF105953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
13028	26677		3.82	3.1E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
13088	26123		1.22	3.1E-01	10945623	NT	Mus musculus peptidoglycan recognition protein-like (Pglyrp-pending), mRNA
74	15979	26336	1.65	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkc), mRNA
264	13483	26515	11.52	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1251	14410	27472	2.35	3.0E-01	AW300400.1	EST_HUMAN	xs63f08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1537	14690	27769	5.77	3.0E-01	AJ006755.1	NT	Balanoptera physalus gene encoding atial natiretic peptide
1838	14984	28084	1.2	3.0E-01	X99082.1	NT	A. immersus putative gene encoding integrase, Mars2 (RP)
3069	18245		0.8	3.0E-01	AB008877.1	NT	Bos taurus mRNA for UDP-glucuronosyltransferase, complete cds
3283	18457		1.33	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyFG gene for polygluturonate lyase, complete cds
3988	17128	30129	1.58	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-261199-001-g01 ST0262 Homo sapiens cDNA
4032	17237	30243	1.16	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4636	17772	30752	1.79	3.0E-01	AJ006755.1	NT	Balanoptera physalus gene encoding atial natiretic peptide
5258	16649	28665	2.33	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-ETC) (GATA-3)
5487	18667	31846	5.1	3.0E-01	BE741626.1	EST_HUMAN	601594903F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3948734 5'
5548	18745	31780	0.64	3.0E-01	AF224698.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
5552	18749	31785	1	3.0E-01	AF220247.1	NT	Canis lupus familiaris hemagglutinin gene, complete cds
5621	18815	31883	4.01	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5621	18815	31884	4.01	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5638	18852	32135	3.87	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
6970	20198	33624	2.82	3.0E-01	D16313.1	NT	Mouse cycloratin 15 gene, complete cds
6999	18518	31511	0.76	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds
7065	20118	33532	1.15	3.0E-01	AF228247.1	NT	Canis lupus familiaris hemagglutinin gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7270	20353	33806	0.96	3.0E-01	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7481	20559	34028	4.3	3.0E-01	10947007	NT	Mus musculus midnolin (Midn-pending), mRNA
7670	20739	34214	1.51	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBLS PspA (pspA) gene, partial cds
8111	21193	34713	1.34	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8588	21649		3.1	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec3f), mRNA
8658	21735	35279	0.48	3.0E-01	270200.1	NT	H. sapiens gene for U5 snRNP-specific 200kD protein
8671	21751	35288	1.23	3.0E-01	BE566083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 6'
9029	22108	35649	0.69	3.0E-01	AF141676.1	NT	Streptomyces sulfonolactams isopenicillin N synthase (pcbc) gene, partial cds
9072	22151		0.82	3.0E-01	7681685	NT	Homo sapiens DKFZP566M0122 protein (DKFZP566M0122), mRNA
9419	22493	36059	1.09	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds, and unknown gene
9773	22813	36391	0.64	3.0E-01	P76389	SWISSPROT	HYPOPHETICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
9927	22967		0.46	3.0E-01	D90904.1	NT	Synechocystis sp. PCC6803 complete genome, 6/27, 630555-761448
10173	23210	36803	0.84	3.0E-01	BF574612.1	EST_HUMAN	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288336 5'
10346	23381	36992	0.45	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetemcomitans TadA (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10346	23381	36993	0.45	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetemcomitans TadA (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10606	23640	37248	0.6	3.0E-01	AW118111.1	EST_HUMAN	Xe03d10.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2608035 3'
10608	23642	37250	2.51	3.0E-01	AB030231.1	NT	Aspergillus oryzae bipA gene for ER chaperone BIP, complete cds
10629	23683	37271	0.76	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 6'
10629	23683	37272	0.76	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
12087	25048	38755	2.16	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:194107 5'
12087	25048	38756	2.16	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:194107 5'
12470	25324		1.3	3.0E-01	P54660	SWISSPROT	PONTICULIN PRECURSOR
12731	26062		1.88	3.0E-01	AJ297691.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
13061	26121		4.49	3.0E-01	6677766	NT	Mus musculus ribose 5-phosphatase isomerase A (Rpia), mRNA
1771	14920		0.94	2.9E-01	AJ248895.1	NT	Mus musculus mas proto-oncogene and igf2i gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1930	15073	28176	0.94	2.9E-01	5174502	NT	Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA
2080	15220	28340	2.36	2.9E-01	AE000736.1	NT	Aquifex acidicus section 68 of 109 of the complete genome
2322	15454	28585	1.01	2.9E-01	AF222718.1	NT	Chrysidium synuroides mitochondrion, complete genome
3253	16427	29445	0.96	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds

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3323	18466	29513	2.88	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171289-001-f12 CT0326 Homo sapiens cDNA
3323	18466	29514	2.88	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171289-001-f12 CT0326 Homo sapiens cDNA
4003	17160	30166	1.12	2.9E-01	AI610838.1	EST_HUMAN	tp21a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2189412 3' similar to gb15050 NIL-2-A ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
4045	17201	30212	0.61	2.9E-01	AI769472.1	EST_HUMAN	w14d10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402803 3' similar to WP:G34F6.7
4183	17333	30325	0.61	2.9E-01	AB016426.1	NT	CE15676;
4185	17345		0.79	2.9E-01	AW002902.1	EST_HUMAN	Cavia porcellus mRNA for glutathione S-transferase, complete cds
4808	17745	30724	0.98	2.9E-01	AA284488.1	EST_HUMAN	w02f10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480395 3'
4805	17940		0.73	2.9E-01	AL163207.2	NT	zs57d12.1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
4957	18087	31063	0.59	2.9E-01	AB019029.1	NT	Homo sapiens chromosome 21 segment HS21C007
5222	18344		0.99	2.9E-01	AI670899.1	EST_HUMAN	Mus musculus gene, complete cds, similar to EXLM1
5320	18087	31063	0.65	2.9E-01	AB019029.1	NT	repetitive element;
5372	18578		1.59	2.9E-01	R37485.1	EST_HUMAN	y77e12.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28281 3'
5511	20137	33555	0.98	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5884	19073	32381	5.27	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5884	19073	32382	5.27	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5887	19085	32397	5.53	2.9E-01	8879862	NT	Mus musculus Eph receptor A8 (Epha8), mRNA
6181	18357	32705	1.55	2.9E-01	AA418145.1	EST_HUMAN	zx67b12.1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5'
6411	19580	32941	1.07	2.9E-01	AI797128.1	EST_HUMAN	w027c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.H L1 repetitive element;
6455	19622	32888	2.22	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
7001	20137	33555	0.71	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
7126	18552	31466	1.4	2.9E-01	AF142328.1	NT	Mus musculus Filin protein (Filin) gene, complete cds; and Uigh protein (Uigh) gene, partial cds
7245	20328	33773	3.11	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR506C
7310	20362	33852	1.54	2.9E-01	AF100988.1	NT	Mus musculus major histocompatibility locus class II region, Fas-binding protein Daxx (DAXX) gene, partial cds: Bmg1 (BING1), tapasin (tapasin), RelGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3- galactosyl transferase (beta1,3-galactosyl tr>
8104	21166	34705	1.61	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8104	21166	34708	1.61	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8343	21424	34949	0.64	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8343	21424	34950	0.64	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8356	21437		0.75	2.9E-01	BF217743.1	EST_HUMAN	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086113 5'
							Buchnera aphidicola plasmid pLeu isclate M1 2-isopropylmalate synthase (leuA) gene, partial cds; 3-isopropylmalate dehydrogenase (leuB) gene, complete cds; and isopropylmalate dehydratase subunit (leuC) gene, partial cds
8534	21615		0.53	2.9E-01	AF197456.1	NT	
8794	21873	35412	0.82	2.9E-01	AU150910.1	EST_HUMAN	AL150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
9125	22204	35747	1.09	2.9E-01	AF225908.1	NT	Arabidopsis thaliana sulfonyleurea receptor-like protein mRNA, complete cds
9233	22311	35853	0.81	2.9E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9447	22563	36125	0.96	2.9E-01	AJ248287.1	NT	Pyrococcus abyssii complete genome; segment 5/6
9447	22563	36126	0.96	2.9E-01	AJ248287.1	NT	Pyrococcus abyssii complete genome; segment 5/6
10405	23440	37047	0.46	2.9E-01	AW294100.1	EST_HUMAN	U1-H-B12-ahg-b-02-Q-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2728714 3'
10405	23440	37048	0.46	2.9E-01	AW294100.1	EST_HUMAN	U1-H-B12-ahg-b-02-Q-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2728714 3'
11133	24205	37830	1.94	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11433	24494	38159	1.79	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11433	24494	38160	1.79	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
							ny55h02.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element
11881	24669	38566	2.71	2.9E-01	AAB35373.1	EST_HUMAN	
11886	24874	38571	3.12	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11188 complete genome; segment 5/6
11900	24888	38587	2.09	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11900	24888	38588	2.09	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
							w288f05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element
12677	25452	32017	1.85	2.9E-01	AW005671.1	EST_HUMAN	MER29 repetitive element
12774	25516		1.89	2.9E-01	V00202.1	NT	D. melanogaster: part of the 44D cuticle gene cluster encoding cuticle gene 1
12777	25519	32001	2.23	2.9E-01	AF062453.1	NT	Homo sapiens TNF-a-inducible RNA binding protein (TIRP) gene, complete cds
13125	25734	31944	1.24	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
13125	25734	31945	1.24	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
13204	25785	31919	1.4	2.9E-01	AF200418.1	NT	Callinectes sapidus cadmium-inducible metallothionein CdMT-I mRNA, complete cds
582	13774		2.04	2.8E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
587	13778		1.96	2.8E-01	U28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1107	14272	27331	3.34	2.8E-01	AF168050.1	NT	Guinea oocyte maturation factor Mos (c-mos) gene, partial cds
1308	14462	27529	2.19	2.8E-01	BE313442.1	EST_HUMAN	801148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1306	14462	27530	2.19	2.8E-01	BE313442.1	EST_HUMAN	801148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1319	14475	27541	1.2	2.8E-01	D88550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1766	14915	28011	1.87	2.8E-01	AW86020.1	EST_HUMAN	QV1-CT0364-120200-085-b05 CT0364 Homo sapiens cDNA
2089	15210	28326	1.49	2.8E-01	AL047620.1	EST_HUMAN	DKFZp586i2321.j1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586i2321
2200	16335	28462	1.51	2.8E-01	AW511195.1	EST_HUMAN	hd44b03.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2542	15667	28781	2.98	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2542	15667	28792	2.98	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2612	15736		2.95	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2730	15848	28958	1.16	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoytransferase, complete cds
3035	16211		1.37	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
3036	16212	28234	2.52	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3036	16212	29235	2.52	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3466	16833	29652	1.05	2.8E-01	AF000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (477)
4103	17257	30257	1.67	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 88 of 70) of the complete genome
4240	17368		0.6	2.8E-01	AE004460.1	NT	Pseudomonas aeruginosa PA01, section 11 of 529 of the complete genome
4315	17458		2.17	2.8E-01	AI090868.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640228 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
4582	17719	30702	2	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4944	18074	31049	0.92	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4950	18080	31056	4.95	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4984	18113	31080	1.52	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCL_CGAP_Brim7 Homo sapiens cDNA clone IMAGE:4180129 5'
5006	18135	31109	3.66	2.8E-01	AI272669.1	EST_HUMAN	qf59c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR6 repetitive element;
5318	18473	31404	0.61	2.8E-01	X60797.1	NT	Mouse Kv3.3 gene for potassium channel protein, exon 2
5428	25504	31802	23.61	2.8E-01	AA349897.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5723	18916	32211	2.57	2.8E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
5938	19124		0.93	2.8E-01	AW892583.1	EST_HUMAN	OM1-BN0024-160200-118-g12 BN0024 Homo sapiens cDNA
6042	19225	32548	0.66	2.8E-01	AA765296.1	EST_HUMAN	oa01406.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:130369; 3' similar to gb:M34539 FK508-BINDING PROTEIN (HUMAN);
6059	19241		0.64	2.8E-01	AA404576.1	EST_HUMAN	zf41101.j1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element;
6305	26212		0.67	2.8E-01	MG8688.1	NT	Bovine 680 bp repeated unit of 1.723 actinella DNA
6347	19517	32874	1.65	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6347	19517	32875	1.65	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6870	20022	33432	7.84	2.8E-01	BF511215.1	EST_HUMAN	UI-H-B14-act-1-04-0-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7146	20280	33721	0.64	2.8E-01	U85300.1	NT	Orthomyx heterodius cytochrome b (cyb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7599	20669		1.14	2.8E-01	U05633.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, chloroplast gene encoding chloroplast protein, partial cds
8284	21368	34884	1.31	2.8E-01	A1346128.1	EST_HUMAN	qp48h01.x1 NCL CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8284	21368	34885	1.31	2.8E-01	A1346128.1	EST_HUMAN	qp48h01.x1 NCL CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8404	21485	35014	2.31	2.8E-01	U51688.1	NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
8712	21792	35328	0.6	2.8E-01	AA911629.1	EST_HUMAN	002h05.s1 NCL CGAP_Co12 Homo sapiens cDNA clone IMAGE:1419993 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
8789	21868		7.72	2.8E-01	BF37847.1	EST_HUMAN	602022987F1 NCL CGAP_Bri67 Homo sapiens cDNA clone IMAGE:4158525 5'
9666	22628	36169	1.14	2.8E-01	U17251.1	NT	Neurospora crassa negative regulator sulfur controller-2 (sccr-2) gene, complete cds
9912	22952		1.18	2.8E-01	L13854.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
10092	23130	36733	0.98	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10092	23130	36734	0.98	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10152	23189	36786	0.46	2.8E-01	AE001310.1	NT	Chlamydia trachomatis section 37 of 87 of the complete genome
10156	23183	36789	0.7	2.8E-01	AF294353.1	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
10265	23300	36868	3.8	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
10519	23534		1.1	2.8E-01	9626154	NT	Fujinami sarcoma virus, complete genome
10561	23596	37202	0.5	2.8E-01	BE969727.2	EST_HUMAN	601684822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839785 3'
10982	24061	37695	1.88	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4109350 5'
10992	24061	37696	1.88	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4109350 5'
11011	24090	37727	3.01	2.8E-01	BF696970.1	EST_HUMAN	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
11119	24191	37823	1.53	2.8E-01	AF051662.1	NT	Drosophila heteroneura fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11556	24611		3.58	2.8E-01	BF674023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273953 5'
11851	24840	38533	1.55	2.8E-01	AJ248285.1	NT	Pyrococcus abyssi complete genome; segment 3/6
11861	24840	38534	1.55	2.8E-01	AJ248286.1	NT	Pyrococcus abyssi complete genome; segment 3/6
12715	25475		12.79	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12846	25562	31967	7.61	2.8E-01	BE178699.1	EST_HUMAN	PM4-HT0606-030400-001-a07 HT0606 Homo sapiens cDNA
12875	25692	31996	1.29	2.8E-01	BE900116.1	EST_HUMAN	601673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955996 5'
13052	26066		1.59	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
489	13883	26717	4.34	2.7E-01 Y17324.1	NT	Rattus norvegicus CDK104 mRNA
628	13813	26835	13.64	2.7E-01 AA450061.1	EST_HUMAN	z39b10.s1 Soares fetal_tetus_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
1290	14446	27512	2.04	2.7E-01 AB004906.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1650	14803		1.63	2.7E-01 X78815.1	NT	Glambilla SR2 gene
1768	14917	28012	3.16	2.7E-01 W58087.1	EST_HUMAN	z02h10.r1 Soares fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:341443 5'
1817	14966	28059	1.48	2.7E-01 P09341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12, CORE PROTEIN P15, CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2204	16057		3.1	2.7E-01 AF04751.1	NT	Rattus norvegicus vesicular monocarboxylate transporter type 2, promoter region and exon 1
2250	15383	28510	0.94	2.7E-01 A137272.1	EST_HUMAN	EST175679 Infant brain, Bento Soares Homo sapiens cDNA clone UH101R 5' end
2250	15383	28511	0.94	2.7E-01 A137272.1	EST_HUMAN	EST175679 Infant brain, Bento Soares Homo sapiens cDNA clone UH101R 5' end
2440	15568	28695	7.07	2.7E-01 Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITT0088PIU (M88), partial
2526	15561	28775	4.36	2.7E-01 A1310859.1	EST_HUMAN	ta43o11.x2 NCL CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element;
3049	16225		0.99	2.7E-01 BF088284.1	EST_HUMAN	GM1-HT0875-080900-385-e05 HT0875 Homo sapiens cDNA
3361	16533	29547	0.66	2.7E-01 8393620	NT	Rattus norvegicus Insulin receptor (Insr), mRNA
4118	17272	30271	1.94	2.7E-01 A1928015.1	EST_HUMAN	w092a11.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4133	17286	30281	0.88	2.7E-01 AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4133	17286	30282	0.88	2.7E-01 AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4140	17292	30286	2.39	2.7E-01 L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
5153	18275		4.46	2.7E-01 AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 GT0286 Homo sapiens cDNA
5381	18583	31452	1.98	2.7E-01 P17277	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (CHOX-1.4)
5807	18902		1.31	2.7E-01 AB03171.1	NT	Astrocystis myriophthalma mitochondrial cyto b gene for cytochrome b, partial cds
6472	19639	32898	0.86	2.7E-01 Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1)
6472	19639	32899	0.86	2.7E-01 Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1)
6745	19801	33293	1.05	2.7E-01 AE001094.1	NT	(TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6745	19801	33294	1.05	2.7E-01 AE001094.1	NT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1)
6918	20233	33667	1.74	2.7E-01 Q61554	SWISSPROT	(TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
7187	20062		0.77	2.7E-01 A1540070.1	EST_HUMAN	Archaeoglobus fulgidus section 13 of 172 of the complete genome
7511	20585	34058	0.92	2.7E-01 Q11079	SWISSPROT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
						FIBRILLIN 1 PRECURSOR
						Id08h08.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2075103 3'
						HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7734	20795	34283	0.87	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7734	20795	34284	0.87	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7885	20919	34425	2.1	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7885	20919	34426	2.1	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7917	20988	34474	0.72	2.7E-01	AA351121.1	EST_HUMAN	EST158740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7917	20988	34475	0.72	2.7E-01	AA351121.1	EST_HUMAN	EST158740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7978	21028	34540	0.68	2.7E-01	L01081.1	NT	Oryzobagus culiculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
8048	21131	34651	0.68	2.7E-01	AA013147.1	EST_HUMAN	ze35b11.1 s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element
8330	21412	34838	0.56	2.7E-01	AW86503.1	EST_HUMAN	MR1-SN0062-100500-002-d09 SN0062 Homo sapiens cDNA
8380	21461	34984	0.59	2.7E-01	R9257.1	EST_HUMAN	ye91h08.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3'
8486	21957	35104	0.83	2.7E-01	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8959	22038	35580	1.4	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
9534	22599	36171	10.56	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9534	22599	36172	10.56	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9537	22602		2.66	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
10005	23043	36636	0.8	2.7E-01	D89680.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
10286	23321	36923	0.9	2.7E-01	AF091848.1	NT	Oryzobagus culiculus calgranulin C mRNA, partial cds
10323	23358	36968	2.06	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc1 isoform a (NF-ATc1) mRNA, complete cds
10455	23490	37099	1.06	2.7E-01	AF150538.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10455	23490	37100	1.06	2.7E-01	AF150538.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10749	23782		0.51	2.7E-01	AB011678.1	NT	Rattus norvegicus mRNA for class I beta-tubulin, complete cds
10765	23798	37418	0.58	2.7E-01	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
10765	23798	37419	0.58	2.7E-01	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
11050	24127	37761	1.98	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11050	24127	37762	1.98	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
							Homo sapiens caveolin-1/2 locus, Contig1, D7S822, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
11061	24137	37772	2.58	2.7E-01	AJ133298.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12816	25942		1.49	2.7E-01	AB008782.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
13034	25981		2.75	2.7E-01	AF217491.1	NT	
482	16013	26710	2.8	2.0E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
493	13688		1.94	2.6E-01	D18459.1	NT	Bos taurus mRNA for mb-1, complete cds
1424	14578	27651	1.77	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1468	14622	27705	1.09	2.6E-01	AB013250.1	NT	Glycine max pseudogene for Bd 30K
1945	15088	28188	7.69	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1945	15088	28189	7.69	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04d10x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfactant locus surfact 3 protein gene (MOUSE);
2159	15295		10.39	2.6E-01	AW733152.1	EST_HUMAN	Human prealbumin gene, complete cds
2220	15354	28485	1.13	2.6E-01	M11844.1	NT	Human prealbumin gene, complete cds
2811	15735		11.68	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5'
3161	16336		1.11	2.6E-01	AW974531.1	EST_HUMAN	EST3386335 MAGC sequences, MAGF Homo sapiens cDNA
3871	16834	29845	0.84	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA (adenine-N6)methyltransferase (dam) gene, complete cds
3733	16894	29899	1.67	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLO) gene, exons 1A, 2, 3, 4, and 5
4215	17364	30352	0.79	2.6E-01	AW959510.1	EST_HUMAN	EST371580 MAGC sequences, MAGF Homo sapiens cDNA
4270	17415	30404	16.93	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
							Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4478	17616	30597	1.71	2.6E-01	AF175293.1	NT	
4617	17754	30735	0.69	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4617	17754	30736	0.69	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4670	17806	30794	1.14	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.1 StrataGene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4770	17905	30887	2.25	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3-1) mRNA, complete cds
4837	17970	30958	1.15	2.6E-01	AF142703.1	NT	Ophrestia radiosa maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
5086	18214	31187	3.63	2.6E-01	H04858.1	EST_HUMAN	yf51e05.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5156	18277		0.61	2.6E-01	AA884625.1	EST_HUMAN	am33b11.1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1468605 3'
5457	18657		1.29	2.6E-01	AB035972.1	NT	Paramacium caudatum gene for PAP, complete cds
5695	18762	31802	0.67	2.6E-01	M98060.1	NT	Acetabacter xylinum cellulose synthase (tcsA) gene, partial cds, CMCax and CcpAx genes, complete cds
							td16a03.x1 NCJ_CGAP_C016 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element
5689	18883		0.84	2.6E-01	AI862398.1	EST_HUMAN	MER35 repetitive element;
							Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, pim-2 protooncogene homolog pim-2h, and shd-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds; and unknown g?
5895	19083	32394	0.64	2.6E-01	AF207550.1	NT	

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6196	26211		2.57	2.6E-01	AE001811.1	NT	Thermoboga maritima section 123 of 136 of the complete genome
6330	19501	32859	1.96	2.6E-01	AI582557.1	EST_HUMAN	is02a12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
6330	19501	32860	1.96	2.6E-01	AI582557.1	EST_HUMAN	is02a12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
6552	19714	33090	0.98	2.6E-01	AL162757.2	NT	Nisseria meningitidis serogroup A strain Z2491 complete genome, segment 6/7
6807	19961	33364	0.74	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3938156 5'
6807	19961	33365	0.74	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3938156 5'
7183	20315	33758	1.04	2.6E-01	AI914380.1	EST_HUMAN	PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7549	20621	34098	0.7	2.6E-01	BE148961.1	EST_HUMAN	GM0-HT0245-031109-085-f04 HT0245 Homo sapiens cDNA
7587	25848		0.96	2.6E-01	AL138077.2	NT	Campylobacter jejuni NCTC1168 complete genome; segment 4/8
7626	20896		0.78	2.6E-01	AA196149.1	EST_HUMAN	zpc92a01.r1 Striatagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:927672 5'
7918	20969	34476	1.73	2.6E-01	R10365.1	EST_HUMAN	y37a03.a1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:129004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);
8033	21116	34634	1.18	2.6E-01	R02411.1	EST_HUMAN	y682a07.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:124212 5'
8088	21170	34685	1.3	2.6E-01	BE144331.1	EST_HUMAN	MR0-HT0166-181195-003-412 HT0166 Homo sapiens cDNA
8529	21610	35148	2.97	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4150396 5'
8605	21696	35223	1.74	2.6E-01	Q10199	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN G11G11.02 IN CHROMOSOME II
8892	21971	35506	4.06	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8892	21971	35507	4.06	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9667	22623	36200	0.92	2.6E-01	X17604.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
9940	22879		0.5	2.6E-01	AF057121.1	NT	Lontra canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10072	23110	36713	1.13	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFFH-G)
10072	23110	36714	1.13	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFFH-G)
10393	23428		0.63	2.6E-01	Q26295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10727	23760		1.09	2.6E-01	Y10196.1	NT	Homo sapiens PHOX gene
10840	23873		0.48	2.6E-01	Y15874.2	NT	Danio rerio mRNA for RPTP-alpha protein
11815	24804		31.14	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
12468	26070		4.14	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12535	25365	32069	3.86	2.6E-01	AF16896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXDY2) gene, complete cds, alternatively spliced

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12922	25607		2.04	2.0E-01	D88425.1	NT	Cavia cbbaya mRNA for serine/threonine kinase, complete cds
13007	25693		1.78	2.0E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
13057	25692		2.36	2.0E-01	AF141325.2	NT	Homo sapiens insulin polyphosphate 1-phosphatase (NPP1) gene, complete cds
13098	15735		1.43	2.0E-01	BE272440.1	EST_HUMAN	601128076F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2860043 5'
13107	25722		2.04	2.0E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
13150	25748		2.4	2.0E-01	U30729.1	NT	Arabidopsis thaliana floral homeotic (AP3) gene, promoter region and partial cds
251	13472	26503	1.87	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
282	13472	26503	1.7	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
286	13484		2.51	2.5E-01	M26501.1	NT	Sterfish (P. ochraceus) cytoplasmic actin gene, complete cds
855	14032	27093	1.23	2.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1085	14251		1.75	2.5E-01	AE002166.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1145	14310	27367	5.45	2.5E-01	T89837.1	EST_HUMAN	ye11g07.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:117468 5'
1767	14916		4.53	2.5E-01	4885408	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
2479	15608		11.21	2.5E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2583	15688	28814	1.22	2.5E-01	6878218	NT	Mus musculus protein-L-isopentate (D-aspartate) O-methyltransferase 1 (Pcmt1), mRNA
2585	15690		1.02	2.5E-01	AA251987.1	EST_HUMAN	zs11a12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
2702	15820	28936	1	2.5E-01	X95310.1	NT	B. taurus mRNA for D-aspartate oxidase
3489	16666		3.34	2.5E-01	AW973471.1	EST_HUMAN	EST385464 IMAGE resequences, MAGM Homo sapiens cDNA
3639	16903	2981E	7.18	2.5E-01	AL181617.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28
3950	17108	30105	1.25	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364760 3'
3950	17108	30106	1.25	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364760 3'
4438	17578		0.88	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4737	17872	30855	0.7	2.5E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-16
4871	18004		1.13	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4878	18009	30993	3.09	2.5E-01	AF007768.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4904	18034	31023	2.3	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4926	18056		3.54	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4954	18084	31060	0.8	2.5E-01	BE886785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4994	18123	31101	0.61	2.5E-01	U83658.1	NT	Rattus norvegicus NF-KB gene, promoter region
5212	18333	31303	0.62	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5212	18333	31304	0.62	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5337	18450		1.08	2.5E-01	AA419208.1	EST_HUMAN	P59 PROTEIN (HUMAN); zv35a05.1 Scores over y (unior NbHOT Homo sapiens cDNA clone IMAGE:755600 5' similar to gb:M88279
5441	18641	31620	12.21	2.5E-01	S83390.1	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2830 nt]
6080	19262	32591	0.6	2.5E-01	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6081	19263		0.81	2.5E-01	AL163207.2	NT	Homo sapiens partial sterin-1 gene
6762	19916	33313	0.82	2.5E-01	AJ251973.1	NT	Homo sapiens partial sterin-1 gene
7190	20055	33485	0.64	2.5E-01	8394138	NT	Rattus norvegicus rabin 3 (RABIN3), mRNA
7507	20581	34054	0.71	2.5E-01	U13992.1	NT	Feline calicivirus CF/68 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene
7536	20609		1.13	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7770	20828	34319	0.62	2.5E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
7814	20869	34365	4.23	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
8028	21111	34630	2.22	2.5E-01	BF109040.1	EST_HUMAN	7157a03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
8039	21122	34642	0.51	2.5E-01	BE960712.1	EST_HUMAN	601653391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198 3'
8421	21502	35034	1.9	2.5E-01	BF038595.1	EST_HUMAN	601459238F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3862809 5'
8591	21672	35210	0.8	2.5E-01	P04492	SWISSPROT	E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K)
8837	21916	35454	4.07	2.5E-01	H53236.1	EST_HUMAN	yq84f07.1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:202501 5'
9076	22155	35668	1.05	2.5E-01	M88626.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9716	22781	36351	18.85	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9716	22781	36352	18.85	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9772	22768	36339	2.44	2.5E-01	AF085184.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9772	22768	36340	2.44	2.5E-01	AF085184.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10303	23338	36943	1.31	2.5E-01	AW581997.1	EST_HUMAN	RC3-ST0188-130100-015-a07 S10188 Homo sapiens cDNA
10550	23685	37163	0.51	2.5E-01	11485652	NT	Porphyrin purpurea chloroplast, complete genome
10763	23798	37416	1.4	2.5E-01	AW152246.1	EST_HUMAN	xg40c10.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element
10767	23800	37422	1.61	2.5E-01	X58491.1	NT	Mouse L1Md LINE DNA
11392	24395	38043	2.96	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
12204	25158	38834	5.16	2.5E-01	AF200628.1	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
12233	26167		6.12	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13024	25674		1.22	2.5E-01	AF325383.1	NT	Delta brassica cytochrome oxidase subunit II (COII) gene, partial cds; mitochondrial gene for mitochondrial product
567	13759	26783	1.41	2.4E-01	AA836316.1	EST_HUMAN	on70404.g1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
871	14047	27113	4.4	2.4E-01	BF576124.1	EST_HUMAN	902132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271678 5'
1332	14489	27657	16.83	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1332	14489	27558	16.83	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1415	14569	27642	0.97	2.4E-01	Y17293.1	NT	Homo sapiens FLI1 gene, partial
1808	15041		28.78	2.4E-01	AF267763.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1949	15092	28193	1.43	2.4E-01	AF261708.1	NT	Zaocys diurnades fructose-1,6-bisphosphatase mRNA, complete cds
2081	15231	28953	1.64	2.4E-01	A1742958.1	EST_HUMAN	wg76405.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371017 3' similar to TR-O60287 O60287 KIAA0512 PROTEIN. ;
2206	15340	28487	1.17	2.4E-01	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2237	15370		1.25	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2336	15467	28602	2.29	2.4E-01	AE000680.1	NT	Aquifex acidicus section 12 of 109 of the complete genome
2602	15726	28845	3.13	2.4E-01	Z36534.1	NT	D.discoideum (AX-K) ponA gene
2820	15834	29045	2.22	2.4E-01	X71783.1	NT	S.pombe swi6 gene
2848	15960	29069	6.27	2.4E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
3202	16377		3.03	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3217	16391	29402	1.51	2.4E-01	X74209.1	NT	H. sapiens AGT gene, PstI fragment of intron 4
3836	17016	30016	0.97	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4141	17293		0.65	2.4E-01	D26960.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
5181	18303	31266	0.65	2.4E-01	AW078596.1	EST_HUMAN	xb18a02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5181	18303	31267	0.65	2.4E-01	AW078596.1	EST_HUMAN	xb18a02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5334	18447	31415	1.89	2.4E-01	U88914.1	NT	Bacillus firmus hypothetical 34.0 kDa protein, hypothetical 8.9 kDa protein, hypothetical 10.1 kDa protein, hypothetical 21.0 kDa protein, putative thiosulfate sulfurtransferase, hypothetical 16.1 kDa transcriptional regulator and hypothetical 18.2 kDa>
5335	18448	31416	1.46	2.4E-01	AB032785.1	NT	Homo sapiens gene for TU12B1-TY, exon 13
5335	18448	31417	1.46	2.4E-01	AB032785.1	NT	Homo sapiens gene for TU12B1-TY, exon 13
5578	18773	31818	0.9	2.4E-01	AB032785.1	EST_HUMAN	wc33405.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5578	18773	31819	0.9	2.4E-01	AB032785.1	EST_HUMAN	wc33405.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5602	18797	31847	0.59	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5772	18964	32266	12.86	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5772	18964	32267	12.86	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5800	18950		0.7	2.4E-01	M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
6010	25815		0.97	2.4E-01	AJ133836.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (calM2 gene)
6016	19200	32517	2.54	2.4E-01	BF592336.1	EST_HUMAN	7154404.x1 NCL CGAP_B18 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4; contains element TAR1 TAR1 repetitive element
6106	19286	32620	2.47	2.4E-01	AF035546.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
6215	19350	32738	2.49	2.4E-01	7661801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6269	19443	32792	0.94	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cda Homo sapiens cDNA clone cdaADE11 5'
6516	19681	33051	0.87	2.4E-01	AA398872.1	EST_HUMAN	270402.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727683 3'
6665	19824	33212	1.59	2.4E-01	AI698989.1	EST_HUMAN	wc82c11.x1 NCL CGAP_Fan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464 PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7498	20573	34046	7.79	2.4E-01	LA3901.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
7802	20954	34481	0.68	2.4E-01	AF228644.1	NT	Mus musculus DXImx48a protein (DXImx48a) mRNA, complete cds
8271	21353	34869	0.5	2.4E-01	X97252.1	NT	M.musculus pah gene and promoter
8271	21353	34869	0.5	2.4E-01	X97252.1	NT	M.musculus pah gene and promoter
8392	21473	34999	1.48	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae r08 and hk08 genes; two component system 08
8392	21473	35000	1.48	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae r08 and hk08 genes; two component system 08
8544	21625	35162	1.29	2.4E-01	AJ012585.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
8798	21877	35416	1.18	2.4E-01	BF242794.1	EST_HUMAN	601877879F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106288 5'
9332	22408	35951	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9332	22408	35962	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9763	22701	36267	8.99	2.4E-01	AI693515.1	EST_HUMAN	wd43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains MER22.b1 TAR1 repetitive element;
9905	22945	36530	0.66	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
9905	22945	36531	0.66	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
10654	23688	37297	1.8	2.4E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11006	24085	37722	2.15	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11074	24149	37788	1.96	2.4E-01	AF030199.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11447	24508	38174	1.8	2.4E-01	BE286817.1	EST_HUMAN	601176415F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5'
11447	24508	38175	1.8	2.4E-01	BE286817.1	EST_HUMAN	601176416F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5'
11478	24537		8.04	2.4E-01	Z21647.1	NT	P.asiatica mosaic virus genomic RNA
12169	25127	38827	1.75	2.4E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
12269	25932		1.35	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive1-like1 (EIL1) mRNA, complete cds
12360	25258		1.62	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative mcf7 protein (mcf7 gene)

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12588	25914		1.95	2.4E-01	V01507.1	NT	Gallus gallus gene coding for α -actin
12839	26151		1.37	2.4E-01	BF228975.1	EST_HUMAN	RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA
13072	25701		1.4	2.4E-01	AJ238044.1	NT	Homo sapiens mRNA for bradykinin B1 receptor (B1BR gene)
13102	25718		4.16	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment H821C081
400	13597	26633	1.39	2.3E-01	S75898.1	NT	aromatase [Poephila gutturalis-zebra finches, ovary, mRNA, 3188 nt]
654	13840		5.53	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
684	13869	26900	29.31	2.3E-01	U67596.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
957	14130	27188	3.57	2.3E-01	BE311883.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1634	14766	27872	1.11	2.3E-01	AJ245480.1	NT	Brassica napus sig gene for S-Hoccy glycoprotein, cultivar T2
1881	14873	27898	1.72	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
2103	15242		1.78	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2517	15843	28764	1.85	2.3E-01	BE297748.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2717	15835	28945	0.98	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2885	14573	27846	1.5	2.3E-01	AB015033.1	NT	Marrubium agarosifolium gyb gene for DNA gyrase subunit B, partial cds, strain:IFO 14967
3028	16204	28227	1.08	2.3E-01	AA601378.1	EST_HUMAN	not6d06.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element THR repetitive element;
3153	16328		7.06	2.3E-01	R21732.1	EST_HUMAN	y971507.s1 Scars placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3456	16623	28844	1.32	2.3E-01	H69836.1	EST_HUMAN	y97110.r1 Scars fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:213283 5'
							GSTA5=glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3944	17103	30100	0.98	2.3E-01	S82821.1	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4046	17202		5.15	2.3E-01	7662133	NT	y17101.r1 Scars placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4470	17610	30588	0.88	2.3E-01	R82252.1	EST_HUMAN	Mus musculus renin (Ren-1c) gene, promoter region
4520	17659		1.91	2.3E-01	L78789.1	NT	Synchoecelis sp. PCC8803 complete genome, 1/27, 1-133859
4573	17710	30693	1.12	2.3E-01	D90899.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4611	17748	30728	2.76	2.3E-01	AF092535.1	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
4676	17811	30800	5.55	2.3E-01	5031984	NT	Mus musculus tulip 1 mRNA, complete cds
5159	18281	31246	0.87	2.3E-01	AB032400.1	NT	
5223	18345		1.03	2.3E-01	M16364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
5260	18379	31345	0.93	2.3E-01	BF574804.1	EST_HUMAN	602132210F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271547 5'
5419	18620	31596	2.47	2.3E-01	AB040845.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
							7k30b06.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476689 3' similar to SW:GAG SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10].
5545	18742	31776	2.03	2.3E-01	BF058381.1	EST_HUMAN	

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5647	18841	32122	5.25	2.3E-01	X86887.1	NT	C. familiaris rom1 gene
5766	18958		0.99	2.3E-01	L39112.1	NT	Vitiforma cornum small subunit ribosomal RNA gene
5870	19060	32367	1.32	2.3E-01	S60371.1	NT	23S rRNA [Leuconostoc camosum, Genomic, 2866 nt]
6062	19244	32569	1.98	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6082	19244	32570	1.98	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6794	19949	33348	0.66	2.3E-01	AF198089.1	NT	Oryctolagus cuniculus cytochrome oxidase subunit VIa (coxVIa2) mRNA, complete cds; nuclear gene for mitochondrial product
7017	20153	33573	4.63	2.3E-01	A1718148.1	EST_HUMAN	as42f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element;
7260	20343	33795	0.86	2.3E-01	8923323	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7440	20517	33989	0.76	2.3E-01	AF000227.1	NT	Secale cereale omega secalin gene, complete cds
7573	20645	34123	2.54	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
7576	20648	34125	5.37	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLCDB08 5'
7576	20648	34126	5.37	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLCDB08 5'
7764	20840		4.26	2.3E-01	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
7789	20845	34338	1.56	2.3E-01	BE888071.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
7931	20981		2.8	2.3E-01	N80983.1	EST_HUMAN	zat12e08.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:292358 5'
7968	21018	34530	0.71	2.3E-01	11416821	NT	Homo sapiens protocadherin alpha cluster (LOC63960), mRNA
7968	21018	34531	0.71	2.3E-01	11416821	NT	Homo sapiens protocadherin alpha cluster (LOC63960), mRNA
8036	21118	34637	0.52	2.3E-01	AL161558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
8183	21265	34788	1.73	2.3E-01	M68931.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8690	21770	35300	0.62	2.3E-01	U57999.1	NT	Mus musculus prosaposin (psapISGP-1) gene, complete cds
8972	22051	35594	0.58	2.3E-01	AW090541.1	EST_HUMAN	xc90a06.x1 NCL CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591554 3'
9089	22168	35715	0.52	2.3E-01	AW864460.1	EST_HUMAN	EST376533 MAGE resequences, MAGH Homo sapiens cDNA
9341	22417	35970	0.64	2.3E-01	AA372184.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9341	22417	35971	0.64	2.3E-01	AA372184.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9780	22820	36398	0.5	2.3E-01	6679318	NT	Mus musculus phosphotyrosine 3-kinase catalytic subunit delta (Ptk3cd), mRNA
9930	22970	36559	0.53	2.3E-01	BE277860.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2966739 5'
9985	23024	36616	0.81	2.3E-01	AW964460.1	EST_HUMAN	EST376533 MAGE resequences, MAGH Homo sapiens cDNA
10037	23075	36675	1.57	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10071	23109	38712	0.63	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0036-281289-001-004 DT0036 Homo sapiens cDNA
10138	23176	38773	2.62	2.3E-01	BE173060.1	EST_HUMAN	MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
10197	23234	38823	2.48	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10658	23692	37302	0.94	2.3E-01	AF201929.1	NT	Murine hepatitis virus strain 2, complete genome
10671	23705		5.89	2.3E-01	BF133577.1	EST_HUMAN	601848155R2 NIH_MGC 59 Homo sapiens cDNA clone IMAGE:4102092 3'
11465	24524	38195	2.24	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11465	24524	38196	2.24	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11633	24713	38404	2.43	2.3E-01	AE002187.2	NT	Chlamydomonas reinhardtii AR39, section 4 of 94 of the complete genome
12099	25079		1.36	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADC Homo sapiens cDNA clone ADCAGH01 5'
12281	25210		3.07	2.3E-01	U45428.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12370	25264		48.78	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT28M6 Homo sapiens cDNA clone HCOE44 5'
12395	25873		1.23	2.3E-01	AA089819.1	EST_HUMAN	chr1424, seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12484	26088	31657	4.08	2.3E-01	AW303623.1	EST_HUMAN	xx21d07.x1 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175
12500	26143	31552	7.05	2.3E-01	BE882484.1	EST_HUMAN	Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTR5.b2 TAR1 repetitive element ;
12563	26378		1.77	2.3E-01	BF66319.1	EST_HUMAN	601507202F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3908689 5'
12612	25411		2.74	2.3E-01	AJ006519.1	NT	602144459F1 NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4287719 5'
12708	25470		1.22	2.3E-01	U49645.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12712	25411		1.84	2.3E-01	AJ006519.1	NT	Pleurodeles waltli distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
13009	25666		2.36	2.3E-01	BF475611.1	EST_HUMAN	Rattus norvegicus mRNA for acid gated ion channel
92	13327	26355	1.13	2.2E-01	A1052190.1	EST_HUMAN	nac39h12.x1 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:3385950 3' similar to contains element
1598	14749	27833	2.74	2.2E-01	AF187850.1	EST_HUMAN	MER38 repetitive element ;
2155	15291	28418	2.19	2.2E-01	M34640.1	NT	0274810 x1 Soares_fetal_liver_spleen_1NFLS.S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to
2476	15603	28728	7.16	2.2E-01	BF677638.1	EST_HUMAN	TR-Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN ;
2654	15777	28890	1.63	2.2E-01	BE618258.1	EST_HUMAN	Homo sapiens PPAR delta gene, promoter region
2654	15777	28891	1.63	2.2E-01	BE618258.1	EST_HUMAN	Fresh-water sponge Emfr1 alpha collagen (COLF1) gene
2946	16123	29136	4.94	2.2E-01	BE156625.1	EST_HUMAN	60205608F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4249969 5'
2946	16123	29137	4.94	2.2E-01	BE156625.1	EST_HUMAN	601462829F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3866190 5'
2987	16163		2.07	2.2E-01	AF020503.1	NT	601462829F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3866190 5'
3479	16646		2.35	2.2E-01	AL161562.2	NT	PM2-HT0353-281289-003-a12 HT0353 Homo sapiens cDNA
							PM2-HT0353-281289-003-a12 HT0353 Homo sapiens cDNA
							Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
							Arabidopsis thaliana DNA chromosome 4, contig fragment Nb_62

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3848	17008	30009	0.62	2.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4211	17380	30349	0.69	2.2E-01	AF213391.1	NT	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4242	17388		0.8	2.2E-01	U68174.1	NT	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds
4328	17471		1.07	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4335	17478	30480	6.62	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4379	17522	30502	2.74	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Meik1) mRNA, complete cds
4379	17522	30503	2.74	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Meik1) mRNA, complete cds
4475	17615	30595	1.07	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4475	17615	30596	1.07	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4947	18077		1.09	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4952	18082	31058	2.2	2.2E-01	AA211216.1	EST_HUMAN	z687c05.1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648968 5'
5156	18278		1.57	2.2E-01	L13299.1	NT	Mus musculus vinculin gene, exon 3
5226	18348	31319	1.34	2.2E-01	BE141035.1	EST_HUMAN	MRO-HT0067-201098-002-c10 HT0067 Homo sapiens cDNA
5863	19053	32360	1.89	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5874	19084		3.75	2.2E-01	D84000.1	NT	Streptococcus sp. PCC6803 complete genome, 19/27, 2392729-2538999
6122	19301	32640	0.78	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6122	19301	32641	0.78	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6845	19998	33405	0.77	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
7166	20299	33742	10.63	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'
7279	20362	33815	1.61	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7279	20362	33816	1.61	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7442	20519	33981	2.36	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7442	20519	33982	2.36	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7655	20723	34169	0.62	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7678	20930	34436	0.88	2.2E-01	AF287967.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
7909	20957	34463	0.71	2.2E-01	AB024553.1	NT	Bacillus halodurans DNA, complete and partial cds, strain C-125
8210	21292		2.45	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
8280	21362	34881	2.68	2.2E-01	Z49933.1	NT	E. coli sepA and sepB genes
8748	21827	35363	0.61	2.2E-01	AJ132918.1	NT	Pan troglodytes MeCP2 gene 3'UTR
9083	22162	35705	0.52	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9083	22162	35706	0.52	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9097	22176	35720	4.53	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
9117	22196	35740	0.48	2.2E-01	U09954.1	NT	Mus musculus ICR/Swiss glycerialdehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
9224	22302		2.88	2.2E-01	AW855039.1	EST_HUMAN	PM3-CT0263-241289-009-507 CT0263 Homo sapiens cDNA
9315	22391	35942	1.98	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
9399	22473	36039	1.13	2.2E-01	BF376394.1	EST_HUMAN	MR1-TN0045-110900-008-002 TN0045 Homo sapiens cDNA
9489	22548	36109	1.42	2.2E-01	W02988.1	EST_HUMAN	z0403.1 Soares melanocyte 2NHM Homo sapiens cDNA clone IMAGE:281591 5'
9507	22773	36345	15.08	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9552	22817	36187	0.76	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)
9563	22705	36271	1.05	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9576	22718	36286	4.29	2.2E-01	M89643.1	NT	Brachydanio rerio ependymin beta and gamma chains (Epd) gene, complete cds
9820	22860	36441	0.65	2.2E-01	Q90980	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
10020	23058	36654	3.84	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds; nuclear gene for chloroplast product
10159	23196	36782	1.53	2.2E-01	BF205507.1	EST_HUMAN	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10380	23415	37024	1.11	2.2E-01	9625671	NT	Human herpesvirus 5, complete genome
10540	23575	37182	0.65	2.2E-01	T59472.1	EST_HUMAN	y63408.1 Stratagene ovary (8937217) Homo sapiens cDNA clone IMAGE:75855 5'
10540	23575	37183	0.65	2.2E-01	T59472.1	EST_HUMAN	y63408.1 Stratagene ovary (8937217) Homo sapiens cDNA clone IMAGE:75855 5'
10580	23615	37220	0.6	2.2E-01	AF069284.1	NT	Pseudomonas aeruginosa quinolone protein ethanoid dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquin>
10659	23693		0.79	2.2E-01	AF071001.1	NT	synthesis A (pqqA) genes, complete cds, and pyrroloquin>
10707	23740	37344	0.57	2.2E-01	AE001562.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10707	23740	37345	0.57	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10853	23886	37605	0.48	2.2E-01	AF049720.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11389	24450	38111	1.65	2.2E-01	AF257772.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11707	24794	38396	5.09	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
11748	23934	37660	3.7	2.2E-01	7706215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
12207	25161		1.33	2.2E-01	BE870359.1	EST_HUMAN	601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
12319	26156		1.96	2.2E-01	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12407	25286		3.24	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12518	18492	31531	1.86	2.2E-01	AW361098.1	EST_HUMAN	RC1-GT0249-141199-021-g04 CT0249 Homo sapiens cDNA
12519	25353		1.47	2.2E-01	AW661922.1	EST_HUMAN	h17b02.x1 NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2972523 3'
13115	26148		3.08	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKG Homo sapiens cDNA clone GKGAI1802 5'
993	14165	27226	1.88	2.1E-01	AA569289.1	EST_HUMAN	nm31e11.s1 NCL CGAP Lip2 Homo sapiens cDNA clone IMAGE:1061804
998	14167	27228	0.72	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1148	14312		2.43	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1225	14385	27446	1.45	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (fnar2), mRNA
1225	14385	27447	1.45	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (fnar2), mRNA
1540	14692	27771	4.29	2.1E-01	AJ249895.1	NT	Mus musculus mas proto-oncogene and lgt2 gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1963	15106	28206	2.15	2.1E-01	AA909824.1	EST_HUMAN	dk73g02.s1 NCL CGAP GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765 COMPLEMENT C3-PRECURSOR (HUMAN);
2224	15358	28488	3.55	2.1E-01	BF696073.1	EST_HUMAN	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2991	16167	29183	2.52	2.1E-01	6912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3533	16698	29709	6.1	2.1E-01	AA639482.1	EST_HUMAN	nc90b10.s1 NCL CGAP_C09 Homo sapiens cDNA clone IMAGE:1159579 3'
3908	17067		5.91	2.1E-01	9838361	NT	Beta vulgaris mitochondrial, complete genome
4125	17279		0.67	2.1E-01	AE001793.1	NT	Thermotoga maritima section 105 of 136 of the complete genome
4166	17315	30310	1.57	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4165	17315	30311	1.57	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4496	17835		1.63	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4699	17834	30819	1.82	2.1E-01	AB010273.1	NT	Homo sapiens pshep47 gene, complete cds
4757	17892	30871	0.93	2.1E-01	X83161.1	NT	P. falciparum mRNA for small GTPase rabt1
5138	18261	31228	0.7	2.1E-01	D13597.1	NT	Lampetra japonica mRNA for alpha-2-macroglobulin, complete cds
5416	18618	31592	6.31	2.1E-01	BF672695.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
7027	20163	33565	1.05	2.1E-01	AJ223392.1	NT	Dobo fragilis mitochondrial 16S rRNA gene, partial
7036	20091	33508	1.8	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7564	20636	34111	0.77	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7564	20636	34112	0.77	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7576	20647		1.88	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7883	20935	34441	1.54	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT19) gene, complete cds
7930	20980	34488	1.38	2.1E-01	AF068637.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7930	20960	34489	1.38	2.1E-01	AF088687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8263	21345		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1b), mRNA
8700	21760	35313	4.76	2.1E-01	U88399.1	NT	Haemophilus influenzae hmcD, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds
8987	22076	35615	0.91	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614.1_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0614.5'
8997	22076	35616	0.91	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614.1_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0614.5'
9159	22237		0.5	2.1E-01	AB022524.1	NT	Homo sapiens APC gene, exon 9
9237	22314	35856	6.7	2.1E-01	Z35786.1	NT	S. cerevisiae chromosome II reading frame ORF YEL025w
9704	22753	36323	0.66	2.1E-01	N42536.1	EST_HUMAN	yy1e10.1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270854.5'
9704	22753	36324	0.66	2.1E-01	N42536.1	EST_HUMAN	yy1e10.1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270854.5'
9713	22778	36346	2.72	2.1E-01	X97378.1	NT	A.thaliana mRNA for ATRantBP1b protein
9817	22857	36437	1.02	2.1E-01	AB038529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 8
10535	23570	37178	1.31	2.1E-01	Z97067.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10569	23604	37209	1.97	2.1E-01	P62824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10576	23611	37216	0.72	2.1E-01	BF574254.1	EST_HUMAN	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831.5'
11776	24768		1.34	2.1E-01	A1141875.1	EST_HUMAN	ga66108.X1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:1691751.3'
11862	24850		1.68	2.1E-01	11036847	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11879	24867	38565	2.6	2.1E-01	BE160422.1	EST_HUMAN	RC3-H10622-040500-013-b11 H10622 Homo sapiens cDNA
12688	25459		1.92	2.1E-01	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
12994	25646		1.39	2.1E-01	BE622149.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675.6'
13156	25753	31926	1.19	2.1E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
206	13428	26460	1.92	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avens, complete cds
547	13740		1.97	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
717	13899	26937	1.37	2.0E-01	M177085.1	NT	O. cuniculus gemline 1gH heavy chain V-H pseudogene, allotype V/He2
833	14011	27067	2.09	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
1038	14204	27261	1.83	2.0E-01	D90905.1	NT	Synechocystis sp. PCC6803 complete genome, 7/27, 781440-820815
1149	14313	27369	2.81	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1283	14439	27508	1.19	2.0E-01	AJ132685.5	NT	Homo sapiens rac1 gene
1336	14493	27563	1.99	2.0E-01	AW394937.1	EST_HUMAN	PW1-H10422-281299-002-c06 H10422 Homo sapiens cDNA
1516	14669	27752	22.4	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1582	14734	27816	2.68	2.0E-01	AB007674.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1588	14740	27821	3.48	2.0E-01	AF280700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1732	14882	27973	0.96	2.0E-01	U22348.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1755	14804		2.58	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1786	14945		3.87	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1941	15084	28185	1.46	2.0E-01	8922238	NT	Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA
2423	15552		1.9	2.0E-01	X82877.1	NT	H. sapiens Nar-D glucose cotransport regulator gene
2955	16132		0.78	2.0E-01	AF074990.1	NT	Homo sapiens full length insert cDNA YH89A11
3576	16741	29758	0.72	2.0E-01	P46607	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3658	16821		0.91	2.0E-01	AW238005.1	EST_HUMAN	xp15b02.x1 NCL CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3798	16959	28963	0.86	2.0E-01	P34641	SWISSPROT	NER21 repetitive element
3802	16963		0.6	2.0E-01	6680797	NT	GED-11 PROTEIN
4688	17823		8.71	2.0E-01	BE826165.1	EST_HUMAN	Mus musculus bone morphogenetic protein 6 (Bmp6), mRNA
5152	18274	31243	6.41	2.0E-01	8922080	NT	QV4-EN0032-180500-223-e03 EN0032 Homo sapiens cDNA
5243	16959	26983	0.6	2.0E-01	P34641	SWISSPROT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5561	18758	31797	2.55	2.0E-01	X56600.1	NT	GED-11 PROTEIN
5859	19049	32355	2.08	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5963	19149	32464	0.82	2.0E-01	X91856.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
6185	19361	32709	5.99	2.0E-01	U15300.1	NT	F. rubripes DNA encoding for valy-IRNA synthetase
6303	19476		0.74	2.0E-01	M75967.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6559	19721	33098	47.65	2.0E-01	X61033.1	NT	Human hepatocyte growth factor gene, exon 1
6659	19818	33206	3.74	2.0E-01	AW360865.1	EST_HUMAN	Mauratus mu class glutathione transferase gene
7445	20522	33995	1.41	2.0E-01	AF250371.1	NT	PM1-CT0247-141088-007-g06 CT0247 Homo sapiens cDNA
7603	20673	34147	0.83	2.0E-01	P54422	SWISSPROT	Mus musculus phosphofructokinase-1 C isozyme (Pfk) gene, exons 3 through 7
8139	21221		6.16	2.0E-01	AF028028.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
8395	21476	35003	3.12	2.0E-01	X91151.1	NT	Andes virus strain O123133 glycoprotein G1 and G2 precursor, gene, partial cds
8921	22001		0.48	2.0E-01	BE562247.1	EST_HUMAN	M. musculus scp2 gene exon 14
9551	22616	36186	1.17	2.0E-01	U82511.1	NT	601344648F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677794 5'
9590	22645	36215	0.62	2.0E-01	U71122.1	NT	Dicystidium discoidium random slug cDNA19 protein (sc19) mRNA, partial cds
9756	22694		5.42	2.0E-01	AE001278.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9947	22986	36579	0.92	2.0E-01	P11420	SWISSPROT	Chlamydia trachomatis section 5 of 87 of the complete genome
10095	23133		0.62	2.0E-01	AF146892.1	SWISSPROT	DAUGHTERLESS PROTEIN
			2.24	2.0E-01	AF146892.1	NT	DAUGHTERLESS PROTEIN
							Homo sapiens filamin 2 (FLN2) mRNA, complete cds

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10247	23282	36878	1.89	2.0E-01	AF088907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10247	23282	36879	1.89	2.0E-01	AF088907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10371	23406	37016	0.67	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10371	23406	37017	0.67	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10419	23454		0.8	2.0E-01	X78388.1	NT	D melanogaster DNA mobile element (hoppe)
10616	23650	37259	0.88	2.0E-01	X97121.1	NT	R. norvegicus mRNA for NTR2 receptor
11079	24154	37791	2.12	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11079	24154	37792	2.12	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11908	24895	38597	1.33	2.0E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
11908	24895	38598	1.33	2.0E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
12666	25443		1.24	2.0E-01	AF206637.2	NT	Pimephales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12699	25965		1.64	2.0E-01	AF302773.1	NT	Homo sapiens rhain-Lm isoform (rhain) mRNA, complete cds
12812	25878	31851	1.63	2.0E-01	AW915297.1	EST_HUMAN	EST1987405 IMAGE resequences, MAGN Homo sapiens cDNA
12852	25662	31966	1.63	2.0E-01	AI023592.1	EST_HUMAN	ov80a10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1848610 3'
12977	25636		17.48	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
113	13344		4.89	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
362	13573	26604	5.58	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
673	13859	26889	1.54	1.9E-01	U32581.2	NT	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds
673	13859	26890	1.54	1.9E-01	U32581.2	NT	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds
680	13866	26897	8.31	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
681	13866	26897	6.7	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
1010	14181		1.72	1.9E-01	7305180	NT	Mus musculus Interleukin 2 receptor, gamma chain (IL2rg), mRNA
1128	14283	27349	5.63	1.9E-01	AA358813.1	EST_HUMAN	EST 67784 Fetal lung II Homo sapiens cDNA 5' end
1401	14555	27629	2.42	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1466	14620		4.34	1.9E-01	AF184823.1	NT	Plasmodium vivax reticulocyte binding protein-2 (bbp-2) gene, complete cds
2456	15584	28711	3.66	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2989	16165	29181	3.81	1.9E-01	U68066.1	NT	Sigmodon hispidus p53 gene, partial cds
3004	16179		7.53	1.9E-01	U00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3482	16650	29666	4.07	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3569	16734	29760	4.94	1.9E-01	R16487.1	EST_HUMAN	yf42f10.1 Soares fetal liver spleen 1NF5 Homo sapiens cDNA clone IMAGE:129547 5'
3907	17066	30055	1.09	1.9E-01	AF264017.1	NT	Rattus norvegicus arylacetamidase deacetylase gene, complete cds
4100	17255	30266	3.68	1.9E-01	AB006784.1	NT	Schistosoma japonicum pombe DNA for cytoplasmic dynein heavy chain, complete cds
4193	17343	30336	1.51	1.9E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4251	17397		1.31	1.9E-01	AE001912.1	NT	Deinococcus radiodurans R1 section 49 of 229 of the complete chromosome 1

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4346	17488	30471	0.88	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-280700-007-404 FN0010 Homo sapiens cDNA
4592	17728	30711	0.8	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
5124	18250		1.08	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5721	18914		5.19	1.9E-01	AW130149.1	EST_HUMAN	x29a07.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5761	18953	32286	8.03	1.9E-01	AF127837.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5962	19148	32463	1.08	1.9E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
6006	19191		2.45	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6457	19624	32987	1.03	1.9E-01	AU1762391.1	EST_HUMAN	wf54h02.x1 NCI_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2394099 3'
6518	19683	33054	1.1	1.9E-01	AW148452.1	EST_HUMAN	xf14c08.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7112	18538	31495	1.54	1.9E-01	R43212.1	EST_HUMAN	y09a12.s1 Soares infant brain T1B1 Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element;
7138	20273	33712	0.74	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7138	20273	33713	0.74	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7409	20487	33957	0.92	1.9E-01	U73846.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
7638	20707	34186	0.78	1.9E-01	U93688.1	NT	Staphylococcus aureus toxic shock syndrome toxin-1 (tsst), enterotoxin (ent), and integrase (int) genes, complete cds
7661	20728	34204	1.38	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (T0PP8) gene, complete cds
7708	20773	34258	2.84	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds
8174	21266	34778	1.83	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8885	21964	35500	13.56	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1188 protein, partial cds
9146	22225	35768	1.5	1.9E-01	M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
9146	22225	35769	1.5	1.9E-01	M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
10079	23117	36719	0.77	1.9E-01	AA912486.1	EST_HUMAN	ol96g10.s1 NCI_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu repetitive element;
10447	23482	37090	0.81	1.9E-01	BE830353.1	EST_HUMAN	RC5-E T0082-060700-022-A02 ET0082 Homo sapiens cDNA
10447	23482	37091	0.81	1.9E-01	BE830353.1	EST_HUMAN	RC5-E T0082-060700-022-A02 ET0082 Homo sapiens cDNA
10880	23965	37593	1.38	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10880	23965	37594	1.38	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
10992	24509	37704	2.18	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12025	25019	38711	2.21	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12047	25028	38735	1.48	1.9E-01	L07344.1	NT	Influenza A/Guangdong/243/72 nucleoprotein (seg 5) gene, 5' end

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
32	13270	26274	1.85	1.8E-01	U73200.1	NT	Mus musculus p16Rip mRNA, complete cds
270	16009	26519	1.47	1.8E-01	AB022000.1	NT	Mus musculus Ctg gene for chaparotin containing TCP-1 gamma subunit, partial cds
381	13589	26625	1.9	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
765	13946	26963	0.78	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
1005	14178	27235	1.8	1.8E-01	A1912212.1	EST_HUMAN	wd7102.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1115	14279	27335	2.14	1.8E-01	AF000580.1	NT	Dictyostelium discoideum plasmid Ddp5, complete genome
1317	14473	27640	6.97	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1533	14696	27765	1.49	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1533	14696	27766	1.49	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1915	15068		1.91	1.8E-01	A1733708.1	EST_HUMAN	qp22d10.x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE ;
1965	15108	28208	2.28	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya6, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2756	15873		3.34	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081289-036-g04 DT0018 Homo sapiens cDNA
2963	16140		2.3	1.8E-01	AF184589.1	NT	Jonopodium acule LEAFY protein (LEAFY2) gene, partial cds
2968	16144	28163	1.18	1.8E-01	AW182300.1	EST_HUMAN	Xj47a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3194	18369	29375	1.61	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3452	16819	28638	0.77	1.8E-01	BF183592.1	EST_HUMAN	G01809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040821 3'
3712	16973	29877	0.87	1.8E-01	H03369.1	EST_HUMAN	Y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3712	16973	29878	0.87	1.8E-01	H03369.1	EST_HUMAN	Y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4453	17553		0.92	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DOB), complete cds
4678	17813	30901	5.61	1.8E-01	AL161596.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4895	18025	31011	2.68	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya6, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5129	18254	31219	0.65	1.8E-01	X79794.1	NT	N. labacum mRNA pNLA-35
5158	18280	31245	1.79	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151299-112-g06 ST0203 Homo sapiens cDNA
5206	18327	31297	2.55	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5218	18340	31313	0.89	1.8E-01	A1439881.1	EST_HUMAN	t57e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5291	18409	31376	1.2	1.8E-01	Y08310.1	NT	M. barkeri mtlaC and mtlaB genes

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5413	18615	31589	0.81	1.8E-01	BE082628.1	EST_HUMAN	RC6-BT0641-300300-011-H03 BT0641 Homo sapiens cDNA
5929	19115	32428	1.19	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
6047	19230	32554	0.95	1.8E-01	N28628.1	EST_HUMAN	yx38108.r1 Soares melanocyte 2NBM Homo sapiens cDNA clone IMAGE:264063 5'
6256	19430	32776	0.89	1.8E-01	6678428	NT	Mus musculus Trf receptor-associated factor 6 (Traf6), mRNA
6256	19430	32777	0.89	1.8E-01	6678428	NT	Mus musculus Trf receptor-associated factor 6 (Traf6), mRNA
6641	19800	33189	1.16	1.8E-01	Q9QY14	SWISSPROT	FORHEAD BOX PROTEIN E3
6688	19846		2.12	1.8E-01	N94853.1	EST_HUMAN	yx2h02.r1 Soares, multiple sclerosis_2NBHSP Homo sapiens cDNA clone IMAGE:278163 5'
7146	20281	33722	1.11	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wslus, complete cds
7146	20281	33723	1.11	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wslus, complete cds
7202	20087	33477	0.87	1.8E-01	BE961353.1	EST_HUMAN	601648361R2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3932247 3'
7604	20874	34148	0.81	1.8E-01	AF001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
8810	21889	35431	0.58	1.8E-01	AW966118.1	EST_HUMAN	EST378191 IMAGE ressequences, MAGI Homo sapiens cDNA
9543	22608	36176	1.58	1.8E-01	M73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9574	22716	36284	1.52	1.8E-01	9626232	NT	Bacteriophage like, complete genome
9692	22741		0.8	1.8E-01	AA4693751.1	EST_HUMAN	h02a06.s1 NC1_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1, L3 L1
9774	22814	36392	0.95	1.8E-01	P15272	SWISSPROT	repetitive element ;
9774	22814	36393	0.95	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9814	22854	36432	1.02	1.8E-01	M26019.1	NT	AMP NUCLEOSIDASE
9814	22854	36433	1.02	1.8E-01	M26019.1	NT	S.commune ordidine-5'-phosphate decarboxylase (URA1) gene, complete cds
9981	23020	36613	0.81	1.8E-01	P08123	SWISSPROT	S.commune ordidine-5'-phosphate decarboxylase (URA1) gene, complete cds
9986	23025	36617	0.71	1.8E-01	U67548.1	NT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
10337	23372						Methanococcus jannaschii section 90 of 150 of the complete genome
10578	23613	37218	0.67	1.8E-01	AF200252.1	NT	Aquafus amplius cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10785	23618	37441	1.46	1.8E-01	X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
10873	23958	37588	2.02	1.8E-01	AB011171.1	NT	Homo sapiens mRNA for KIA0559 protein, partial cds
10917	24000	37633	5	1.8E-01	X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
10974	20281	33722	3.05	1.8E-01	U38908.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, hollin and lysis genes, complete cds
10974	20281	33723	3.05	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wslus, complete cds
10975	24054	37688	4.41	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wslus, complete cds
11270	24338	37976	2.08	1.8E-01	AF019107.1	NT	Dicotyledon discoidium unknown (DG1041) gene, complete cds
11551	24806	38284	1.41	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
					AW275728.1	EST_HUMAN	xp40h10.x1 NC1_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2742883 3'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11750	23938	37563	8.94	1.8E-01	X57033.1	NT	B laurus mRNA for potassium channel
12061	25042	38751	3.48	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r) mRNA
12124	25104	38808	1.77	1.8E-01	AA095094.1	EST_HUMAN	op2788.seq F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12239	25183		1.79	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome
12306	25224	32103	1.28	1.8E-01	BF348623.1	EST_HUMAN	602019828F1 NCLCGAP_Bim87 Homo sapiens cDNA clone IMAGE:4155318 5'
12719	14473	27540	1.18	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
12811	25541		3.28	1.8E-01	Q86682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETTI PROTEIN) (PTP PROTEIN)
12942	25620		20.8	1.8E-01	R24494.1	EST_HUMAN	yf48h10.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12988	25643		4.98	1.8E-01	Y11114.1	NT	E dispar mRNA for hexokinase (hvk1)
13035	26134	31548	1.7	1.8E-01	9508952	NT	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcolce), mRNA
581	13782	26801	6.4	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815788 5'
828	14006	27063	3.16	1.7E-01	X53330.1	NT	P dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
983	14156		1.79	1.7E-01	P39616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1083	14249	27305	0.82	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1083	14249	27306	0.89	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1880	15006	28113	2.44	1.7E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
2038	16179		3.23	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2922	16100	29112	2.13	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hprt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2922	16100	29113	2.13	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hprt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2953	16159	29188	1.47	1.7E-01	AA336909.1	EST_HUMAN	EST141651 Erdemetal tumor Homo sapiens cDNA 5' end
3081	16237	29257	1.09	1.7E-01	AJ238736.1	NT	Naja naja atra ctk-1 gene, exons 1-3
3081	16237	29258	1.09	1.7E-01	AJ238736.1	NT	Naja naja atra ctk-1 gene, exons 1-3
3174	16349	29355	1.65	1.7E-01	AF081614.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3451	16618	29637	0.81	1.7E-01	N55763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3534	16699	29710	1.52	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpC gene, adpD gene, adpE gene and adpF gene
4049	17205	30215	6.06	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment; partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4881	17816		2.49	1.7E-01	X52936.1	NT	Schistosoma gregaria alpha repellent DNA
4894	18014	30968	0.59	1.7E-01	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4961	18090	31088	1.31	1.7E-01	A1247635.1	EST_HUMAN	qh57a09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808.3' similar to contains OFR.b1 OFR repetitive element;
5231	18353		1.07	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1b (ae) gene, complete cds
5272	18391	31359	0.72	1.7E-01	BF030010.1	EST_HUMAN	601557260F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827167.5'
5312	18429	31396	0.91	1.7E-01	D37951.1	NT	Rattus norvegicus mRNA for MIBP1 (c-myc intron binding protein 1), complete cds
5524	18721	31737	1.88	1.7E-01	AA470686.1	EST_HUMAN	het13a02.s1 NC1 CGAP_C03 Homo sapiens cDNA clone IMAGE:881066.3' similar to gb:M17886.60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5524	18721	31738	1.88	1.7E-01	AA470686.1	EST_HUMAN	het13a02.s1 NC1 CGAP_C03 Homo sapiens cDNA clone IMAGE:881066.3' similar to gb:M17886.60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5710	18903	32198	0.92	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6459	19626	32968	12.64	1.7E-01	H72118.1	EST_HUMAN	ys02g06.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:213658.3'
6517	19662	33052	0.72	1.7E-01	A1370976.1	EST_HUMAN	ta26c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492.3'
6517	19662	33053	0.72	1.7E-01	A1370976.1	EST_HUMAN	ta26c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492.3'
6992	18511	31503	0.75	1.7E-01	BE300286.1	EST_HUMAN	600944087T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960248.3'
7019	20155		1.94	1.7E-01	AF026562.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
7140	20275		0.99	1.7E-01	Z92910.1	NT	Homo sapiens HFE gene
7369	20448	33911	1.38	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7448	20525	33998	8.51	1.7E-01	BE734179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3943964.5'
7649	20718	34195	1.21	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLF0 PROTEIN)
7666	26850	34208	0.64	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
8045	21126	34548	1.26	1.7E-01	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
8150	21232	34752	0.75	1.7E-01	AF150669.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8472	21553	35083	7.35	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8472	21553	35084	7.35	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8895	21974	35511	0.5	1.7E-01	AW992873.1	EST_HUMAN	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
8925	22004	35543	1.93	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
9045	22124	35668	0.94	1.7E-01	AF217413.1	NT	Homo sapiens neurodin 3 isoform gene, complete cds, alternatively spliced
9045	22124	35667	0.94	1.7E-01	AF217413.1	NT	Homo sapiens neurodin 3 isoform gene, complete cds, alternatively spliced
9198	22276	35814	0.51	1.7E-01	R77002.1	EST_HUMAN	y66g02.r1 Soares_placenta_Nb2HP Homo sapiens cDNA clone IMAGE:144242.5'
9369	22444	36005	0.53	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184.5'
9369	22444	36006	0.53	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184.5'
9789	22829	36407	9.03	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9899	22939	36524	0.54	1.7E-01	AW977455.1	EST_HUMAN	EST389564 IMAGE resequences, MAGO Homo sapiens cDNA
9899	22939	36525	0.54	1.7E-01	AW977455.1	EST_HUMAN	EST389564 IMAGE resequences, MAGO Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9918	22955	36543	2.08	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9992	23031	36621	0.47	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
9992	23031	36622	0.47	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
10013	23051	36645	0.93	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10438	23473		2.77	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10605	23639	37247	1.59	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
10607	23641	37249	1.89	1.7E-01	AA627972.1	EST_HUMAN	h960607.s1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:U25081 TRANSFORMING PROTEIN RHOC (HUMAN);
10919	24002	37636	9.54	1.7E-01	BE930835.1	EST_HUMAN	801286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
11045	24122	37766	2.12	1.7E-01	AA814617.1	EST_HUMAN	cf43a03.s1 NCL_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426824 3'
11373	24434	38030	6.81	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11373	24434	38091	6.81	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11657	24738	38427	1.71	1.7E-01	AA883375.1	EST_HUMAN	44509.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460297 3'
12011	24995		1.5	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
12042	25023	38727	1.67	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FORN) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12042	25023	38728	1.67	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FORN) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12142	25117	38825	2	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
12275	26087		1.45	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12567	25920		1.18	1.7E-01	AI824404.1	EST_HUMAN	ts89g05.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2214872 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
12607	25600	31972	7.24	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
128	13356	26388	1.7	1.6E-01	AF217532.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
697	18986	26913	1.16	1.6E-01	R31497.1	EST_HUMAN	y175112.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:1355599 5'
1561	14703	27783	4.26	1.6E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1910	15093		1.27	1.6E-01	AJ235272.1	NT	Rickettsia prowazekii strain Madrid E, complete genome, segment 3/4
1977	15120	28221	2.14	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2041	15182		1.43	1.6E-01	U10334.1	NT	Craosotrea gigas RNA polymerase II largest subunit mRNA, partial cde
2457	16063	28712	1.09	1.6E-01	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2562	15687	28813	2.73	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2657	16134	28149	14.1	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2957	16134	29150	14.1	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3723	16884	29889	1.23	1.0E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol AB13 gene
3723	16884	29890	1.23	1.0E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol AB13 gene
3872	17031	30030	0.82	1.0E-01	AE000962.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4107	17261		2.8	1.0E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 83 of the complete chromosome
4144	17296	30288	1.21	1.0E-01	AF084456.1	NT	Critidia fasciculata trypanoxin 1 (bn1) gene, complete cds
4448	17598	30569	10.91	1.0E-01	AF179680.1	NT	Homo sapiens apelin gene, complete cds
4578	17715		2.49	1.0E-01	AW968601.1	EST_HUMAN	EST380677 IMAGE:2869699 3' similar to TR:075984 075984
4586	17723		4.39	1.0E-01	6783319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
5060	18188	31162	1.39	1.0E-01	AA088343.1	EST_HUMAN	z84h09.s1 StrataGene colon (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955
5083	18211	31183	1.8	1.0E-01	AJ008356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV ;
5083	18211	31184	1.8	1.0E-01	AJ008356.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
5345	18458		0.93	1.0E-01	AF045283.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
5503	18702	31719	0.81	1.0E-01	L40608.1	NT	Gallus gallus smooth muscle/non-muscle myosin light chain kinase gene, exon 29
5639	18833	31909	2.9	1.0E-01	AW197496.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5639	18833	31910	2.9	1.0E-01	AW197496.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5651	18845	32126	1.99	1.0E-01	AF034716.1	NT	HYPOTHETICAL 127.6 KD PROTEIN ;
6152	19328	32674	0.73	1.0E-01	BE25803.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN ;
6558	19720	33096	2.06	1.0E-01	AL161588.2	NT	Rattus norvegicus CCAA7enhancer binding protein epsilon (cebpe) gene, complete cds
6558	19720	33097	2.06	1.0E-01	AL161588.2	NT	RG3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
6939	20252	33698	0.79	1.0E-01	AB046786.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6965	20213	31485	0.66	1.0E-01	BF683630.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7103	18530	34001	4.15	1.0E-01	AW291215.1	EST_HUMAN	Homo sapiens mRNA for KIAA1566 protein, partial cds
7451	20528	34001	0.71	1.0E-01	Z46632.1	NT	602139855F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301004 5'
7955	21005	34516	1.63	1.0E-01	AW246359.1	EST_HUMAN	U1H-B12-agi-B-06-0-UI.st NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7982	21031	34544	0.84	1.0E-01	6783237	NT	S.cerevisiae chromosome X reading frame ORF YJR132w
7986	21035		1.03	1.0E-01	AU136528.1	EST_HUMAN	2822248.5p100 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
8063	21136	34657	1.62	1.0E-01	L49349.1	NT	Mus musculus Ca<2+>-dependent activator protein for secretion (Cadps), mRNA
8215	21297		0.53	1.0E-01	BE244087.1	EST_HUMAN	AU136525 PLACET1 Homo sapiens cDNA clone PLACE1004466 5'
8310	21392	34916	0.77	1.0E-01	U38243.1	NT	Cerilla gorilla endrogen receptor gene, partial exon
							TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607
							Bacteroides vulgatus beta-lactamase (ctxA) gene, complete cds and mobilization protein (mobA) gene, complete cds

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8833	21912	35450	1.08	1.6E-01	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410
9026	22105	35646	0.77	1.6E-01	R13673.1	EST_HUMAN	yf60h08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:26873 5'
9133	22212		0.74	1.6E-01	L36861.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
9171	22249	35792	1.85	1.6E-01	Z49501.1	NT	S. cerevisiae chromosome X reading frame ORF YJR001w
9311	22367		0.78	1.6E-01	AF11167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9851	22891		1.77	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041199-011-01 ST0200 Homo sapiens cDNA
9854	22894	36475	1.99	1.6E-01	Z49501.1	NT	S. cerevisiae chromosome X reading frame ORF YJR001w
9891	22931		1.16	1.6E-01	BE155694.1	EST_HUMAN	PM2-HT0353-270100-004-f11 HT0353 Homo sapiens cDNA
10826	23859	37482	0.5	1.6E-01	11128018	NT	Homo sapiens nuclear autoantigen (GS2NA), mRNA
10893	23977	37809	2.34	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
11244	24313	37951	1.34	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11244	24313	37952	1.34	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11249	24318	37958	1.62	1.6E-01	BE259649.1	EST_HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
11377	24438		3.6	1.6E-01	AF106094.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11697	24694	38386	7.53	1.6E-01	6671552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Aptb1), mRNA
12277	25207	38363	3.89	1.6E-01	AV719585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
12597	25402	32043	2	1.6E-01	L14933.1	NT	Rat convertase PC5 mRNA, 5' end
12630	25423		1.38	1.6E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-H01_1 LT0074 Homo sapiens cDNA
12733	25893		11.64	1.6E-01	AB045310.1	NT	Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds
12833	25615		2.71	1.6E-01	AK024496.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
13029	25678		5.04	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
13054	25680	31964	1.69	1.6E-01	9506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
13080	25694		1.4	1.6E-01	BE267894.1	EST_HUMAN	601125459F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345038 5'
13199	25782		1.29	1.6E-01	BF672698.1	EST_HUMAN	602162004F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293145 5'
258	13477	26508	1.7	1.6E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
258	13477	26509	1.7	1.6E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
600	15984		2.5	1.6E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
805	13985	27037	1.38	1.6E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS210084
1116	14281	27337	1.44	1.6E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGG522 myosin heavy chain, 3'UTR
1121	14288	27341	2.7	1.6E-01	AJ251895.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1137	14302		1.85	1.6E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1243	14402	27463	2.37	1.6E-01	AW195516.1	EST_HUMAN	w839d1.1.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2696085 3'

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1304	14480	27526	3.22	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1304	14480	27527	3.22	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1511	14664	27749	1.38	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekkt) mRNA, complete cds
1957	15100	28200	0.88	1.5E-01	AW444451.1	EST_HUMAN	UI-H-BI3-ekb-b-09-D-JL1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733841 3'
2980	16186		0.9	1.5E-01	AW572516.1	EST_HUMAN	xi56a02.x2 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X56072_mai
3100	16278	29290	0.91	1.5E-01	M81441.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3118	16294	29308	0.82	1.5E-01	O78887	SWISSPROT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3433	16601	29620	6.78	1.5E-01	AA035049.1	EST_HUMAN	NADHUBIQUINONE OXIDOREDUCTASE CHAIN 4
3454	16621	29841	0.73	1.5E-01	Z23104.1	NT	cd88d05.s1 NCL CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3454	16621	29842	0.73	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
3851	17011	30011	2.35	1.5E-01	U09964.1	NT	L.stagnalis mRNA for G protein-coupled receptor
3887	17028	30026	0.83	1.5E-01	7108358	NT	L.stagnalis mRNA for G protein-coupled receptor
3981	17040	30037	0.77	1.5E-01	M97882.1	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3970	17128	30131	2.45	1.5E-01	AW655983.1	EST_HUMAN	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3987	17144	30149	0.68	1.5E-01	AJ003165.1	NT	XYNA; Thermotoga bacterium; xyna; 4182 base-pairs
3987	17144	30150	0.69	1.5E-01	AJ003165.1	NT	h107006.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
4161	17312	30308	1.16	1.5E-01	AW366659.1	EST_HUMAN	Populus trichocarpa cv. Trichobal ABI3 gene
4210	17359	30348	0.87	1.5E-01	Z12828.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
4200	17442	30428	9.85	1.5E-01	AL163284.2	NT	RC2-HT0149-191098-012-c09 HT0149 Homo sapiens cDNA
4947	17980	30969	1.54	1.5E-01	BF687665.1	EST_HUMAN	B napus mitochondrion DNA for ORF158
4874	15891	29002	2.33	1.5E-01	BF695381.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
5114	16242	31207	1.9	1.5E-01	AL161560.2	NT	Homo sapiens cDNA clone IMAGE:4068223 5'
5370	18573	31441	1.91	1.5E-01	P07696	SWISSPROT	602083269F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4247537 5'
5399	18601	31671	1.33	1.5E-01	AF266852.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5443	18643		5.95	1.5E-01	P16196	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5655	18849	32131	4.8	1.5E-01	AW850754.1	EST_HUMAN	Chimpan erodolus MHC class II beta chain (hclbeta) gene, complete cds
5697	18891	32182	6.89	1.5E-01	U65016.1	NT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN)
5697	18891	32183	6.88	1.5E-01	U65016.1	NT	(SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
6029	19212	32532	0.82	1.5E-01	4506810	NT	IL3-CT0219-100200-064-F10 CT0219 Homo sapiens cDNA
							Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
							Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
							Homo sapiens sodium channel, voltage-gated, type VI, alpha polypeptide (SCN6A) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6128	19307	32847	1.71	1.5E-01	6756559	NT	Mus musculus DNA methyltransferase 2 (Dnm2), mRNA
6128	19307	32848	1.71	1.5E-01	6756559	NT	Mus musculus DNA methyltransferase 2 (Dnm2), mRNA
6168	19344	32890	2.19	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6324	19408	32852	3.49	1.5E-01	BE727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6376	19545		1.99	1.5E-01	4508396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6474	19641	33002	1.74	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6631	25828	33179	3.68	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6681	19820	33207	4.73	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (CSORF3), mRNA
6672	19831	33220	1.51	1.5E-01	P48508	SWISSPROT	GLUTAMATE--CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6719	19876	33267	2.35	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6823	19976	33383	0.86	1.5E-01	AA714780.1	EST_HUMAN	hw30d10.s1 NCL_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241971 3'
6852	20005	33414	2.24	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7118	19544	31500	6	1.5E-01	AW970295.1	EST_HUMAN	EST382376 MAGE resequences, MAGK Homo sapiens cDNA
7158	25840		0.8	1.5E-01	AA811545.1	EST_HUMAN	ob73102.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element LTR2 repetitive element
7365	20444		4.73	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7550	20622	34099	1.63	1.5E-01	AI973157.1	EST_HUMAN	wf52z08.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
7764	20823	34314	0.88	1.5E-01	AF289073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7764	20823	34315	0.88	1.5E-01	AF289073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7775	20832	34322	1.68	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BNO-akk-005-0-UI.71 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7775	20832	34323	1.68	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BNO-akk-005-0-UI.71 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7919	20970	34477	0.79	1.5E-01	U46560.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of <i>bst1-1</i> (SOL3) gene, complete cds
8248	21330	34846	0.99	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK66 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8414	21495	35026	1.1	1.5E-01	AA970317.1	EST_HUMAN	o085g12.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062
8507	21588		1.06	1.5E-01	BE884799.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN)
8594	21676		14.14	1.5E-01	C16800.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8628	21708	35245	1.87	1.5E-01	L27835.1	NT	C16800 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-529H09 5'
8793	21872	35411	2.17	1.5E-01	DB4476.1	NT	Pangasinanodon gigas growth hormone (GH) mRNA, complete cds
8814	21893		0.79	1.5E-01	P43446	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
9038	22117	35660	3.12	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
							Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9305	22381	35932	2.55	1.5E-01	N74226.1	EST_HUMAN	2259e06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296866 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human ;
9394	22459	36033	1.34	1.5E-01	BF585465.1	EST_HUMAN	GVO000404 Human Paotais Differential Display Homo sapiens cDNA
9401	22475		2.52	1.5E-01	AV754819.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAHB12 5'
9605	22660		0.84	1.5E-01	AU130007.1	EST_HUMAN	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5'
9652	21055	34609	6.7	1.5E-01	U00455.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
10022	23050	36656	0.71	1.5E-01	M77144.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
10125	23163	36761	7.82	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10125	23163	36762	7.82	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10407	23442	37049	2.59	1.5E-01	X68952.1	NT	P. lentusculus mRNA for integrin beta subunit
10495	23530		0.51	1.5E-01	AB027759.1	NT	Mesocricetus auratus mRNA for collagen type XVII, complete cds
10516	23551	37161	2.38	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI CGAP_P22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10516	23551	37162	2.38	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI CGAP_P22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10598	23633	37242	1.22	1.5E-01	U40932.1	NT	Danio rerio transcription factor Pax9b (Pax9) mRNA, complete cds.
10761	23794	37413	1.69	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
10761	23794	37414	1.69	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
10935	24017	37849	1.67	1.5E-01	BE088492.1	EST_HUMAN	CM2-BT0688-210300-122-411 BT0688 Homo sapiens cDNA
10935	24017	37850	1.67	1.5E-01	BE088492.1	EST_HUMAN	CM2-BT0688-210300-122-411 BT0688 Homo sapiens cDNA
11063	24139	37773	4.46	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11063	24139	37774	4.46	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11331	24394	38042	1.38	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-026-D04 CN0024 Homo sapiens cDNA
11925	24911		1.34	1.5E-01	AI193704.1	EST_HUMAN	q72e01.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1744536 3' similar to gb:M17887 60S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
12232	25953		38.98	1.5E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
12629	25422		1.84	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12633	25426		1.23	1.5E-01	AJ238332.1	NT	Mus musculus mRNA for death inducer-abliterator-1 (Dlc-1)
12696	25976		5.64	1.5E-01	R83077.1	EST_HUMAN	yp87e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194130 5'
12749	25496		1.52	1.5E-01	AP001514.1	NT	Bacillus halodurans genomic DNA, section 8/14
12778	25520	32002	1.41	1.5E-01	6695413	NT	Lymphocystis disease virus 1, complete genome
12807	26000		2.59	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDA GD04 5'
12932	25896	31857	7.88	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11108 complete genome; segment 1/6

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13183	25769	31632	6.61	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
13227	26138		2.26	1.5E-01	9631284	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
310	13628		1.23	1.4E-01	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV856P to TCRBV21S2A2 region
933	14108		3.24	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5-)methyltransferase, complete cds
1288	14444		2.99	1.4E-01	T91864.1	EST_HUMAN	yd54c01.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:112032 3'
1787	14936		1.46	1.4E-01	6879980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1790	14939	28032	1.84	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1654	15097		1.27	1.4E-01	AW135741.1	EST_HUMAN	UI-H-B11-act-a-09-0-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
2042	15183		14.84	1.4E-01	AA720815.1	EST_HUMAN	my72d07.s1 NCL CGAP_GGB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2544	15669	28793	1.02	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYL TRANSFERASE PRECURSOR (GPAT)
2853	15967	28077	3.34	1.4E-01	A933496.1	EST_HUMAN	wm74d01.x1 NCL CGAP_U2 Homo sapiens cDNA clone IMAGE:2441665 3'
4289	17434	30421	9.45	1.4E-01	A169094.1	EST_HUMAN	b56d02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4289	17434	30422	9.45	1.4E-01	A169094.1	EST_HUMAN	b56d02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4352	17465	30475	4.28	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
							z16b01.s1 Soares fetal liver spleen INFLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gb:X01057_rna1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element;
4631	17869		0.7	1.4E-01	AA776287.1	EST_HUMAN	Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2)
4798	17933	30920	0.79	1.4E-01	5433861	NT	(PDE4A), mRNA
5322	18436	31406	0.62	1.4E-01	AJ005180.1	NT	Lycopodium obscurum genomic RAPD band 26
5421	18622	31568	6.21	1.4E-01	T90877.1	EST_HUMAN	yef5c11.s1 Stratiogene lung (#637210) Homo sapiens cDNA clone IMAGE:117812 3'
5444	18644	31821	4.33	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5444	18644	31622	4.33	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6427	19595	32961	3.17	1.4E-01	BE328891.1	EST_HUMAN	hr67c02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
6611	19771	33161	4.45	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6811	19771	33162	4.45	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6701	19856	33240	3.7	1.4E-01	AW082786.1	EST_HUMAN	x671d12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
6716	19873		1.51	1.4E-01	BE266536.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6739	19895	33286	2.48	1.4E-01	BF376533.1	EST_HUMAN	QV1-UM00036-080300-103-009 UM00036 Homo sapiens cDNA
7278	20359		0.71	1.4E-01	AL118568.1	EST_HUMAN	DKFZp761A0910.1 1761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5'
7545	20617		1.78	1.4E-01	AW016373.1	EST_HUMAN	UI-H-B10-act-c-09-0-U1.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7618	20888		0.73	1.4E-01	AI762827.1	EST_HUMAN	w04f12.x1 NCL CGAP_CL11 Homo sapiens cDNA clone IMAGE:2389295 3' similar to SW:ICE4_HUMAN P49662 CASPASE-4 PRECURSOR ;

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7621	20651	34167	0.63	1.4E-01	TS3770.1	EST_HUMAN	ye0011.2 Stratagene placenta (#637225) Homo sapiens cDNA clone IMAGE:68973 5' similar to contains
7799	20855	34345	0.95	1.4E-01	U85B45.1	NT	Alu repetitive element
7832	20982	34490	1.02	1.4E-01	A1305192.1	EST_HUMAN	Oryctolagus cuniculus fructose 1,6, biphosphate aldolase (AldB) gene, complete cds
8162	21244		0.54	1.4E-01	BF310286.1	EST_HUMAN	q190512.x1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8670	21760		1.32	1.4E-01	AV659047.1	EST_HUMAN	607894760.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124199 5'
							AV659047 GLC Homo sapiens cDNA clone GLCF5H06 3'
8984	22063		0.6	1.4E-01	A1436093.1	EST_HUMAN	h92b12.x1 Soares NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to
9114	22182	35798	4.04	1.4E-01	AA307073.1	EST_HUMAN	TR:002710 002710 GAG POLYPROTEIN.
9194	22272	35810	0.76	1.4E-01	AW023636.1	EST_HUMAN	EST178182 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9322	22396	35951	1.07	1.4E-01	R62746.1	EST_HUMAN	df58903.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9322	22398	35952	1.07	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9388	22463	36027	8.52	1.4E-01	BF310959.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
							607893465.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9475	22532	36096	1.72	1.4E-01	W93411.1	EST_HUMAN	z09404.r1 Soares_fetal_heart NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains
9547	22612	36180	0.54	1.4E-01	X73293.1	NT	element KER repetitive element ;
9547	22612	36181	0.54	1.4E-01	X73293.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9558	22623	36194	1.65	1.4E-01	Y10196.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9558	22623	36195	1.65	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
							Homo sapiens PHEX gene
9949	21092	34607	1.81	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IAL), and
10009	23047	36641	0.54	1.4E-01	X66092.1	NT	zinc finger protein (DNZ1) genes, complete cds
							C.perfringens ORF for putative membrane transport protein
10192	23229	36821	0.86	1.4E-01	AF023813.1	NT	Macromitrium levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein,
10293	23328	36931	0.81	1.4E-01	AW021908.1	EST_HUMAN	partial cds
10293	23328	36932	0.81	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10463	23498	37109	0.76	1.4E-01	BF375285.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10463	23498	37110	0.76	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
10680	23714		0.51	1.4E-01	T84293.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
10825	23858	37481	0.7	1.4E-01	Z98117.1	NT	yc47d03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:111365 5'
10948	24030		1.32	1.4E-01	AA811480.1	EST_HUMAN	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
11081	24156	37793	2.57	1.4E-01	R53400.1	EST_HUMAN	cg9a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:130364 3'
11282	24348	37885	1.69	1.4E-01	AW104982.1	EST_HUMAN	y70c05.r1 Soares breast 2NB-Bst Homo sapiens cDNA clone IMAGE:154088 5'
11354	24416	38071	1.58	1.4E-01	T96102.1	EST_HUMAN	xc79e10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603274 3'
							ye47g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120930 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11354	24418	38072	1.58	1.4E-01	T98102.1	EST_HUMAN	ye4/g10 r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120930 5'
11356	24418	38075	2.35	1.4E-01	P08848	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
11572	24627	38306	1.85	1.4E-01	X68092.1	NT	C. perfingens ORF for putative membrane transport protein
11613	20617		1.57	1.4E-01	AW015373.1	EST_HUMAN	U1H-B10-eat-c-09-0-111.st NC1_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11757	23943	37570	2.07	1.4E-01	U28780.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11816	24805		1.51	1.4E-01	X52102.1	NT	M.musculus p16K gene for 16 kDa protein
12038	25020	38724	10.18	1.4E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
12560	25382	32038	4.68	1.4E-01	X74773.1	NT	P. salina plastid gene secY
12574	2639C		3.28	1.4E-01	11968117	NT	Rattus norvegicus deamin (Dcp), mRNA
12605	25405		1.71	1.4E-01	BE964835.2	EST_HUMAN	601659490R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3885671 3'
12627	26175		2.83	1.4E-01	BE513802.1	EST_HUMAN	601315538F1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:3634329 5'
12724	25482		7.52	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycineamide ribonucleotide transformylase (GART) genes, complete cds
12742	25483		4.02	1.4E-01	D84004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2858761-3002965
12834	25193		3.2	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12928	25612		1.45	1.4E-01	X69192.1	NT	V. planifolia mRNA for methyltransferase
13084	25977		3.36	1.4E-01	D82883.1	NT	Mus musculus mRNA for prolidase, complete cds
13178	25785		1.68	1.4E-01	AW377998.1	EST_HUMAN	MRO-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
332	13546	26576	2.27	1.3E-01	4759487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
332	13546	26577	2.27	1.3E-01	4759487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
542	13735	26769	1.88	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
653	13839	26866	2.43	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
653	13839	26867	2.43	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
867	14043	27108	1.55	1.3E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
917	14092	27157	1.26	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1052	14218	27274	2.14	1.3E-01	AL117078.1	NT	Borrelia cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1151	14315		2.04	1.3E-01	AL115265.1	NT	Borrelia cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1242	14401	27462	1.67	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1475	14628		0.97	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1905	15048	28159	1.02	1.3E-01	6680957	NT	Mus musculus procollagen, type XI, alpha 1 (Col11a1), mRNA
2014	15154	28259	2.73	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2239	15372		1.09	1.3E-01	AJ243578.1	NT	Rhodopsin/opsin/opsin acidophila pucB5, pucA5, pucB6, pucA7, pucB8, pucA8 and pucC genes and ORF151
2364	15495		1.38	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2455	15583		3.31	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2653	15776	28889	2.78	1.3E-01	M86918.1	NT	Garassius auratus keratin type I mRNA, complete cds
3440	16608	29626	1.21	1.3E-01	AF198779.1	NT	Homo sapiens transcription factor IG-HM enhancer 3, JM11 protein, JM1 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds, and L-type calcium channel α_2
3539	16704	29715	1.11	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3816	16976	29979	0.95	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (117)
3816	16976	29980	0.85	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (117)
3822	16962	29985	1.55	1.3E-01	A3032159.1	NT	Homo sapiens DD4 gene for dihydrolipoyl dehydrogenase 4 [AKR1C4], exon 2
3905	17064	30063	0.68	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
4096	17251		1.08	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4162	13839	26856	0.88	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Gillingham/93/UK RNA for capsid protein (ORF2), strain HUNLV/Gillingham/93/UK
4162	13839	26867	0.88	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Gillingham/93/UK RNA for capsid protein (ORF2), strain HUNLV/Gillingham/93/UK
4257	17402		0.82	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4274	17419		3.74	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081299-036-e03 DT0018 Homo sapiens cDNA
4281	17426	30415	1.82	1.3E-01	AF028805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4302	17445	30431	21.62	1.3E-01	AW273741.1	EST_HUMAN	xv23110.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4434	17574		1.19	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4601	17738	30717	0.61	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4656	17792	30778	2.54	1.3E-01	BE272339.1	EST_HUMAN	801128096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2690063 5'
4748	17883	30865	0.73	1.3E-01	BF679654.1	EST_HUMAN	602154306F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295544 5'
5314	18431	31401	0.78	1.3E-01	AP000003.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 994001-1166000 nt, position (517)
5440	18640	31619	1.01	1.3E-01	AW466988.1	EST_HUMAN	ha07606.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1
5478	18677	31680	1.83	1.3E-01	AW804417.1	EST_HUMAN	L1 repetitive element
5618	18812		0.92	1.3E-01	AF107793.1	NT	QV0-UM00093-100400-189-a06 UM0093 Homo sapiens cDNA
							Emeritella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5702	18995		0.67	1.3E-01	AF056980.1	NT	Hepatitis C virus 68 CL10 genome polyprotein gene, partial cds
5842	19032	32338	0.72	1.3E-01	BF210920.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6107	19287	32821	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6107	19287	32822	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6612	19772	33163	18.92	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6698	19856	33246	2.25	1.3E-01	X88891.1	NT	C. jacchus intron 4 of visual pigment gene (red allele)
6827	20242		0.74	1.3E-01	W26387.1	EST_HUMAN	2563 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
6974	20202	33628	0.7	1.3E-01	BE782926.1	EST_HUMAN	601465957F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3869079 5'
6974	20202	33629	0.7	1.3E-01	BE782926.1	EST_HUMAN	601465957F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3869079 5'
7155	20289		0.74	1.3E-01	BF529580.1	EST_HUMAN	602044345F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181866 5'
7412	20490		1.97	1.3E-01	H48664.1	EST_HUMAN	y3302.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'
8146	21228		0.79	1.3E-01	BE272336.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
8180	21242	34762	1.88	1.3E-01	11423284	NT	Homo sapiens PRO611 protein (PRO611), mRNA
8192	21274	34797	1.32	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
8469	21650	35080	0.56	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8540	21821		4.24	1.3E-01	Z74102.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL054c
8580	21661		4.96	1.3E-01	8923019	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8725	21805	35342	1.26	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
9149	22227	35770	0.57	1.3E-01	R11172.1	EST_HUMAN	y33911.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP-RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9149	22227	35771	0.57	1.3E-01	R11172.1	EST_HUMAN	y33911.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP-RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9420	22494	38060	0.69	1.3E-01	11068003	NT	Plutella xylostella granubovirus, complete genome
9420	22494	38061	0.69	1.3E-01	11068003	NT	Plutella xylostella granubovirus, complete genome
9872	22634	36204	4.19	1.3E-01	AF023126.1	NT	Oryzias latipes cuniculus H+K+ATPase alpha 2c subunit mRNA, complete cds
9873	23012		0.73	1.3E-01	N86348.1	EST_HUMAN	J7537F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7537 5' similar to B-CELL
10257	23252		1.07	1.3E-01	8353940	NT	RECEPTOR ASSOCIATED PROTEIN (BAP) 29
10335	23370	36980	0.95	1.3E-01	AW851599.1	EST_HUMAN	Rattus norvegicus peptidyl arginine deiminase, type IV (Pd4), mRNA
10603	25864	37244	1.08	1.3E-01	AL163246.2	NT	MR2-CT0222-201089-001-e01 CT0222 Homo sapiens cDNA
10743	23776	37389	0.65	1.3E-01	AU121237.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
10797	23830	37454	0.45	1.3E-01	AW247836.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10868	23953		2.31	1.3E-01	BF330999.1	EST_HUMAN	2820637.3prine NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820637 3'
11455	24515		1.34	1.3E-01	BF022708.1	EST_HUMAN	MR4-BT0358-130700-010-h08 BT0358 Homo sapiens cDNA

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Probe Seq ID NO:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11529	24585		3.2	1.3E-01	6671745	NT	Mus musculus collagen 2, muscle (Clt2), mRNA
11616	24667	38354	2.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4251346 5'
11616	24667	38355	2.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4251346 5'
11895	24883	38581	7.98	1.3E-01	BE279449.1	EST_HUMAN	601198052F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3504804 5'
12000	24985		1.41	1.3E-01	AF012836.1	NT	Thermococcus litoralis trehalose/maltose transporter operon including trehalose/maltose binding protein (malE) and inner membrane proteins MalF (malF) and MalG (malG) genes, complete cds
12023	25007	38708	1.72	1.3E-01	BE619364.1	EST_HUMAN	601473398F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3876208 5'
12052	25033	38739	1.52	1.3E-01	BF683555.1	EST_HUMAN	602139760F1 NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4300983 5'
12399	25279	32080	2.13	1.3E-01	BE618346.1	EST_HUMAN	601482741F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3866003 5'
12543	25368		6.39	1.3E-01	AJ242790.1	NT	Gallus gallus scyc1 gene for lymphocytin, exons 1-3
12964	25627		1.31	1.3E-01	AB026829.1	NT	Ephydra fluvialis mRNA for eALK-6, complete cds
12995	25647		1.87	1.3E-01	AW001114.1	EST_HUMAN	TR-O60287 O60287 KIAA0639 PROTEIN. ;
394	13631	26868	13.87	1.2E-01	AH21744.1	EST_HUMAN	tf39602.x1 NCI CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2088539 3' similar to gb:U05760_ma1
437	13237		1.42	1.2E-01	U66912.1	NT	ANNEXIN V (HUMAN);
551	13753		3.82	1.2E-01	AF039442.1	NT	Dictyostellum discoideum ORF DG1016 gene, partial cds
1408	14562	27636	2.32	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1408	14562	27637	2.32	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1414	14568		3.35	1.2E-01	AV735249.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1419	14572		0.94	1.2E-01	AL445086.1	NT	AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1536	14689		0.94	1.2E-01	AA897474.1	EST_HUMAN	Thermoplasma acidophilum complete genome, segment 4/5
1680	14812	27897	1.1	1.2E-01	Q14934	SWISSPROT	el49e09.s1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671
1682	14834	27919	2.88	1.2E-01	AJ285402.1	EST_HUMAN	Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1808	14957		25.75	1.2E-01	X89211.1	NT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOLASMIC 4 (T CELL TRANSCRIPTION FACTOR
1970	15113		1.68	1.2E-01	AW449368.1	EST_HUMAN	NFAT3(NF-ATC4) (NF-A3)
2293	15368	28514	1.68	1.2E-01	BF248480.1	EST_HUMAN	qt66f09.x1 NCI CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1890553 3'
2450	15578		0.99	1.2E-01	Z21405.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
2636	15779	28893	1.84	1.2E-01	AW996556.1	EST_HUMAN	UI-H-B13-ek9-e-10-O-J1.s1 NCI CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2734554 3'
2905	16053	29098	1.16	1.2E-01	U18018.1	NT	601821587F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4046224 5'
2987	16143	29162	1.9	1.2E-01	AJ720470.1	EST_HUMAN	HSAAAEZT1 TEST1, Human adult Testis tissue Homo sapiens cDNA
							QV3-BN0046-220300-129-f10 BN0046 Homo sapiens cDNA
							Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
							as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:U05095
							60S RIBOSOMAL PROTEIN L30 (HUMAN);

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3001	16177	29198	3.44	1.2E-01	M16364.1	NT	Human creatine kinase-B mRNA, complete cds
3088	18244	29285	0.91	1.2E-01	X58882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3302	16476	29498	2.52	1.2E-01	AW370698.1	EST_HUMAN	QV1-BT0259-261089-021-405 BT0259 Homo sapiens cDNA
3330	16503		0.74	1.2E-01	U67600.1	NT	Methanococcus jannaschii section 142 of 160 of the complete genome
3568	16733		0.66	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3610	16774	29789	1.12	1.2E-01	X58882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3610	16774	29780	1.12	1.2E-01	X58882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3694	16733		1.22	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3895	17024		0.95	1.2E-01	BF128551.1	EST_HUMAN	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053688 3'
4298	17441	30426	2.1	1.2E-01	Z54255.1	NT	P. clarkii mRNA; repeat region (ID 2MR17)
4298	17441	30427	2.1	1.2E-01	Z54255.1	NT	P. clarkii mRNA; repeat region (ID 2MR17)
4431	17571	30562	0.59	1.2E-01	M15861.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
4942	18072		1.94	1.2E-01	X73416.1	NT	W. savatensis mitochondrial ori
5364	18367	31433	0.89	1.2E-01	AA744369.1	EST_HUMAN	ny63c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'
5416	18617	31591	0.93	1.2E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5425	18626	31601	2.5	1.2E-01	W33035.1	EST_HUMAN	z08d02.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5'
5484	18683	31700	1.65	1.2E-01	Z98268.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5622	18816	31885	1.14	1.2E-01	Z48234.1	NT	M.domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6329	19500	32858	1.9	1.2E-01	BE620945.1	EST_HUMAN	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896613 5'
6377	19546	32903	0.81	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI
6428	19596	32962	2.28	1.2E-01	AW845275.1	EST_HUMAN	IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
6493	19659	33022	1.52	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6861	19723	33101	0.58	1.2E-01	AA747535.1	EST_HUMAN	ny85601.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269024 3'
6785	19940	33338	1.18	1.2E-01	BF347985.1	EST_HUMAN	60202312F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158386 5'
7154	20288	33731	0.64	1.2E-01	H47789.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:193759 5'
7154	20288	33732	0.64	1.2E-01	H47789.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:193759 5'
7772	20829	34320	0.62	1.2E-01	AJ271741.1	NT	Homo sapiens partial ILF3 gene for interleukin enhancer binding factor 3 (alternative transcripts drbp76, drbp76 gamma, drbp76 alpha and ILF3)
8076	21158		1.13	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-280300-002-409 BN0137 Homo sapiens cDNA
8149	21231	34751	2.45	1.2E-01	AI913753.1	EST_HUMAN	wc89g03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW-GST2_HUMAN
8197	21279	34801	0.64	1.2E-01	Q02369	SWISSPROT	Q99735 MICROSMAL GLUTATHIONE S-TRANSFERASE II;
8504	21585	35119	0.65	1.2E-01	AI832681.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (C1-B22)
							at71b10.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST-E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8590	21871		10.76	1.2E-01	AW083652.1	EST_HUMAN	xc49407.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
8611	21691		3.76	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8649	21729	35266	1.09	1.2E-01	J03956.1	NT	N. crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8649	21729	35267	1.09	1.2E-01	J03956.1	NT	N. crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8800	21879		1.02	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
8887	21968		1.44	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
8920	21989		0.77	1.2E-01	X15191.1	NT	M. musculus DNA fragment of Apolipoprotein B gene
9771	22787	36338	1.3	1.2E-01	X77981.1	NT	S. cerevisiae HXT5 gene
10209	23245	36835	0.9	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CUAKE08 5'
11125	24197		2.55	1.2E-01	D28184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
11320	24393		3.03	1.2E-01	BE962324.2	EST_HUMAN	601655578R1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3846283 3'
11414	24475		1.73	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11533	24589	38264	2.78	1.2E-01	AF190483.1	NT	Homo sapiens dynein intermediate chain DNAIL (DNAIL) gene, exon 17
11593	24648	38328	1.72	1.2E-01	R40249.1	EST_HUMAN	Y80c02.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28880 3'
11798	24788		2.47	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
12161	25128		2.09	1.2E-01	AV656033.1	EST_HUMAN	AV656033 GLC Homo sapiens cDNA clone GLCFB12 3'
12522	25355		4.37	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
12614	25126	31544	2	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12732	25486		1.65	1.2E-01	AF189892.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin gene, partial cds
12734	13763		18.32	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12863	25574		1.4	1.2E-01	X53981.1	NT	R. norvegicus NF88 gene for 68kDa neurofilament
12968	25529	31981	4.89	1.2E-01	A1299903.1	EST_HUMAN	gn20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12992	25544		3.46	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12997	26050		6.44	1.2E-01	O98433	SWISSPROT	CYCLIN T
13031	26676	31060	1.47	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
13221	25795		1.23	1.2E-01	AF090141.1	NT	Chryseobacterium marisnigrae GOB-1 carboxypeptidase gene, complete cds
578	13770	26792	1.56	1.1E-01	A1561003.1	EST_HUMAN	h18d08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3'
630	13815	26838	1.33	1.1E-01	AA566006.1	EST_HUMAN	h18d08.x1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_mai1 HEME OXYGENASE 1 (HUMAN);

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1079	14245	27302	1.61	1.1E-01	BF697308.1	EST_HUMAN	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1109	14274		1.65	1.1E-01	AL161960.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1186	16031	27405	3.67	1.1E-01	AW972158.1	EST_HUMAN	EST384142 MAGE resequences, MAGL Homo sapiens cDNA
1278	14435	27505	1.88	1.1E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2888767-3002965
1549	14701	27780	2.75	1.1E-01	AU140363.1	EST_HUMAN	AU140363 PLACE2 Homo sapiens cDNA clone IMAGE:2000403 5'
2255	15388		1.73	1.1E-01	AJ008701.1	NT	Homo sapiens mRNA for putative serine/threonine protein kinase, partial
2388	15519		2.02	1.1E-01	6758215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
2603	15999		1.08	1.1E-01	6978676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2833	15756		1.27	1.1E-01	AW821809.1	EST_HUMAN	RCO-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
2917	16095	29107	0.89	1.1E-01	S82418.1	NT	interleukin-12 p35 subunit (ntice, Genomic, 700 nt, segment 4 of 6)
3098	16274	29288	0.81	1.1E-01	F03285.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
3422	16591		1.55	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Caona1g), mRNA
3508	16676	29886	2.09	1.1E-01	BE383186.1	EST_HUMAN	601308878F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3540	16705	29716	1.47	1.1E-01	X62135.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3580	16745	29763	0.71	1.1E-01	R96946.1	EST_HUMAN	Y62g08.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains Alu repetitive element
3673	16836	29848	0.7	1.1E-01	Y07696.1	NT	A. Immeus gene for transposase
3791	16952		0.96	1.1E-01	P97384	SWISSPROT	ANNEXIN XJ (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3800	16961	29965	1.28	1.1E-01	X52708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4226	17374	30359	1.2	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4226	17374	30360	1.2	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4233	17380		0.83	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
4367	17510		11.45	1.1E-01	AF157068.1	NT	Drosophila melanogaster kirsch protein (klar) mRNA, complete cds
4401	17544	30528	0.76	1.1E-01	AW802056.1	EST_HUMAN	IL5-JM0070-020500-068-g08 JM0070 Homo sapiens cDNA
4762	17897	30877	0.92	1.1E-01	S44657.1	NT	Tape-1= integral membrane protein TAPA-1 (ntice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7)
4853	18083	31069	1.23	1.1E-01	Y07696.1	NT	A. Immeus gene for transposase
5134	17380		0.75	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
5787	18979		2.59	1.1E-01	AA747216.1	EST_HUMAN	nx76a03.s1 NCL CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1288140 similar to contains Alu repetitive element; contains element MER35 repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5857	19047	32353	1.32	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5894	19082	32393	0.97	1.1E-01	AL110985.1	NT	Bcl-2 chimeric strain T4 cDNA library under conditions of nitrogen deprivation
5927	19113	32425	0.96	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5'
5927	19113	32426	0.98	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5'
5958	19144	32459	1.79	1.1E-01	X68851.1	NT	S. pombe sea gene encoding protein kinase
5992	19177	32498	5.15	1.1E-01	M86533.1	NT	Providencia reitgeri penicillin G amidase gene
6150	19326	32671	1.68	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
6171	19347	32693	1.37	1.1E-01	BE769152.1	EST_HUMAN	PM3-F10024-130600-004-F12 FT0024 Homo sapiens cDNA
6191	19367	32716	7.73	1.1E-01	AW830899.1	EST_HUMAN	RC3-CT0254-280899-011-e01 CT0254 Homo sapiens cDNA
6554	19716	33092	0.61	1.1E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6582	19724	33102	1.52	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6602	19762	33150	0.84	1.1E-01	AI216307.1	EST_HUMAN	cg76d06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6742	19898	33289	3.88	1.1E-01	O69535	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6843	19996		2.73	1.1E-01	AF032922.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6934	20249	33684	2.74	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (P(GB), mRNA
7193	20058	33468	0.74	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7193	20058	33469	0.74	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7337	26217		1.01	1.1E-01	BF382758.1	EST_HUMAN	601816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050863 5'
7456	26845	34007	0.98	1.1E-01	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt position (6/7)
7706	20771	34255	7.51	1.1E-01	BF684628.1	EST_HUMAN	602140876F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7708	20771	34256	7.51	1.1E-01	BF684628.1	EST_HUMAN	602140876F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7833	20886	34391	2.16	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
7872	20926		0.64	1.1E-01	Z14098.1	NT	B. subtilis gene encoding hypothetical polyketide synthase
7873	20927	34433	3.06	1.1E-01	AA788784.1	EST_HUMAN	af31b06.s1 Scores_parathyroid_tumor_NHPPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483
8155	21237	34758	1.58	1.1E-01	U87492.1	NT	CHROMOGGRANIN A PRECURSOR (HUMAN);
8403	21484	35012	1.55	1.1E-01	AA493574.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8403	21484	35013	1.55	1.1E-01	AA493574.1	EST_HUMAN	rh04g10.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8449	21530	35059	1.26	1.1E-01	X91293.1	NT	rh04g10.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8489	21570		0.94	1.1E-01	AW817918.1	EST_HUMAN	H. sapiens IL15 gene
8546	21627	35165	2.31	1.1E-01	AL134349.1	EST_HUMAN	PM1-S10270-080200-001-f05 ST0270 Homo sapiens cDNA
9018	22097	35637	5.67	1.1E-01	U02492.1	NT	DKFZ547P194.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZ547P194 5'
							Pediococcus acidilactici H plasmid pSMB74 pediocin ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9113	22192	35737	1.04	1.1E-01	AI807474.1	EST_HUMAN	wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element;
9210	22288	35830	0.5	1.1E-01	AF050081.1	NT	Homo sapiens C16orf3 large protein mRNA, complete cds
9243	22320	35863	2.25	1.1E-01	AA192183.1	EST_HUMAN	z93b12.11 Stratiote muscle 937209 Homo sapiens cDNA clone IMAGE:827743 5'
9243	22320	35864	2.25	1.1E-01	AA192183.1	EST_HUMAN	z93b12.11 Stratiote muscle 937209 Homo sapiens cDNA clone IMAGE:827743 5'
9335	22411	35984	0.71	1.1E-01	Y12727.1	NT	P. furiosus partial dph5 gene and arg1 gene
9366	22441	36001	2.78	1.1E-01	T72675.1	EST_HUMAN	yd19i03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gbM81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9392	22467		0.83	1.1E-01	BE893280.1	EST_HUMAN	601436972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
9622	22677		0.89	1.1E-01	BE142305.1	EST_HUMAN	CM3-1T10142-271099-026-g11 HT0142 Homo sapiens cDNA
9696	22745		2.33	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
10114	23152		0.77	1.1E-01	AL161543.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10410	23445		1.23	1.1E-01	R80590.1	EST_HUMAN	y96a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147064 3'
10544	23578	37188	1.29	1.1E-01	U60529.1	NT	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
10814	23987	37631	1.38	1.1E-01	AF245277.1	NT	Dichytetium discoidium kinesin Unc104/KIF1a homolog (Unc104) mRNA, complete cds
11044	16274	29288	1.78	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
11162	24233		2.47	1.1E-01	AF169032.1	NT	Carassius auratus actin beta A precursor, mRNA, complete cds
11300	24388	38007	3.11	1.1E-01	R23708.1	EST_HUMAN	yh35f12.71 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
11483	24542	38212	2.6	1.1E-01	Z11910.1	NT	Z. mobilis tgt and lig genes encoding RNA guanine transglycosylase and DNA ligase
11483	24542	38213	2.6	1.1E-01	Z11910.1	NT	Z. mobilis tgt and lig genes encoding RNA guanine transglycosylase and DNA ligase
11510	24568	38245	1.69	1.1E-01	BE02074.1	EST_HUMAN	601676924F1 NIH_MGC_27 Homo sapiens cDNA clone IMAGE:3959888 5'
11588	24638	38319	3.21	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11971	24958		1.33	1.1E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
12378	25266		3.78	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-003 NT0112 Homo sapiens cDNA
12649	25910		3.18	1.1E-01	BE074556.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
13136	25738	31947	1.98	1.1E-01	BF239763.1	EST_HUMAN	601906350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1228	14388		1.51	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (LYSOSOMAL DNASE II)
1301	14457	27523	2.18	1.0E-01	AU985498.1	EST_HUMAN	we88d01.x1 NCI_CGAP_Kic11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13 MER7 repetitive element;
1423	14577	27650	2.3	1.0E-01	AL151504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
2558	15883	28808	1.01	1.0E-01	AW451365.1	EST_HUMAN	UH-HB13-alc-d-07-Q-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3813	16973	29976	1.11	1.0E-01	BF239763.1	EST_HUMAN	601906489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
4084	17220	30228	2.6	1.0E-01	BF366703.1	EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4527	17865	30651	1.44	1.0E-01	AE002265.2	NT	Chlamydia pneumoniae AR39, section 91 of 94 of the complete genome
4677	17812		0.76	1.0E-01	AI792349.1	EST_HUMAN	ar32c04.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4834	17967	30955	2.17	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
5039	18167	31143	2.17	1.0E-01	AW952344.1	EST_HUMAN	EST364414 IMAGE resequences, MAGB Homo sapiens cDNA
5281	18350	31346	0.61	1.0E-01	BE989100.1	EST_HUMAN	60128898F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613552 5'
5436	18636		9.49	1.0E-01	W88490.1	EST_HUMAN	zh52h04.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416895 3'
5634	18731		0.67	1.0E-01	X54015.1	NT	X.campestis genes for sensor and regulator protein
6001	19186		1.08	1.0E-01	AK024472.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
6148	19325	32670	13.08	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6465	19632	32893	0.9	1.0E-01	AA481879.1	EST_HUMAN	zv41g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:766258 3' similar to contains
6479	19646	33008	0.72	1.0E-01	AA406039.1	EST_HUMAN	L1.13 L1 repetitive element;
7164	20297		1.87	1.0E-01	R23821.1	EST_HUMAN	zab7c12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743082 3'
7914	20965		2.39	1.0E-01	Y12488.1	NT	yh34h06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element;
8118	21200	34721	0.69	1.0E-01	AA861091.1	EST_HUMAN	M.musculus wtn gene
8141	21223	34741	2.17	1.0E-01	AF260225.1	NT	ak32g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407896 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8141	21223	34742	2.17	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8689	21769		0.66	1.0E-01	AW189797.1	EST_HUMAN	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
9387	22462	36026	1.12	1.0E-01	AF102855.2	NT	x08b01.x1 NCJ_CGAP_U14 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40S
9695	22744	36314	0.87	1.0E-01	R44993.1	EST_HUMAN	RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.13 TAR1 repetitive element;
9707	22756		1.9	1.0E-01	M76729.1	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synapton mRNA, complete cds
9750	22688		3.15	1.0E-01	AE001501.1	NT	Human pro-alpha1(V) collagen mRNA, complete cds
9784	22761	36331	0.55	1.0E-01	W01955.1	EST_HUMAN	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
10028	23064	36681	1.88	1.0E-01	BF240154.1	EST_HUMAN	z066c10.s1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:327282 3'
10139	23177	36774	8.92	1.0E-01	AB046799.1	NT	60190568F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
10139	23177	36775	8.92	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10347	23382		1.06	1.0E-01	AW957425.1	EST_HUMAN	Homo sapiens mRNA for KIAA1579 protein, partial cds
10351	23386	36995	0.62	1.0E-01	T51955.1	EST_HUMAN	EST369916 IMAGE resequences, MAGB Homo sapiens cDNA
10337	23672	37179	1.27	1.0E-01	BE792750.1	EST_HUMAN	y628a06.s1 Stratagene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
10894	23978		1.77	1.0E-01	AU159127.1	EST_HUMAN	60158460F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3693908 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11286	24352	37991	2.17	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11286	24352	37992	2.17	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11885	24984	38874	3.64	1.0E-01	BE790543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
11814	24803		1.75	1.0E-01	AF000400.1	NT	Escherichia coli O167:H7 genomic DNA, prophage (Sakai-VT1) inserted region, substrain:RIMD 0509952
12364	25633		1.73	1.0E-01	BE537719.1	EST_HUMAN	601055554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12609	25408		1.73	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12839	28119		3.11	1.0E-01	U52891.1	NT	Gonyalax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
12973	25633		1.8	1.0E-01	BE537719.1	EST_HUMAN	601055554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
13045	26085		25.82	1.0E-01	U68834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
13117	25729		6.58	1.0E-01	AF001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
13219	26106		1.45	1.0E-01	AE002138.1	NT	Ureaplasma urealyticum section 39 of 59 of the complete genome
2839	15953	28060	0.96	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-Ril) mRNA, complete cds
2847	15961	29070	0.94	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2847	15961	29071	0.94	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3340	16313	29528	1.31	9.9E-02	AF09810.1	NT	Homo sapiens neurixin III-alpha gene, partial cds
7110	18336	31492	8.66	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blastidin S deaminase, complete cds
8099	21181	34089	0.69	9.9E-02	AW103088.1	EST_HUMAN	x443c09.x1 NC1_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
8099	21181	34700	0.69	9.9E-02	AW103088.1	EST_HUMAN	x443c09.x1 NC1_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
9457	22573	36139	1.35	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
12132	25112	38816	3.67	9.9E-02	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
577	13759		2.18	9.8E-02	X56338.1	NT	O. sativa RAMy3C gene for alpha-amylose
3214	16388	29398	3.66	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4339	17482	30463	9.93	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4339	17482	30464	9.93	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7651	20719		0.98	9.8E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9454	22570		1.16	9.8E-02	M61943.1	NT	Human laminin B1 chain gene, exon 26
11747	23833	37559	1.73	9.8E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
12332	26240		1.29	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1381	14538	27611	1.92	9.7E-02	AB005808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1617	14769		1.01	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2335	15466	28601	2.56	9.7E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-095-024 HT0516 Homo sapiens cDNA
4091	17246		4.05	9.7E-02	Q09795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5461	18661	31639	0.59	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5461	18661	31640	0.59	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
6138	19316	32657	1.39	9.7E-02	AF099189.1	NT	EST366546 MAGC resequenced, MAGC Homo sapiens cDNA
7450	20527	34000	3.05	9.7E-02	AW954476.1	EST_HUMAN	Bacillus subtilis complete genome (section 16 of 21); from 2957771 to 3213410
8171	21253	34774	1.54	9.7E-02	Z39119.1	NT	yw41c03.s1 Weizmann Offractory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8171	21253	34775	1.54	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Offractory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
9050	22129	35673	1.49	9.7E-02	A1953984.1	EST_HUMAN	wx78b09.x1 NC1 CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb.X52851_mai
11472	24531		1.72	9.7E-02	U56337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
2073	15213	28330	1.33	9.6E-02	A1080721.1	EST_HUMAN	Mus musculus ligatin (Lgtn) mRNA, partial cds
2073	15213	28331	1.33	9.6E-02	A1080721.1	EST_HUMAN	oz47d11.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4484	17604	30582	6.67	9.6E-02	Z32686.2	NT	oz47d11.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
5117	18244	31209	0.95	9.6E-02	AW966230.1	EST_HUMAN	Protein fibrinolytic fibrinolytic opsonin, strain H4320
6231	19408		2.75	9.6E-02	BE010039.1	EST_HUMAN	EST378303 MAGC resequenced, MAGC Homo sapiens cDNA
8017	21068		0.79	9.6E-02	6678753	NT	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
8571	21652		0.65	9.6E-02	AU137084.1	EST_HUMAN	Mus musculus lymphocyte antigen 78 (Ly78), mRNA
9744	22808	36386	1.49	9.6E-02	AV687898.1	EST_HUMAN	AU137084 PLAGE1 Homo sapiens cDNA clone PLAGE1005740 5'
10078	23114	36876	1.34	9.6E-02	BE694895.1	EST_HUMAN	AV687898 GKC Homo sapiens cDNA clone GKCAAH02 5'
10245	23280	36876	1.04	9.6E-02	AJ243211.1	NT	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'
10245	23280	36877	1.04	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10325	23360	36970	0.62	9.6E-02	BF677270.1	EST_HUMAN	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10354	23389	36998	1.56	9.6E-02	AB013985.1	NT	602086769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250989 5'
10354	23389	36999	1.56	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10465	23500	37113	3.43	9.6E-02	P08174	SWISSPROT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10981	24060	37694	5.27	9.6E-02	Z76702.1	NT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
12019	25003	38704	2.8	9.6E-02	AA825755.1	EST_HUMAN	Mycobacterium tuberculosis H37Rv complete genome, segment 102162
13015	25668		1.7	9.6E-02	H14599.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
							ym19h03.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13143	25743	31949	1.41	9.8E-02	AJ295624.1	NT	Callus gallus ALPHA 10 nACHR gene for alpha 10 subunit of nicotinic acetylcholine receptor, exons 1-5
4217	17366	30355	2.16	9.8E-02	AW982395.1	EST_HUMAN	GM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
5782	18974	32280	0.88	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7455	20532	34006	4.64	9.8E-02	AB03473.1	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
7741	20802	34292	7.77	9.5E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7876	18974	32280	0.81	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
8084	21146	34666	2.85	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8084	21146	34667	2.85	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10918	24001	37634	4.09	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10918	24001	37635	4.09	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
12104	25084		1.82	9.5E-02	7657416	NT	Mus musculus ccd Ozlen-m homolog 3 (Drosophila) (Odz3), mRNA
13097	25715		2.81	9.5E-02	AF272782.1	NT	Arabidopsis thaliana putative transcription factor (MYB110) mRNA, complete cds
1880	15024	28130	3.95	9.4E-02	BF671063.1	EST_HUMAN	602150892F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
3985	17142	30147	4.64	9.4E-02	Z33059.1	NT	M capitulum DNA for GONTIG MC073
6447	19614	32978	0.95	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
7769	20827	34318	0.68	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and p35 gene, partial cds
8789	21878		2.5	9.4E-02	Z46863.1	NT	Acinetobacter sp. eyeD, cobQ, sodM, lyeS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes
11174	20827	34318	1.9	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and p35 gene, partial cds
12214	26011		7.72	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
13198	25780	31936	4.84	9.4E-02	U27699.1	NT	Human pepHBT-1 betaine-GABA transporter mRNA, complete cds
3054	16230		2.37	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3094	16270		8.03	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3329	16502	29521	2.17	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4298269 5'
4268	17413	30400	3.17	9.3E-02	BE391943.1	EST_HUMAN	601286502F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4288	17413	30401	3.17	9.3E-02	BE391943.1	EST_HUMAN	601286502F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4857	17890		1.82	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA08 5'
5779	18971		0.67	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8442	21523	35052	0.56	9.3E-02	AW566007.1	EST_HUMAN	EST08 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9324	22400		0.5	9.3E-02	AL113179.1	NT	Botrytis chereae strain T4 cDNA library under conditions of nitrogen deprivation
9911	22951	35537	2.3	9.3E-02	BE062631.2	EST_HUMAN	601655988F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
10394	23429	37035	3.6	9.3E-02	Q18034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10394	23429	37036	3.6	9.3E-02	Q18034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10526	23561		3.96	9.3E-02	AW206117.1	EST_HUMAN	U1-H-B11-40x-1-05-0-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723563 3'
12465	25933		2.08	9.3E-02	AJ249890.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
12805	25964		22.03	9.3E-02	AW468850.1	EST_HUMAN	Ind2h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810887 3'
13139	26010					NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1, 3-galactosyl tr>
238	13460	26486	2.87	9.3E-02	AF100956.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13460	26487	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13460	26488	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2302	15434		3.08	9.2E-02	R54156.1	EST_HUMAN	yp9107.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:41618 5'
3247	16421	29437	3.7	9.2E-02	Q26631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3379	16551	29564	1.01	9.2E-02	AA634354.1	EST_HUMAN	nt76901.s1 NCI CGAP_Cc3 Homo sapiens cDNA clone IMAGE:926136 3'
3876	16839		1.14	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
4353	17496		1.05	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4425	17565		0.88	9.2E-02	BE289722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860176 5'
4760	17895	30876	3.44	9.2E-02	X96402.1	NT	G. gallus Mla-CK gene
8198	21280	34802	1.82	9.2E-02	T49920.1	EST_HUMAN	ya9c09.r1 Stratagene placenta (#937226) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb-X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
8370	21451	34974	2.18	9.2E-02	X95256.1	NT	H. vulgare xylose isomerase gene
13120	28201		1.2	9.2E-02	1146872	NT	Podospira anserina mitochondrion, complete genome
436	13236	26237	2.23	9.1E-02	X77665.1	NT	O. cuticulus K12 keratin gene
3760	16921		0.97	9.1E-02	AW372569.1	EST_HUMAN	PM2.BT0349-161299-001-f02 BT0349 Homo sapiens cDNA
4607	17744	30723	1.78	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, cortig fragment No. 54
5848	19038	32345	1.23	9.1E-02	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7459	26218		0.61	9.1E-02	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
7549	20618	34094	12.21	9.1E-02	AW160658.1	EST_HUMAN	au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781668 5'
7852	20907	34411	0.95	9.1E-02	AP000061.1	NT	Aeropyrum pernix genomic DNA, section 47
7887	20939	34445	1.02	9.1E-02	U39073.1	NT	Mus musculus thymoprotein zeta mRNA, complete cds
9124	22203	35746	0.96	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10542	23676		1.46	9.1E-02	T02994.1	EST_HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3'end
10674	23708	37316	1.02	9.1E-02	S74059.1	NT	Tg616-Cy1 actin [Tritoneautes gratilla=sea urchins, embryos, Genomic, 527/5 nt]

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10703	23736	37341	0.8	9.1E-02	Y11187.1	NT	A. italiana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
11441	24602	38170	2.13	9.1E-02	AF037625.1	NT	Rana catesbeiana dihydropyridine receptor mRNA, complete cds
12151	25121		7.04	9.1E-02	8633494	NT	Bacteriophage Mu, complete genome
12393	26124		1.42	9.1E-02	AA179901.1	EST_HUMAN	z38H12.s1 StrataGene muscle 937209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
12473	25326		1.32	9.1E-02	AF052895.1	NT	Rattus norvegicus cell cycle protein p55ODC gene, complete cds
12996	26954		13.49	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B much, exons 1-11
13290	25789		1.27	9.1E-02	AF226888.1	NT	Bombay motif fibrin heavy chain Fib-H (fib-H) gene, complete cds
							FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
763	13944	26990	5.89	9.0E-02	P15328	SWISSPROT	h39g10.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176842 3' similar to contains Alu repetitive element;
1664	14816	27899	7.33	9.0E-02	BE220482.1	EST_HUMAN	IL5-JM0067-240300-050-106 UM0067 Homo sapiens cDNA
2484	16862	28710	1.18	9.0E-02	AW801364.1	EST_HUMAN	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2884	15978	29088	4.99	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2884	15978	29089	4.99	9.0E-02	AF138522.1	NT	Dictyostellium discoideum spore coat structural protein SP65 (cdtE) gene, complete cds
3417	16586	29603	1.11	9.0E-02	AF279135.1	NT	cardiac steroid-binding globulin [Salmifil schreus=squirrel monkeys, liver, mRNA, 1474 nt]
4414	17555	30541	0.6	9.0E-02	S88757.1	NT	cardiac steroid-binding globulin [Salmifil schreus=squirrel monkeys, liver, mRNA, 1474 nt]
4414	17555	30542	0.6	9.0E-02	S88757.1	NT	cardiac steroid-binding globulin [Salmifil schreus=squirrel monkeys, liver, mRNA, 1474 nt]
4790	17925	30913	2.03	9.0E-02	X85740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
6118	19298	32634	7.2	9.0E-02	W58037.1	EST_HUMAN	z683a12.r1 Species fetal lung, NBHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:S52174 S52174 small G protein - human ;
6860	20012		0.93	9.0E-02	BF062851.1	EST_HUMAN	7H33403 x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3320845 3' similar to contains Alu repetitive element;
							Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
12819	25546		1.82	9.0E-02	AF022236.1	NT	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1469	14623	27706	1.25	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1469	14623	27707	1.25	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2460	15587	28714	1.64	8.9E-02	BE153572.1	EST_HUMAN	PMO-HT0339-251189-003-d01 HT0339 Homo sapiens cDNA
4316	17459		1.68	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranF102 protein (AtranF102) gene, partial cds
5972	19158	32474	2.7	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alo-f-08-0-UJ.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088294 3'
5972	19158	32475	2.7	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alo-f-08-0-UJ.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088294 3'
5987	19172	32494	3.34	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7343	20423	33886	1.6	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHYLENETETRAHYDROFOLATE CYCLOHYDROLASE]
7731	20763		1.77	8.9E-02	Z78021.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC8pA20F8
8240	21322	34839	1.19	8.9E-02	P29475	SWISSPROT	NITRIC OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8323	21405	34932	0.76	8.9E-02	BF701665.1	EST_HUMAN	602128111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8323	21405	34933	0.76	8.9E-02	BF701665.1	EST_HUMAN	602128111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8797	21876	35415	5.85	8.9E-02	AA308319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9819	22859	36439	0.84	8.9E-02	AI285627.1	EST_HUMAN	qu55cd05.x1 NCJ CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1 MER10 repetitive element;
9819	22859	36440	0.84	8.9E-02	AI285627.1	EST_HUMAN	qu55cd05.x1 NCJ CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1 MER10 repetitive element;
9834	22973	36565	0.63	8.9E-02	AA339356.1	EST_HUMAN	EST144454 Fetal brain Homo sapiens cDNA 5' end
12213	25962		1.8	8.9E-02	P19524	SWISSPROT	MYOSIN-2 ISOFORM
12366	26262		3.82	8.9E-02	BF689318.1	EST_HUMAN	602129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
12637	26366		2.75	8.9E-02	9880220	NT	Mus musculus hippocampus abundant gene transcript 1 (Hiat1), mRNA
12684	26993		2	8.9E-02	U29895.1	NT	Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds
12827	26199		1.16	8.9E-02	U40463.1	NT	Ceratitis capitata mariner transposon transposase gene, complete cds
12880	26133		1.54	8.9E-02	AE001514.1	NT	Helicobacter pylori, strain J99 section 76 of 132 of the complete genome
1404	14558	27632	0.96	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
4012	17169	30177	1.07	8.8E-02	AA259128.1	EST_HUMAN	EST11695 Uterus Homo sapiens cDNA 5' end
4145	17297		5.23	8.8E-02	O00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT (TAFII135) (TAFII130) (TAFII130)
4418	17559		0.75	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA
7716	20780		0.71	8.8E-02	D17520.1	NT	Sheep mRNA for angiotensinogen, complete cds
9188	22266	35807	2.07	8.8E-02	AA151872.1	EST_HUMAN	zn66a05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
11380	24441	38099	2.79	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:36356848 5'
11380	24441	38100	2.79	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:36356848 5'
11541	24597	38273	5.25	8.8E-02	AL040129.1	EST_HUMAN	DKFZp434D1313_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313 5'
12443	25314	32060	1.19	8.8E-02	Z71661.1	NT	S.cerevisiae chromosome XIV reading frame ORF YNL285w
3785	18946	29853	4.17	8.7E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3785	16946	29954	4.17	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xc28STS protein (Xc28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4829	17992	30950	1.4	8.7E-02	AF178638.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5211	18332		1.07	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5429	18828	31605	5.49	8.7E-02	AA288875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5429	18829	31606	5.49	8.7E-02	AA288875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6884	20212	33642	0.63	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6884	20212	33643	0.63	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7188	20053	33463	0.57	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TAT-binding protein 1 mRNA, partial cds
8046	21129		0.56	8.7E-02	AA28432.1	EST_HUMAN	z120e03.s1 Soerees ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:713692 3'
8713	21793	35329	0.66	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
8713	21793	35330	0.66	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
10951	24033		2.01	8.7E-02	L04788.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11591	24644	38326	1.48	8.7E-02	AJ007763.1	NT	Glucobacter oxydans tRNA-Ile and tRNA-Ala genes
12431	25306		2.2	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12648	25432		2.85	8.7E-02		NT	Mus musculus nidogen 2 (Nid2), mRNA
13033	25680		2.05	8.7E-02	X65292.1	NT	G. gallus mRNA for vigilin
1281	14437	27506	7.73	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2317	15449	28591	2.2	8.6E-02	BE408667.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3257	16431	29448	2.35	8.6E-02	L05488.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3734	16895		3.68	8.6E-02	AF153362.1	NT	Dietosleilium discoidium adenyl cyclase (acrA) gene, complete cds
3880	17039		0.6	8.6E-02	U29187.1	NT	Mus musculus long incubation piron protein (Prnpb) and prion-like protein (Prnd) genes, complete cds
4609	17748	30725	0.66	8.6E-02	U68179.1	NT	Oryctolagus cuniculus galecetin-3 gene, untranslated exon and 5' flanking region
5330	19443		1.02	8.6E-02	AB011163.1	NT	Homo sapiens mRNA for KIAA0591 protein, partial cds
6219	19394	32743	4.74	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
6504	19670	33035	1.29	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6504	19670	33036	1.29	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7755	20814	34306	0.89	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (R-RELATED RECEPTOR)
8115	21197	34716	1.09	8.6E-02	5730066	NT	Homo sapiens Smf2-related CBP activator protein (SRCAP) mRNA
8115	21197	34717	1.09	8.6E-02	5730066	NT	Homo sapiens Smf2-related CBP activator protein (SRCAP) mRNA
8261	21343	34860	0.96	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8324	21408		0.76	8.0E-02	U60168.1	NT	Dictyostellium discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
9938	22977	36568	1.24	8.0E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
9975	23014		1.4	8.0E-02	AF0662153.1	EST_HUMAN	h20c08.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872846 3'
10356	23391	37001	1.07	8.0E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
11188	24257	37892	1.82	8.0E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11188	24257	37893	1.82	8.0E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11527	24583	38259	3.02	8.0E-02	BF303606.1	EST_HUMAN	601895437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11527	24583	38260	3.02	8.0E-02	BF303606.1	EST_HUMAN	601895437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11724	23910	37534	7.67	8.0E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11875	24863	38559	2.29	8.0E-02	AF283660.1	NT	Bacillus stearothermophilus BarFI methylase (FIM) and BarFI restriction endonuclease (FIR) genes, complete cds
2470	15597	28722	2.59	8.0E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5292	18410		0.66	8.5E-02	N76915.1	EST_HUMAN	yy46h08.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:245823 5'
5786	18978	32283	0.73	8.5E-02	AA985491.1	EST_HUMAN	cg83b07.s1 NCL CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1692917 3' similar to gb:K01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5826	19016		1.99	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
6135	19314	32653	6.61	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8805	21884	35424	1.98	8.5E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
10041	23079	36680	3.27	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10041	23079	36681	3.27	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10572	23607	37212	0.64	8.5E-02	X76731.1	NT	V annodyles gene for annododyoxin C
10702	23735	37340	0.82	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11424	24485		8.03	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11446	24507	38173	3.82	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12873	25886		2.76	8.5E-02	AJ005586.1	NT	Anthrithum majus mRNA for MYB-related transcription factor
13070	25700		2.44	8.5E-02	AA362934.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA 5' end
2732	18070	28961	4.05	8.4E-02	W69330.1	EST_HUMAN	z444e11.r1 Soares fetal heart NBH1919W Homo sapiens cDNA clone IMAGE:343532 5'
5427	18627	31603	9.84	8.4E-02	BE267153.1	EST_HUMAN	601180436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534933 5'
6828	19881	33388	1.46	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00030 protein, partial cds
8218	21300	34821	6.95	8.4E-02	BE095074.1	EST_HUMAN	CH8-BT0760-260400-162-d05 BT0760 Homo sapiens cDNA
9043	22122	35664	1.15	8.4E-02	AF218690.1	NT	Homo sapiens atracrin precursor (ATRIN) gene, exon 2

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10571	23606	37211	1.84	8.4E-02	AI735184.1	EST_HUMAN	as88g10.x1 Barstead colon HPLURB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:088312
10631	23665		0.48	8.4E-02	AV730682.1	EST_HUMAN	O88312 GOS 4.;
12351	26264	32114	1.87	8.4E-02	R79408.1	EST_HUMAN	AV730682 HTF Homo sapiens cDNA clone HTF8M/G04 5'
3682	16845	29653	7.77	8.3E-02	P76334	SWISSPROT	Y63H12.1 Soares placenta N12HP Homo sapiens cDNA clone IMAGE:145895 5'
3709	16870	29873	0.75	8.3E-02	A1436797.1	EST_HUMAN	HYPOPHYSAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3709	16870	29874	0.75	8.3E-02	A1436797.1	EST_HUMAN	th82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2126210 3'
4417	17558		0.68	8.3E-02	M54984.1	NT	th82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2126210 3'
6389	19558	32917	0.74	8.3E-02	A1942338.1	EST_HUMAN	C.thummi A2b region open reading frame, complete cds
6496	19662	33025	2.87	8.3E-02	AF052683.1	NT	wo79111.x1 NCJ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2481581 3'
8169	21251	34771	3.08	8.3E-02	AF19587.1	NT	Homo sapiens protocadherin 43 gene, exon 1
8202	21294		1.06	8.3E-02	AA653285.1	EST_HUMAN	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Drp2) mRNA, complete cds
8495	21576		1.31	8.3E-02	AA987873.1	EST_HUMAN	cg88g08.s1 NCJ CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.t1 L1 L1
8738	22803	36377	1.09	8.3E-02	AW583503.1	EST_HUMAN	repetitive element;
9751	22689		2.02	8.3E-02	AL161595.2	NT	cg81110.s1 NCJ CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
10549	23584		0.72	8.3E-02	AF020409.1	NT	ia05h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
12448	26128		1.81	8.3E-02	BE958458.1	EST_HUMAN	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE.;
1410	14584		9.13	8.2E-02	Y08170.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
1525	14678	27759	2.03	8.2E-02	AF167077.2	NT	Dichostellum discoides DocA (docA) mRNA, complete cds
3141	16317		1.97	8.2E-02	AL163206.2	NT	601844770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928983 5'
3804	17063		1.35	8.2E-02	AL161498.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
4114	17268	30268	0.99	8.2E-02	AL163206.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
4399	17542	30523	6.59	8.2E-02	P48980	SWISSPROT	Homo sapiens chromosome 21 segment HS21C006
4399	17542	30524	6.59	8.2E-02	P48980	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4399	17542	30525	6.58	8.2E-02	P48980	SWISSPROT	Homo sapiens chromosome 21 segment HS21C006
5192	18314	31282	3.43	8.2E-02	U76009.1	NT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5450	18650	31628	1.46	8.2E-02	BE997030.1	EST_HUMAN	LEUCOCYTE ANTIGEN CD97 PRECURSOR
7165	20298	33741	3.16	8.2E-02	AF309955.1	EST_HUMAN	LEUCOCYTE ANTIGEN CD97 PRECURSOR
7910	20962		0.58	8.2E-02	AF743341.1	EST_HUMAN	Mus musculus zinc transporter (Znt-3) gene, complete cds
8905	21894		0.59	8.2E-02	U28397.1	NT	601439676F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
8971	22050	35593	3.24	8.2E-02	AF743341.1	EST_HUMAN	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
9799	22839	36416	4.88	8.2E-02	X04197.1	NT	AV743341 CB Homo sapiens cDNA clone CBLANF07 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9965	23004	36599	2.27	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355596 5'
12454	25318	32094	3.93	8.2E-02	AE002246.2	NT	Chlamydia pneumoniae AR39, section 73 of 94 of the complete genome
12686	25498	32021	1.43	8.2E-02	AW862195.1	EST_HUMAN	QV4-CT0361-021299-049-b01 CT0361 Homo sapiens cDNA
12909	25875		2.58	8.2E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1524	14677	27758	0.96	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcI, and mdcM genes), complete cds
5873	19063	32371	1.03	8.1E-02	AE004006.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
6509	19674	33043	0.89	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7347	20427		0.83	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7796	20816		0.99	8.1E-02	AI692681.1	EST_HUMAN	wd0808.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8535	21616	35151	0.56	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8535	21616	35152	0.56	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
10116	23154		1.83	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
10685	23719		0.7	8.1E-02	AW269778.1	EST_HUMAN	x45b11.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816061 3'
10858	23891	37511	0.47	8.1E-02	AW450487.1	EST_HUMAN	UI-H-B13-ako-g-01-Q-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
10858	23891	37512	0.47	8.1E-02	AW450487.1	EST_HUMAN	UI-H-B13-ako-g-01-Q-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
11790	24780	38477	1.99	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
959	14132	26246	7.61	8.0E-02	AW954663.1	EST_HUMAN	EST368723 MAGC resequences, MAGC Homo sapiens cDNA
1733	16046	27874	11.83	8.0E-02	U60315.1	NT	Malus domestica virus subtype 1, complete genome
1733	16046	27875	11.83	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1852	15095	28196	4.4	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
2447	15575	28704	0.93	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-508 BT0347 Homo sapiens cDNA
2447	15575	28705	0.93	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2541	15686		3.21	8.0E-02	BF246744.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2881	14290	27336	1.55	8.0E-02	M23449.1	NT	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4076619 5'
2965	16141	29159	1.05	8.0E-02	AL445067.1	NT	Dicystosium discoidum cyclic nucleotide phosphodiesterase gene, complete cds
3919	17078	30075	0.93	8.0E-02	AW966118.1	EST_HUMAN	Thermoplasma acidophilum complete genome, segment 5/5
4182	17332		0.74	8.0E-02	4593034	NT	EST378191 MAGC resequences, MAGC Homo sapiens cDNA
4635	18065		6.87	8.0E-02	X72794.1	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
5038	18166	31142	0.82	8.0E-02	M28071.1	NT	Mimulus gene for gelatinase B
6012	18166	32513	3.59	8.0E-02	AF275948.1	NT	Herpesvirus salmieri transformant-associated protein (STP), and dihydrolipoate reductase (DHFR) genes, complete cds, and small nuclear RNAs (snRNAs)
							Homo sapiens ABCA1 (ABCA1) gene, complete cds

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7330	19196	32513	1.61	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8319	21401	34926	2.41	8.0E-02	AL114993.1	NT	Bd.1yis. chineesa strain T4 cDNA library under conditions of nitrogen deprivation
9589	22644	36213	1.38	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9589	22644	36214	1.38	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10361	23366		0.49	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
11032	24111	37747	2.64	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12127	25107	38811	1.63	8.0E-02	4507608	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 9 (TNFSF9) mRNA
12486	25337	32061	3.54	8.0E-02	AJ005376.1	NT	Drosophila orena hunchback region
13134	17332	17332	1.85	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2243	15376	28504	3.37	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859510 5'
3043	16219	29240	12.53	7.9E-02	AI592020.1	EST_HUMAN	ai98c08.x1 Barslead colon HP-LRB7 Homo sapiens cDNA clone IMAGE:1737646 3' similar to gb:Z26876
3953	17111	30110	4.47	7.9E-02	6681044	NT	80S RIBOSOMAL PROTEIN L38 (HUMAN);
3953	17111	30111	4.47	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r). mRNA
4932	18082		1.16	7.9E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
6836	19989		1.14	7.9E-02	BF368016.1	EST_HUMAN	RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA
8221	21303	34824	3.1	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of Mif2 Smt4p (SMT4) gene, complete cds
10234	23269	38859	5.6	7.9E-02	A1081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611.
10234	23269	38860	5.6	7.9E-02	A1081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611.
13008	25684		1.27	7.9E-02	A1761639.1	EST_HUMAN	wg06th01.x1 Soares NSF_F8_9W_OT_PA_F_S1 Homo sapiens cDNA clone IMAGE:2370097 3'
1237	14396	27457	1.49	7.8E-02	A1793275.1	EST_HUMAN	ou59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element ;
1237	14396	27458	1.49	7.8E-02	A1793275.1	EST_HUMAN	ou59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element ;
4915	18045	31035	0.6	7.8E-02	BE836331.1	EST_HUMAN	PVX3-FN0058-140700-005-709 FN0058 Homo sapiens cDNA
5198	17003		2.97	7.8E-02	BE260048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
7023	20087	33504	1.1	7.8E-02	UB2895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7223	20087	33505	1.1	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8985	22084	35604	0.93	7.8E-02	BE897947.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
9081	22180	35702	0.69	7.8E-02	X78344.1	NT	S. cerevisiae CAT8 gene
9253	22330	35877	0.8	7.8E-02	AF233437.1	NT	Homo sapiens FVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9253	22330	35878	0.8	7.8E-02	AF233437.1	NT	Homo sapiens FVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9561	22703	36259	0.9	7.8E-02	AA469354.1	EST_HUMAN	nc88b06.r1 NCI CGAP_P1 Homo sapiens cDNA clone IMAGE:771731
10006	23044	36637	0.55	7.8E-02	Z89124.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814
10901	23985	37816	2.19	7.8E-02	U32323.1	NT	Human interleukin-11 receptor alpha chain gene, complete cds
12910	25802	31973	1.35	7.8E-02	U72847.1	NT	Homo sapiens envoplakin (EVPL) gene, exons 15 through 18
1431	15038	27659	1.22	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3677	16840		2.01	7.7E-02	AJ238083.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and A/U repeat elements
8093	21175	34690	5.38	7.7E-02	AA402949.1	EST_HUMAN	zu53d11.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN.;
10040	23078	36579	4.88	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10336	23371	36981	0.84	7.7E-02	AI318662.1	EST_HUMAN	ta80b08.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S
10336	23371	36982	0.84	7.7E-02	AI318662.1	EST_HUMAN	RIBOSOMAL PROTEIN L38 (HUMAN);
11262	24331	37972	3.98	7.7E-02	11422757	NT	ta80b08.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S
3474	16641	29660	3.1	7.6E-02	BE514432.1	EST_HUMAN	RIBOSOMAL PROTEIN L38 (HUMAN);
3494	16661	29673	0.98	7.6E-02	AA296447.1	EST_HUMAN	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
							601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
							EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
							Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
3649	18812	29825	0.96	7.6E-02	AJ400877.1	NT	
6222	19397	32746	0.69	7.6E-02	AI061275.1	EST_HUMAN	an25g02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1899730 3'
6486	19653	33015	1.14	7.6E-02	BE378328.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9570	22712	36280	1.11	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
10101	23139		0.99	7.6E-02	AL138078.2	NT	Campylobacter jejuni NGTC11168 complete genome; segment 5/6
10424	23459	37064	0.5	7.6E-02	BE708002.1	EST_HUMAN	RC1-HT0545-020800-017-d06 HT0545 Homo sapiens cDNA
10557	23592		1.04	7.6E-02	BE959338.2	EST_HUMAN	601854915F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
10815	23848	37469	0.97	7.6E-02	X92656.1	NT	L. esculentum mRNA for fructose phosphatase translocator

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10815	23848	37470	0.97	7.0E-02	X92656.1	NT	L. esculentum mRNA for triose phosphate translocator
11974	24959	38661	1.93	7.0E-02	AW988645.1	EST_HUMAN	QV3-BN0046-160400-151.c04 BN0046 Homo sapiens cDNA
807	13987	27039	1.66	7.5E-02	5902093	NT	Homo sapiens soluble carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
807	13987	27040	1.96	7.5E-02	5902093	NT	Homo sapiens soluble carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1971	15114	28214	0.99	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4630	17766	30748	0.74	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
5974	19159	32477	1.45	7.5E-02	A1848714.1	EST_HUMAN	wq24h09.xt NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472257 3'
8533	21614	35150	1.28	7.5E-02	A1864367.1	EST_HUMAN	w52b02.xt NCI_CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
8705	21785	35318	1.36	7.5E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000284 5'
10238	23273		0.49	7.5E-02	BF221730.1	EST_HUMAN	7c61c05.xt NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element MER27 repetitive element;
10711	23744	37350	0.73	7.5E-02	BF208909.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
10816	23849	37471	0.82	7.5E-02	X79480.1	NT	C.fini DSM 20113 16S rDNA
490	13684	26718	1.41	7.4E-02	AW838547.1	EST_HUMAN	RC5-LT0054-260100-011-H09.LT0054 Homo sapiens cDNA
1489	14642		1.21	7.4E-02	AF030027.1	NT	Equine herpesvirus 4 strain NS80567, complete genome
2648	15771		0.96	7.4E-02	6755089	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
3683	16846	28854	1.21	7.4E-02	A1807885.1	EST_HUMAN	wf43h01.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4826	17959	30946	1.19	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4914	18044	31034	2.65	7.4E-02		NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
5056	18184	31159	4.42	7.4E-02	6878442	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchlp), mRNA
6624	19784		1.69	7.4E-02	R17477.1	EST_HUMAN	yg14g06.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
6717	19875	33266	0.66	7.4E-02	AF030422.1	NT	Electrophorus electricus acetylcholinesterase catalytic subunit precursor gene, complete cds
7636	20705	34184	0.84	7.4E-02	AA605132.1	EST_HUMAN	no71d02.6t NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3'
8085	21167	34663	1.11	7.4E-02	BE880112.1	EST_HUMAN	601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895294 5'
8699	21779	35312	1.26	7.4E-02	U6089.1	NT	Human periodic tyrosinase protein 2 (PW2) gene, exons 15 to 21, and complete cds
9367	22442	36002	1.08	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.yt NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
9367	22442	36003	1.08	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.yt NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN
9639	21082	34593	0.58	7.4E-02	A1672939.1	EST_HUMAN	015127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9639	21082	34594	0.58	7.4E-02	A1672939.1	EST_HUMAN	015127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9639	21082	34594	0.58	7.4E-02	A1672939.1	EST_HUMAN	we74d02.xt Soares_Dickgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
9639	21082	34594	0.58	7.4E-02	A1672939.1	EST_HUMAN	we74d02.xt Soares_Dickgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10019	23057	36653	1	7.4E-02	U62203.1	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
10146	23184	36780	0.49	7.4E-02	BF512678.1	EST_HUMAN	UI-H-BW1-ang-8-06-QJ1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3069898 3'
11266	24335	37975	1.48	7.4E-02	AA059167.1	EST_HUMAN	z64601.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381720 5'
11914	24901	38604	1.42	7.4E-02	AI125063.1	EST_HUMAN	ap011007.s1 Barstead acilia HPL RB3 Homo sapiens cDNA clone IMAGE:1726285 3' similar to gb:MB6482
12409	25258		1.22	7.4E-02	11525893	NT	GLIA MATURATION FACTOR BETA (HUMAN);
12692	26101		3.74	7.4E-02	AW379431.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12870	25580	31995	2.61	7.4E-02	BF035039.1	EST_HUMAN	CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
12892	25585	31968	1.44	7.4E-02	AJ223459.2	NT	601453813F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857738 5'
481	13676	26708	1.15	7.3E-02	BE984961.2	EST_HUMAN	Aspergillus nidulans prnD, prnX, prnA genes
481	13676	26709	1.15	7.3E-02	BE984961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886208 3'
702	13885	26917	2.65	7.3E-02	AE001789.1	NT	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
1510	16040	27748	3.26	7.3E-02	AW900261.1	EST_HUMAN	Thermoloba maritima section 101 of 136 of the complete genome
1893	16050		15.79	7.3E-02	AL163302.2	NT	CM0-NNT004-130300-284-g08 NN1004 Homo sapiens cDNA
5112	18240		1.02	7.3E-02	U12283.1	NT	Homo sapiens chromosome 21 segment HS21C102
6582	19744	33126	1.48	7.3E-02	AA779977.1	EST_HUMAN	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
7633	20702	34180	2.37	7.3E-02	P05143	SWISSPROT	z24402.s1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
7633	20702	34181	2.37	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7981	21030		0.58	7.3E-02	BF316087.1	EST_HUMAN	PROLINE-RICH PROTEIN MP-3
8361	21442		1.36	7.3E-02	7662107	NT	601896047F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125515 5'
8596	21677	35214	0.5	7.3E-02	Y10887.2	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
9411	22485		1.17	7.3E-02	AB011090.1	NT	Mus musculus cdk5 gene, exon 1, partial
11492	19744	33126	1.78	7.3E-02	AA779977.1	EST_HUMAN	Homo sapiens mRNA for KIAA0518 protein, partial cds
122	13352	26382	0.6	7.2E-02	AE000882.1	NT	z24402.s1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
122	13352	26383	0.6	7.2E-02	AE000882.1	NT	gb:U02426.2BS PROTEASE SUBUNIT 4 (HUMAN);
1505	14658	27739	2.6	7.2E-02	AL163301.2	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039834 (section 88 of 148) of the complete genome
1505	14658	27740	2.6	7.2E-02	AL163301.2	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039834 (section 88 of 148) of the complete genome
2814	15738		3.34	7.2E-02	U14794.1	NT	Homo sapiens chromosome 21 segment HS21C101
3991	17148	30154	0.63	7.2E-02	AW298322.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
							Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
							UI-H-BW0-ajl-a-05-QJ1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4465	17605	30563	3.07	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
5402	18604	31576	2.73	7.2E-02	U67631.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5403	18605	31577	8.76	7.2E-02	P11120	SWISSPROT	CALMODULIN
6244	19418		1.11	7.2E-02	BF217596.1	EST_HUMAN	601883905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096224 5'
7318	20400	33863	1.32	7.2E-02	BF216086.1	EST_HUMAN	601883588F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7335	20416	33878	0.7	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7359	20438		1.53	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8382	21483	34987	0.6	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8382	21483	34988	0.6	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
9264	22341		0.57	7.2E-02	Y17217.1	NT	Lactococcus lactis cspE gene
9775	22815		0.51	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9811	22851	36430	2.19	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAU001 5'
9861	23000	36596	4.88	7.2E-02	L14551.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
10118	23156	36754	0.96	7.2E-02	BF126399.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026438 5'
10206	23242	36833	2.34	7.2E-02	AW873187.1	EST_HUMAN	Hq24111.x1 NCI_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
10385	23430	37037	0.8	7.2E-02	AA768204.1	EST_HUMAN	aa62607.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10560	23585	37201	2.15	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10592	23725	37331	5.57	7.2E-02	BE565003.1	EST_HUMAN	601734926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
10716	23749		3.47	7.2E-02	BE530214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
10837	23870	37492	0.55	7.2E-02	AA706897.1	EST_HUMAN	2j28f05.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451641 3'
11153	24224	37853	4.14	7.2E-02	AF048874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
12315	25230	32104	2.12	7.2E-02	AA773596.1	EST_HUMAN	af81a04.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12380	25253		3.83	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
12411	25290		2.05	7.2E-02	AA584465.1	EST_HUMAN	nc05r08.s1 NCI_CGAP_Phet Homo sapiens cDNA clone IMAGE:1099839 3'
12474	25327		4.23	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12488	25937		7.37	7.2E-02	AW900962.1	EST_HUMAN	CM4-NN1009-200300-118-c11 NN1009 Homo sapiens cDNA
13048	25687		1.63	7.2E-02	AA401779.1	EST_HUMAN	2d57c12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:126454 5'
1953	15096	28197	2.05	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2368	15497	26623	6.8	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092881 5'
8091	21173	34687	1.08	7.1E-02	AI125264.1	EST_HUMAN	cd92a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736022 3'
10866	23898	37521	0.53	7.1E-02	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12193	25150		6.48	7.1E-02	BE304784.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
541	13734	26758	1.4	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1529	14662		1.28	7.0E-02	X96877.1	NT	Martellia Mctc-1 gene
1801	14960	28044	1.18	7.0E-02	AA056343.1	EST_HUMAN	2166104.s1 Striatagene colon (#937204) Homo sapiens cDNA clone IMAGE:509599 3'
3095	16271	29296	2.02	7.0E-02	AW138152.1	EST_HUMAN	UI-H-B11-acy-c-07-Q-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
4004	17161	30167	0.65	7.0E-02	AA815438.1	EST_HUMAN	al65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 80S
4155	17307	30301	1.19	7.0E-02	BE070284.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN).
4268	17403		1.14	7.0E-02	AW792962.1	EST_HUMAN	QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA
4330	17473	30459	1.19	7.0E-02	AF077821.1	NT	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
5045	18173	31150	7.97	7.0E-02	BF381987.1	EST_HUMAN	601816281F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4050071 5'
5493	18922		0.92	7.0E-02	Y09143.2	NT	Lumbricus rubellus mRNA for cyclophilin B
7560	20632	34107	0.9	7.0E-02	AV689285.1	EST_HUMAN	AY689285 GK Homo sapiens cDNA clone GKCCAE08 5'
7782	20838	34331	0.68	7.0E-02	Y19187.1	NT	Gallus gallus mRNA for partial aczanin, XL spliced variant (acc gene)
9299	22375	35926	1.24	7.0E-02	9628113	NT	African swine fever virus, complete genome
9797	22837	36415	1.31	7.0E-02	K02901.1	NT	Rat Ig gamma epsilon H-chain gene C-region, 3' end
10158	23195	36791	0.88	7.0E-02	U27266.1	NT	Human myosin binding protein H (MyBP-H) gene, complete cds
11654	24733	38424	2.6	7.0E-02	AA724295.1	EST_HUMAN	ah98a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837
13022	25673	31958	1.2	7.0E-02	11421638	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
527	13720	28744	7.08	6.9E-02	AL163210.2	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
527	13720	28745	7.08	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1364	14518		1.58	6.9E-02	4507968	NT	Homo sapiens chromosome 21 segment HS21C010
3893	17052	30051	1.34	6.9E-02	Q06364	SWISSPROT	Homo sapiens regulator of G2-selective protein signaling (ZGAP1) mRNA, and translated products
3893	17052	30052	1.34	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5302	18419	31389	4.11	6.9E-02	Z76163.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5316	18433	31403	0.83	6.9E-02	M34956.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA24F7
7793	20849		0.87	6.9E-02	AF164967.1	NT	M. hyorhins 115 kDa protein (p115) gene, complete cds
8242	21324		1.14	6.9E-02	U12022.1	NT	Canine distemper virus strain A79/17, complete genome
8750	21829	36368	1.01	6.9E-02	BE567435.1	EST_HUMAN	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
							601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8750	21829	35367	1.01	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9320	22398	35949	0.67	6.9E-02	U22967.1	NT	Barbale duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
11374	24435	38092	1.46	6.9E-02	S81752.1	NT	DPH2L -candidate tumor suppressor gene [ovarian cancer critical region of deletion] [human, 9 week fetal and placental tissues, mRNA, 2233 nt]
11374	24435	38093	1.46	6.9E-02	S81752.1	NT	DPH2L -candidate tumor suppressor gene [ovarian cancer critical region of deletion] [human, 9 week fetal and placental tissues, mRNA, 2233 nt]
12346	25251		10.94	6.9E-02	X74315.1	NT	X laevis XFD2 mRNA for fork head protein
12524	25357		1.56	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFQ HOMOLOG
12770	25513		3.37	6.9E-02	AF195963.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1932	15075	28177	1.18	6.8E-02	AA496759.1	EST_HUMAN	ae30102.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1932	15075	28178	1.18	6.8E-02	AA496759.1	EST_HUMAN	ae30102.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1956	15099	28199	3.85	6.8E-02	AF156673.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
4575	17810		0.84	6.8E-02	BE141076.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSCR14) gene, complete cds
6759	19914		0.65	6.8E-02	P20792	SWISSPROT	CELL SURFACE RECEPTOR DAF-1 PRECURSOR
7040	20093		0.99	6.8E-02	BE061890.1	EST_HUMAN	RC1-BT0264-090300-017-c09 BT0254 Homo sapiens cDNA
7432	20509	33981	8.22	6.8E-02	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
7861	20915	34420	0.6	6.8E-02	U16856.1	NT	Dictyostelium discoideum myosin heavy chain kinase A (MYCK A) mRNA, complete cds
8483	21564	35096	6.03	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/8
8483	21564	35100	6.03	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/8
12141	26165		1.47	6.8E-02	T03214.1	EST_HUMAN	FB4A9 Fetal brain, Stragene Homo sapiens cDNA clone FB448 3' end similar to LINE-1
12276	25206		1.64	6.8E-02	AA758014.1	EST_HUMAN	ah6705.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'
12906	25599		1.34	6.8E-02	AW975839.1	EST_HUMAN	EST387948 MAGE resequences, MAGN Homo sapiens cDNA
12972	25632		2.3	6.8E-02	8910595	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
13203	26091	31660	1.24	6.8E-02	8978885	NT	Rattus norvegicus Growth factor independent-1 (Gfi1), mRNA
1558	14711		2.71	6.7E-02	AF115636.1	NT	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OrmyTAP1*01 allele, complete cds
1942	15035	28186	2.17	6.7E-02	AJ220285.1	EST_HUMAN	hg79604.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841408 3'
3811	16871	29973	4.48	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOX-D4 (HOXA-A)
4065	17221	30229	0.74	6.7E-02	U63783.1	NT	Cyprinus carpio Rap1b mRNA, complete cds
4065	17221	30230	0.74	6.7E-02	U53783.1	NT	Cyprinus carpio Rap1b mRNA, complete cds
7969	21019	34532	0.88	6.7E-02	W57759.1	EST_HUMAN	ztd20g11.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341262 3' similar to contains
8034	21117	34635	0.74	6.7E-02	X62695.1	NT	Alu repetitive element; contains element L1 repetitive element ; H. sapiens DNA for cGMP phosphodiesterase (exons 4-22)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8034	21117	34636	0.74	6.7E-02	X62895.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8633	21713	35250	0.73	6.7E-02	AW082888.1	EST_HUMAN	xb561c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2680788 3'
9800	22840	36417	0.59	6.7E-02	AW137359.1	EST_HUMAN	U14-B11-acc-g-01-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
9800	22840	36418	0.59	6.7E-02	AW137359.1	EST_HUMAN	U14-B11-acc-g-01-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
1379	14534	27608	0.98	6.6E-02	AI735509.1	EST_HUMAN	at12609.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to
2252	15385	28573	3.73	6.6E-02	AJ289241.1	NT	SW141N1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. ;
3552	16717	29731	12.38	6.6E-02	R64306.1	EST_HUMAN	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3567	16732	29748	3.11	6.6E-02	7108357	NT	Y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3567	16732	29749	3.11	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4191	17341	30334	1.81	6.6E-02	AF260226.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5053	18221	31191	12.07	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5093	18221	31192	12.07	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5130	18255	31220	0.64	6.6E-02	AA393244.1	EST_HUMAN	z14807.1 Soares testis_NHT_Homo sapiens cDNA clone IMAGE:728052 5' similar to gb104270 TUMOR
5130	18255	31221	0.64	6.6E-02	AA393244.1	EST_HUMAN	NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6714	19872	33254	3.92	6.6E-02	X06411.1	NT	z14807.1 Soares testis_NHT_Homo sapiens cDNA clone IMAGE:728052 5' similar to gb104270 TUMOR
6749	19905	33298	0.62	6.6E-02	P25159	SWISSPROT	P. vulgaris mRNA for chalcone synthase
6749	19905	33299	0.62	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
6937	19905	33298	0.68	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
6937	19905	33299	0.68	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
8133	21215	34736	1.51	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8689	21749	35287	0.77	6.6E-02	AF06055.1	NT	Dicystidium discoidium darlin (darA) gene, complete cds
8679	22058		0.93	6.6E-02	O60673	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
9121	22200	35741	1.28	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
9121	22200	35742	1.28	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
10157	23194	36790	0.54	6.6E-02	A1458752.1	EST_HUMAN	957g06.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149498 3'
10292	23327	36930	1.5	6.6E-02	Y07848.1	NT	Homo sapiens EWS, gar22, rrp22 and bam22 genes
10327	23362		0.65	6.6E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
10710	23743	37349	0.49	6.6E-02	BF694659.1	EST_HUMAN	602080508F2 NIH_JMGC_81 Homo sapiens cDNA clone IMAGE:4245936 5'
11205	24274	37911	4.95	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0064.010600-006-a12 SN0064 Homo sapiens cDNA
12761	25505		4.84	6.6E-02	9637981	NT	Mus musculus DIPB gene (DipB), mRNA
13124	25733		1.26	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region

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696	13786	26805	1.57	6.5E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3954178 5'
1011	14183	27245	1.3	6.5E-02	7706068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1422	14576	27649	3.38	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1773	14922	28016	2.04	6.5E-02	AE000764.1	NT	Aquifex acidicus section 96 of 109 of the complete genome
5676	18870	32156	2.07	6.5E-02	AA443991.1	EST_HUMAN	zv46h12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038
6673	19832	33221	0.73	6.5E-02	BF665340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
7113	18539	31496	1.02	6.5E-02	U22861.1	NT	602118687F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:4276029 5'
10147	23186	36781	0.57	6.5E-02	BE963200.2	EST_HUMAN	Azotobacter vinelandii ATCC 8046 negative regulator MucB (mucB) gene, partial cds
10147	23186	36782	0.57	6.5E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3865637 3'
10683	23717	37323	0.81	6.5E-02	BF106300.1	EST_HUMAN	601823511F1 NIH_MGC 77 Homo sapiens cDNA clone IMAGE:4043138 5'
10876	23960	37589	4.45	6.5E-02	AA196648.1	EST_HUMAN	z32g06.s1 Soares NIH-MP_u_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12163	25129		3.78	6.5E-02	M21496.1	NT	Rabbit microsomal epoxide hydrolase
12633	25363		3.67	6.5E-02	AF102993.1	NT	Nectria haematococca kinesis related protein 2 (KRP2) gene, complete cds
589	13780	26789	1.49	6.4E-02	X94549.1	NT	A.cantares precursor of peridinin-chlorophyll-protein (PCP) gene
1770	14919	28013	0.99	6.4E-02	AE001777.1	NT	Thermoboga maritima section 89 of 136 of the complete genome
1770	14919	28014	0.99	6.4E-02	AE001777.1	NT	Thermoboga maritima section 89 of 136 of the complete genome
5566	18763	31803	1.11	6.4E-02	A191956.1	EST_HUMAN	q607b01.x1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR8 repetitive element
6239	19413	32761	2.64	6.4E-02	AF032733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6239	19413	32762	2.64	6.4E-02	AF032733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6532	19896	33069	1.23	6.4E-02	A1672896.1	EST_HUMAN	we73g12.x1 Soares Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346790 3'
6957	20270	33708	4.11	6.4E-02	BE974448.1	EST_HUMAN	601680425R2 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3950503 3'
8531	21812		2.47	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 6a (zeta) (Cot6a), mRNA
8865	21944	35478	4.17	6.4E-02	AA083305.1	EST_HUMAN	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9327	22403	35955	0.98	6.4E-02	AF160195.1	EST_HUMAN	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
9785	22825		0.61	6.4E-02	BE834083.1	EST_HUMAN	RC1-OT0083-150600-014-g06 OT0083 Homo sapiens cDNA
9918	22958	36545	1.87	6.4E-02	AB011126.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10468	23503	37116	0.45	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10468	23503	37117	0.45	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
12008	24993	38697	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (h-LA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12008	24993	38698	1.88	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12427	26048		2.7	6.4E-02	AF107890.1	NT	Human sapiens mucin 5B (MUC5B) gene, partial cds
12479	26331	32056	2.81	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
							Mus musculus major histocompatibility locus class III regions Hec70t gene, partial cds; smRNP, G7A, NG23, MUS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
1793	14942	28035	2.51	6.3E-02	AF109905.1	NT	HEAT SHOCK PROTEIN 70 HOMOLOG
3692	18854		2.29	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6284	19438	32785	1.12	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
7391	20469		1.84	6.3E-02	X97869.1	NT	H.sapiens gene encoding La autoantigen
9491	22548	36111	0.99	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Domina gene, exons 1-3
10218	23264	36843	3.52	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: GNR-152
10478	23513		1.31	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GKC Homo sapiens cDNA clone GKCAHE01 5'
10954	19438	32785	2.36	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
2549	15874	28797	1.04	6.2E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4365	17508	30499	4.22	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
							Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI1) mRNA, complete cds
4458	17598		1.03	6.2E-02	AF271235.1	NT	complete cds
4705	17840		5.66	6.2E-02	Q62191	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO82)
6335	20250	33685	0.76	6.2E-02	D49530.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds.
7805	20861	34354	0.86	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8016	21067		0.58	6.2E-02	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
9148	26225		0.92	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9544	22609	36177	0.47	6.2E-02	AA778450.1	EST_HUMAN	af20a06.st Soares, total Tetus_N52HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9881	22730	36300	1.19	6.2E-02	6677898	NT	Mus musculus stromal cell derived factor receptor 2 (Sdf2), mRNA
11415	24476	38140	1.42	6.2E-02	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
11629	24709	38401	1.54	6.2E-02	AJ242735.1	NT	Metarhizium anisopliae mRNA for Glycylproline (chyl) gene
12263	26191		3.63	6.2E-02	AJ000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12617	25415		1.24	6.2E-02	BE793085.1	EST_HUMAN	601583773F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937842 5'
							737h08.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to
12703	25467	32024	3.61	6.2E-02	BF112039.1	EST_HUMAN	TR:Q9Y4S6 Q9Y4S8 HYPOTHETICAL 30.3 KD PROTEIN. [1];
266	13485	26516	3.63	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
4089	17254		2.85	6.1E-02	U73325.1	NT	Arabidopsis thaliana K ⁺ inward rectifying channel protein (AtKIC1) gene, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6240	19414		1.57	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8458	21539	35068	3.65	6.1E-02	X99268.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8861	21940	35474	0.6	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
8861	21940	35475	0.6	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
10967	24048	37681	3.9	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0818-110500-136-C08 HT0818 Homo sapiens cDNA
12134	25114	38818	1.86	6.1E-02	AB025333.1	NT	Epitretus burgeri mRNA for RNA polymerase III largest subunit, partial cds
12218	26083		30.03	6.1E-02	X70969.1	NT	S. japonicum mRNA for serine-enzyme
12836	25957		1.58	6.1E-02	AI866611.1	EST_HUMAN	t25907.x1 NCI_QGAP_Ox35 Homo sapiens cDNA clone IMAGE:2292901 3'
12993	25645		6.43	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1291	14447	27513	1.58	6.1E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2740	15857	28969	1.17	6.0E-02	AW968848.1	EST_HUMAN	EST380924 IMAGE resequences, MAGI Homo sapiens cDNA
2832	15946		1.43	6.0E-02	AB031289.1	NT	Mesocostoides corli mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
3002	13335	26362	1.53	6.0E-02	AA188730.1	EST_HUMAN	zp78cd4.t1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3002	13335	26363	1.53	6.0E-02	AA188730.1	EST_HUMAN	zp78cd4.t1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3301	16475	29496	2.07	6.0E-02	AA372376.1	EST_HUMAN	EST184266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3301	16475	29497	2.07	6.0E-02	AA372376.1	EST_HUMAN	EST184266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3725	16886		0.76	6.0E-02	BE964443.2	EST_HUMAN	601658160R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
5514	18712		1.01	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011199-013-b04 BT0253 Homo sapiens cDNA
6845	19515	32872	1	6.0E-02	AI807537.1	EST_HUMAN	wf48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.1 L1 L1 repetitive element
7127	18553	31467	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7127	18553	31468	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7338	20418	33880	2.37	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5'
7857	20912	34417	1.78	6.0E-02	AI204275.1	EST_HUMAN	qf58b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754199 3'
8617	21597		0.46	6.0E-02	11468495	NT	Recinononates americana mitochondrion, complete genome
9472	22529	35092	1.29	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_QGAP_G06 Homo sapiens cDNA clone IMAGE:2237362 3'
9472	22529	35093	1.29	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_QGAP_G06 Homo sapiens cDNA clone IMAGE:2237362 3'
9608	22661	36233	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial GLV gene for immunoglobulin light chain variable region, exons 1-2
9608	22661	36234	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial GLV gene for immunoglobulin light chain variable region, exons 1-2
10109	23147	36746	0.72	6.0E-02	AA309797.1	EST_HUMAN	EST180664 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10109	23147	36747	0.72	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
11618	24669		1.42	6.0E-02	AA128386.1	EST_HUMAN	zn87c08.t1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565166 5' similar to gb:X68181.60S RIBOSOMAL PROTEIN L31 (HUMAN); wf69103.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60288
12921	25606		5.12	6.0E-02	AI809273.1	EST_HUMAN	RC1-DT0001-250100-012-e10 DT0001 Homo sapiens cDNA
239	13461	28489	5.86	5.9E-02	AW934719.1	EST_HUMAN	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
3048	16224	29246	2.77	5.9E-02	AF190289.1	NT	Duck parvovirus strain 90-2193 capsid protein (VP3) gene, partial cds
4864	17997		0.77	5.8E-02	AF168111.1	NT	Mus musculus trophoblast related homeobox 5 (Drosophila) (trx5), mRNA
8817	21896	35435	2	5.9E-02	9055249	NT	601877609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105994 5'
9650	21093		0.97	5.9E-02	BF242748.1	EST_HUMAN	Mus musculus follistatin-like (Fstl), mRNA
11026	24104		7.39	5.9E-02	6679870	NT	602076548F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243834 5'
11835	24824		1.35	5.9E-02	BF572539.1	EST_HUMAN	Gallus gallus HIC9 telomere junction
11850	24839		1.37	5.9E-02	AJ240733.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
966	14129		6	5.8E-02	D90110.1	NT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
1693	14845	27929	0.97	5.8E-02	O61768	SWISSPROT	Thermotoga maritima section 87 of 136 of the complete genome
3753	16914	29917	1.68	5.8E-02	AE001775.1	NT	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4474	17614	30593	6.79	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4474	17614	30594	6.79	5.8E-02	AW051927.1	EST_HUMAN	qh5610.1.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4669	17804	30792	4.84	5.8E-02	AI247505.1	EST_HUMAN	qh5610.1.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4669	17804	30793	4.84	5.8E-02	AI247505.1	EST_HUMAN	gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4696	17831		2.1	5.8E-02	AF066264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1), mRNA, complete cds
7855	20910	34414	2.76	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
7855	20910	34415	2.76	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8866	21045	35479	0.81	5.8E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12365	25261		1.86	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12681	26180		4.55	5.8E-02	AA604269.1	EST_HUMAN	no75et1.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
							eu63605.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
3123	16299	29312	1.14	5.7E-02	AI081644.1	EST_HUMAN	CE08811
3139	16315	29328	1.09	5.7E-02	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3902	17061	30060	2.3	5.7E-02	AF166791.1	EST_HUMAN	EST137865 MAGI resequences, MAGI Homo sapiens cDNA
4807	17941		0.95	5.7E-02	M95099.1	NT	Bos taurus lysozyme gene (cow 3), complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6000	19185		0.67	5.7E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7630	20699	34175	0.68	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7630	20699	34176	0.68	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7710	20775	34260	0.72	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
7710	20775	34261	0.72	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8349	21430	34954	1.45	5.7E-02	AJ286090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv9.2 gene)
10055	23093	36695	0.82	5.7E-02	6681260	NT	Mus musculus ect2 oncogene (Ect2), mRNA
11464	24523	38193	3.14	5.7E-02	A1752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC.cn18b09 random
11464	24523	38194	3.14	5.7E-02	A1752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC.cn18b09 random
11630	24710		1.66	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12688	25669		19.03	5.7E-02	D50320.1	NT	Pig DNA for SPAT-2, complete cds
12769	25512		2.17	5.7E-02	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12853	26042		3.04	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
13012	26165		5.21	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
13171	25759	31929	1.18	5.7E-02	R48513.1	EST_HUMAN	y64d10.s1 Soares breast 2NtHst Homo sapiens cDNA clone IMAGE:153523 3' similar to contains L1 repetitive element
1556	14709	27789	1.1	5.6E-02	AF094455.1	NT	Hydroxyle rotundifolia ribosomal protein L16 (p16) gene, intron, chloroplast gene for chloroplast product
2362	15493		1.95	5.6E-02	BE904308.1	EST_HUMAN	601494578F2 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896810 5'
4763	17998	30878	1.37	5.6E-02	AB013100.1	NT	Lycopodium esculentum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4818	17951	30936	1.31	5.6E-02	AA290599.1	EST_HUMAN	z945c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
6799	19954	33354	5.87	5.6E-02	AW172708.1	EST_HUMAN	x02c10.s1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:O94979 O94979 KIAA0905 PROTEIN ;
7031	20167	33689	1.02	5.6E-02	AA866182.1	EST_HUMAN	od47f12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element/contains element L1 repetitive element ;
7301	20383	33842	3.3	5.6E-02	BE008001.1	EST_HUMAN	QV0.BN0147.290400-214-g07 BN0147 Homo sapiens cDNA
8010	21060	34572	1.32	5.6E-02	A1183583.1	EST_HUMAN	q684g11.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1734308 3'
9002	22081	35523	2.52	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
9002	22081	35624	2.52	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
10017	23055	36651	1.18	5.6E-02	AA482884.1	EST_HUMAN	n48g07.s1 NCI_CGAP_A1V1 Homo sapiens cDNA clone IMAGE:323245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11863	24851		2.42	5.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2720	15938	28948	7.33	5.6E-02	X97869.1	NT	H. sapiens gene encoding La autoantigen
3288	18460	29481	3.33	5.5E-02	875550.1	NT	Mus musculus SH3 domain protein 1B (SH3d1B), mRNA
4332	17475	30459	0.98	5.5E-02	L41561.1	NT	Gallid herpesvirus mRNA fragment
5778	18868	32272	3.49	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
6149	18968	32272	4.32	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7535	20608	34083	1.65	5.5E-02	875590.2	NT	Mus musculus tuftelin 1 (Tuft1), mRNA
8311	21393	34917	0.87	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1), mRNA, complete cds
8311	21393	34918	0.87	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1), mRNA, complete cds
9855	22895	36476	0.76	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9855	22895	38477	0.76	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9951	22990	36583	1.24	5.5E-02	U69482.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
11271	24339	37877	6.31	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB), >
3084	18260		0.85	5.4E-02	AJ277468.1	NT	Oryza sativa rbb13-1 gene for putative Bowman Birk trypsin inhibitor
3309	18476		8.19	5.4E-02	BE073468.1	EST_HUMAN	RC8-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
4020	17177	30186	0.61	5.4E-02	U85806.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8318	21398		1.18	5.4E-02	Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2395281 to 2613730
9271	22347	35897	0.51	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10938	24020	37653	1.86	5.4E-02	U20780.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11453	24513	38180	1.36	5.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
11453	24513	38181	1.36	5.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
12463	26850		3.72	5.4E-02	U44894.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1078	14244	27300	1.55	5.3E-02	AW391248.1	EST_HUMAN	QVG-ST0213-021298-062-a09 ST0213 Homo sapiens cDNA
1078	14244	27301	1.55	5.3E-02	AW391248.1	EST_HUMAN	QVG-ST0213-021298-062-a09 ST0213 Homo sapiens cDNA
1535	14688	27789	20.57	5.3E-02	T84759.1	EST_HUMAN	ye37f12.11 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01506
2566	15591	28816	3.22	5.3E-02	AJ276403.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
3008	16184	29207	0.97	5.3E-02	M58417.1	NT	Pseudomonas putida figS gene
3008	16184	29208	0.97	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3221	16395	29406	4.83	5.3E-02	AJ276403.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
5200	18321	31290	7.98	5.3E-02	M80463.1	NT	Pseudomonas putida figS gene
							Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5434	18634	31812	2.39	5.3E-02	AE000527.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
5434	18634	31813	2.39	5.3E-02	AE000527.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
6228	19403	32783	1.14	5.3E-02	M85289.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
7024	20180	33580	4.02	5.3E-02	9695413	NT	Lymphocystis disease virus 1, complete genome
7241	20325	33769	1.37	5.3E-02	U32832.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7517	20560		2.3	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
8061	21073	34585	0.68	5.3E-02	P38742	SWISSPROT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION
8600	21681		0.68	5.3E-02	U10098.1	NT	Mus musculus 129/Sv cystatin G (cs3) gene, complete cds
9325	22401	35954	1.73	5.3E-02	X03127.1	NT	Podospira anserina mitochondrial epsilon-sen DNA
10462	23497		0.61	5.3E-02	Y07807.1	NT	D. rerio mRNA for zp-23 POU gene, splice variant (neurula, 9-16 hpf and posttranscription, 20-28 hpf)
10538	23573	37180	0.79	5.3E-02	X68432.1	NT	B. rerio pou3f mRNA for transcription factor
13173	25761	31931	1.55	5.3E-02	AF276815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2358	15489		64.04	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3183	16358	29363	2.39	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3183	16358	29364	2.39	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4050	17208	30216	0.8	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
4393	17536	30515	3.31	5.2E-02	U07192.1	NT	Human steroid hormone receptor Nrr-1 mRNA, complete cds
5287	18406	31373	0.66	5.2E-02	AB035201.1	NT	Rattus norvegicus mRNA for thyroglobulin, complete cds
6040	19223	32545	0.64	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6233	19408		0.94	5.2E-02	AI830965.1	EST_HUMAN	wj80e04.x1 NC1 CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element
7424	20501	33972	1.23	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8386	21470		2.39	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9931	22971	36560	2.16	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
9931	22971	36561	2.16	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
12725	25483		1.6	5.2E-02	Q03030	SWISSPROT	Oxalacetate decarboxylase ALPHA CHAIN
2437	15563		0.98	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073.1 5'47 (lynorm: hfr1) Homo sapiens cDNA clone DKFZp547D073 5'
5161	18283	31248	0.89	5.1E-02	BE567423.2	EST_HUMAN	601653565R2 NIH_MGC.55 Homo sapiens cDNA clone IMAGE:3833361 3'
5251	18372		0.96	5.1E-02	AL138077.2	NT	Campylobacter jejuni NCTC11108 complete genome, segment 4/6
5349	18482		0.74	5.1E-02	U72397.1	NT	Bacteriophage 80 alpha holin and amidase genes, complete cds
6812	18966	33370	0.79	5.1E-02	AF280369.1	NT	HIV-1 patient 96 from Italy protease (pol) gene, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6997	18516	31508	1.73	5.1E-02	BF378625.1	EST_HUMAN	QV0-UM0051-250800-350-508 UM0051 Homo sapiens cDNA
8447	21528	35055	0.82	5.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8447	21528	35056	0.82	5.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8542	21623	35160	1.42	5.1E-02	AJ131966.1	NT	Spodoptera littoralis mRNA for 3-dehydrodysone 3beta-reductase
9086	22165	35710	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9086	22165	35711	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
10014	23052	36646	4.27	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10384	23419	37028	1.9	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
11068	24143	37778	1.81	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
11068	24143	37779	1.81	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
12736	25487	26721	1.81	5.1E-02	AF082467.1	NT	Cucumis melo polygalacturonase precursor (NPG3) mRNA, complete cds
495	13690	26721	2.8	5.0E-02	AF088004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1231	14390	27452	2.82	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
2047	15188	28299	5.08	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-FPIF-S) (PROTEIN APROTEIN C) CONTAINS: PEPTIDE P-C
2879	14182	27244	10.88	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3418	16587		1.36	5.0E-02	7305610	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3684	16947		1.01	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3775	16936	29842	5.9	5.0E-02	U12769.2	NT	Artheraea pernyi period clock protein homolog mRNA, complete cds
4941	18071		1.05	5.0E-02	P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
6258	19432	32779	0.64	5.0E-02	AF036264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6438	19605		1.28	5.0E-02	AJ242825.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7128	18554	31469	0.58	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
7709	20774	34259	10.04	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
7913	20964		0.67	5.0E-02	AW062464.1	EST_HUMAN	MR0-CT0084-100899-002-g10 CT0084 Homo sapiens cDNA
10403	23438	37045	1.37	5.0E-02	AF305288.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fis3) mRNA, complete cds
10855	23888		0.55	5.0E-02	BF213280.1	EST_HUMAN	601844753FT NIH_MGC.55 Homo sapiens cDNA clone IMAGE:4070101 5'
11782	24772	38468	2.26	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
12229	26004		4.7	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
231	13452		11.82	4.9E-02	M14290.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
380	13588	26623	4.18	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
380	13588	26624	4.18	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2937	18114	29126	0.71	4.9E-02	U32636.1	NT	Zea mays phytoene synthase (Y1) gene, complete cds
3360	16532	29546	1.85	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3660	16823		0.85	4.9E-02	AA188940.1	EST_HUMAN	z448a12.s1 Stratagene HNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632926 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
3681	16844	29851	0.78	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3681	16844	29852	0.78	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4964	18093	31069	2.64	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
4964	18093	31070	2.64	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
5498	18685	31702	1.62	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5498	18685	31703	1.62	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7292	20374	33831	1.79	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8815	21894		1.07	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8942	22021		0.61	4.9E-02	BE931532.1	EST_HUMAN	MRQ-HT0408-170800-003-608 HT0408 Homo sapiens cDNA
8954	22033	35676	0.97	4.9E-02	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10500	23535	37145	0.64	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
10802	23835	37439	1.57	4.9E-02	L41161.1	NT	Mus musculus SM22 alpha gene, exon 1
10802	23835	37460	1.57	4.9E-02	L41161.1	NT	Mus musculus SM22 alpha gene, exon 1
11687	24696	38378	3.46	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12957	25624		3.23	4.9E-02	M19384.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
340	13552	26562	1.19	4.9E-02	D16471.1	NT	Human mRNA, Xq terminal portion
341	13552	26562	2.61	4.9E-02	D16471.1	NT	Human mRNA, Xq terminal portion
501	13696	26726	11.53	4.9E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2347	15478	28610	2.08	4.8E-02	W51983.1	EST_HUMAN	gc49b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30998 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3280	16454	29478	1.79	4.8E-02	X17144.1	NT	Tetrahymena tostrata histone H3II and histone H4II intergenic DNA
4793	17928		1.06	4.8E-02	Z54280.1	NT	S. crofta gene for skeletal muscle tyrosine receptor
5237	18359	31328	0.98	4.8E-02	U91914.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
8332	21414	34940	1.41	4.8E-02	AV1388497.1	EST_HUMAN	MR2-ST0129-221098-012-b02 ST0129 Homo sapiens cDNA
9329	22405	35957	1.01	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9329	22405	35958	1.01	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
11219	24286	37928	1.84	4.8E-02	X61236.1	NT	S. cerevisiae NUM1 gene, involved in nuclear migration control
11219	24286	37929	1.84	4.8E-02	X61236.1	NT	S. cerevisiae NUM1 gene, involved in nuclear migration control
12511	25350		1.46	4.8E-02	9632893	NT	Streptococcus thermophilus bacteriophage Sf19, complete genome
6122	18248	31214	0.74	4.7E-02	6981261	NT	Rattus norvegicus Nestlin (Nes), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6989	20197	33623	3.34	4.7E-02	W01153.1	EST_HUMAN	yz2709.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element
7025	20161	33581	0.69	4.7E-02	BF986625.1	EST_HUMAN	602143554F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5'
7025	20161	33582	0.69	4.7E-02	BF986625.1	EST_HUMAN	602143554F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5'
7058	20111	33527	1.71	4.7E-02	M62752.1	NT	Rat statin-related protein (st) gene, complete cds
8445	21526	35083	9.44	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
9154	22232	35777	1.31	4.7E-02	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
9176	22254		2.97	4.7E-02	AB026676.1	NT	Gallus gallus Wpici-8 gene, complete cds
9428	22502	36068	7.75	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
9936	22975		0.7	4.7E-02	AI873042.1	EST_HUMAN	ve79c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
11852	24841	38535	1.43	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11852	24841	38536	1.43	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
12446	26182		4.31	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLC Homo sapiens cDNA clone GLCBK02 3'
281	13499	26531	0.69	4.6E-02	BE153883.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
758	13839	26984	2.89	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1320	14476		1.49	4.6E-02	AI014255.1	EST_HUMAN	em50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P90533
1390	14544	27620	5.39	4.6E-02	AV727059.1	EST_HUMAN	IP90533 LIMA ; contains element LTR1 repetitive element ;
2557	15682	28807	2.34	4.6E-02	AW236023.1	EST_HUMAN	xt2403.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN
2869	13495	26531	1.78	4.6E-02	BE153553.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1 ;
3073	16249	29270	0.84	4.6E-02	BE153883.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3410	16249	29270	0.59	4.6E-02	BE153883.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3585	16249	29270	0.94	4.6E-02	BE153883.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4239	17385		0.92	4.6E-02	AF220365.1	NT	Mus musculus nucleolar RNA helicase II/Gu (dab21) gene, complete cds
5852	19042	32348	1.57	4.6E-02	AF076962.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (Gnrh2) gene, complete cds
6359	19529	32887	3.67	4.6E-02	XG1624.1	NT	C. reinhardtii etb2 (etbB) mRNA
6359	19529	32888	3.67	4.6E-02	XG1624.1	NT	C. reinhardtii etb2 (etbB) mRNA
6938	20251	33687	1.41	4.6E-02	AI149574.1	EST_HUMAN	qq08000.x1 Soares_placenta_8t08weeks_2NbHP8t09W Homo sapiens cDNA clone IMAGE:1713971 3' similar to contains L1 t3 L1 repetitive element ;
8007	21057	34589	0.63	4.6E-02	6978720	NT	Rattus norvegicus Cathepsin H (Cth), mRNA
8956	21935	35472	3.81	4.6E-02	BE154006.1	EST_HUMAN	PM0-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
11689	24687	38377	3.39	4.6E-02	AA913328.1	EST_HUMAN	o127f09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13078	25708		3.14	4.6E-02	X57808.1	NT	Human germline immunoglobulin lambda light chain gene
460	13655	26693	2.24	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1245	14404	27465	1.52	4.5E-02	AF005730.1	NT	Marburg virus strain M/S-Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1245	14404	27465	1.52	4.5E-02	AF005730.1	NT	Marburg virus strain M/S-Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1847	14933	28095	4.93	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2177	15312	28440	2.2	4.5E-02	AE003904.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
3817	16977	29081	5.04	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6360	19530	32889	1.63	4.5E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6636	19795	33184	0.84	4.5E-02	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7018	20154	33574	0.59	4.5E-02	L28487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
7018	20154	33574	0.59	4.5E-02	L28487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
8587	21668	35207	2.24	4.5E-02	AF036684.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
10155	23162	36788	4.2	4.5E-02	AA325216.1	EST_HUMAN	EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein
10305	23340	36945	0.47	4.5E-02	X95508.1	NT	A. europaeum mRNA for legumin-like protein
10421	23456	37061	0.79	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12442	25313	32089	2.61	4.5E-02	11418013	NT	Homo sapiens ret finger protein-like 3 (RFPL3), mRNA
12891	26051	31684	3.79	4.5E-02	AA191097.1	EST_HUMAN	z43111.1 Stratagene hNT neuron (8937233) Homo sapiens cDNA clone IMAGE:632493 5'
227	13449		4.35	4.4E-02	BE972733.1	EST_HUMAN	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
1050	14216	27273	0.77	4.4E-02	L18295.1	NT	Drosophila melanogaster extracellular (EXO) mRNA, complete cds
2163	15299		6.82	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2559	15694	28809	1.31	4.4E-02	AW876475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 P10012 Homo sapiens cDNA
3730	16891	28895	1.68	4.4E-02	AF159160.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4750	17885	30866	1.33	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4750	17885	30867	1.33	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7267	20350	33802	0.59	4.4E-02	AF093824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7267	20350	33803	0.59	4.4E-02	AF093824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8952	22031	35572	2.34	4.4E-02	AA173969.1	EST_HUMAN	nr13903.s1 NCI_OGAP_S51 Homo sapiens cDNA clone IMAGE:129221 3'
11326	24389	38034	2.84	4.4E-02	AF060689.1	NT	Hepatitis E virus strain HEV-JUS2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11477	24536	38206	3.08	4.4E-02	AA498739.1	EST_HUMAN	aa33304_r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
12158	25126		4.55	4.4E-02	AB040926.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
12347	26192		1.65	4.4E-02	BF241245.1	EST_HUMAN	001878746F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
802	13982	27034	7.25	1.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2634	15757	28871	1.55	4.3E-02	AF704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBA0H08 5'
3516	16682	29663	9.18	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3749	16910		1.21	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6625	19785	33172	4.94	4.3E-02	P30427	SWISSPROT	PLECTIN
6625	19785	33173	4.94	4.3E-02	P30427	SWISSPROT	PLECTIN
6871	20023	33433	0.8	4.3E-02	AA652266.1	EST_HUMAN	ns99c12.s1 NCI CGAP_P12 Homo sapiens cDNA clone IMAGE:1188886
8711	21791	35327	0.68	4.3E-02	AF293359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
9001	22080	35621	1.32	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
9001	22080	35622	1.32	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
12412	25291		1.2	1.3E-02	AL139077.2	NT	(Campylobacter jejuni NCTC11168 complete genome; segment 4/6
845	14023	27081	1.74	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
889	14065		2.4	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
919	14094	27159	1.61	4.2E-02	AW003845.1	EST_HUMAN	w34g01.x1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR-Q63291 Q63291 L1 RETROPOSIN, ORF2 MRNA ; contains L1.3 L1 repetitive element ;
1758	14907		1.37	4.2E-02	AL445088.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
1819	14968	28060	0.99	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
3754	16915	29918	1.66	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4885	17998	30982	0.59	4.2E-02	BF342995.1	EST_HUMAN	602017105F1 NCI CGAP_Bn54 Homo sapiens cDNA clone IMAGE:4152872 5'
5735	18828	32224	0.74	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5735	18928	32225	0.74	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7122	18548	31460	0.61	4.2E-02	BE268285.1	EST_HUMAN	601124598F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2988319 5'
7685	20760	34244	4.35	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7717	20781	34287	0.61	4.2E-02	AV730347.1	EST_HUMAN	AV730347 HTF Homo sapiens cDNA clone HTFAVH04 5'
9010	22089	35631	3.82	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10367	23402	37013	1.46	4.2E-02	Q16950	SWISSPROT	T-BRAIN-1 PROTEIN (T-BRAIN PROTEIN 1) (TBR-1) (TES-56)

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11295	24361	39002	1.52	4.2E-02	AA976118.1	EST_HUMAN	on33b11.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558461 3' similar to gb:M65280 INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11597	24640	38320	2.83	4.2E-02	BE815922.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11597	24640	38321	2.83	4.2E-02	BE815922.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11795	24785	38483	1.52	4.2E-02	AF176458.1	NT	PRRS isolate PRRSV/38 envelope glycoprotein gene, complete cds
12728	26109		6.64	4.2E-02	A1983494.1	EST_HUMAN	w49g10.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
13076	26705		1.17	4.2E-02	D14711.1	NT	Staphylococcus aureus HSP10 and HSP60 genes
523	13716	28743	1.85	4.1E-02	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
2741	15958	28970	1.06	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
4005	17162	30168	0.61	4.1E-02	BE297236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
4005	17162	30169	0.61	4.1E-02	BE297236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
4595	17732		8.4	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180400-164-106 NN0012 Homo sapiens cDNA
5229	18351		0.61	4.1E-02	X85980.1	NT	L monocytogenes type 3 partial lap gene (strain 443)
5759	18951	32253	1.06	4.1E-02	BE251894.1	EST_HUMAN	601107635F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
5759	18951	32254	1.06	4.1E-02	BE251894.1	EST_HUMAN	601107635F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
7022	20158		0.98	4.1E-02	X75881.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
7248	20331	33778	1.38	4.1E-02	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7682	20747	34228	1.79	4.1E-02	7662347	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
7778	20834	34325	20.08	4.1E-02	L02110.1	NT	Mus musculus proviral retroviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
7942	20992	34502	2.81	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds, mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
8402	21483	35011	0.74	4.1E-02	P07857	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8845	21924	35462	0.79	4.1E-02	P34887	SWISSPROT	CUTICLE COLLAGEN 34
9355	22430	35988	0.87	4.1E-02	AA372398.1	EST_HUMAN	EST84291 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end
13112	26110	31666	9.91	4.1E-02	AJ271909.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
3316	16489	29507	3.85	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3900	17059	30058	1.09	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5495	18694	31710	5.31	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6343	19513	32870	0.98	4.0E-02	BF110434.1	EST_HUMAN	7n52h07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3566380 3' similar to TR:076296 O75296 R29124 1.;
7867	20921	34428	5.99	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7929	20979		0.71	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
7943	20983	34503	0.8	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7943	20983	34504	0.8	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7980	21029	34543	0.61	4.0E-02	AF288163.1	NT	Homo sapiens erythrocyte tropomodulin (E-TMOD) gene, exon 7
8914	21993	35532	2.52	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8944	22884		0.63	4.0E-02	BF679376.1	EST_HUMAN	60215388.F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
9889	22909	35495	2.46	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thid: fumarate reductase subunit A
10190	23227		1.08	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
12073	25054		1.52	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Car+ ATPase
12333	25909	31859	16.34	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1144	14308	27368	2.79	3.9E-02	BF516149.1	EST_HUMAN	UI-H-BW1-ans-h-09-D-UJ.Lst NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1375	14530	27603	2.15	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
2016	15166	28261	3.22	3.9E-02	AJ403386.1	NT	Mus musculus DNA for desmin-binding fragment DesD7
2789	15884		1.97	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5246	18367	31334	0.67	3.9E-02	AW392417.1	EST_HUMAN	RC8-ST0258-171199-021-C09 ST0258 Homo sapiens cDNA
5279	18398	31366	0.9	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5279	18398	31367	0.9	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5949	19039	32346	1	3.9E-02	BE968841.1	EST_HUMAN	60164687.F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933642 5'
5977	19182	32482	0.65	3.9E-02	BF675203.1	EST_HUMAN	602138132.F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7203	20068	33478	0.97	3.9E-02	BE271437.1	EST_HUMAN	601140729.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
8023	21106	34623	1.44	3.9E-02	BF239613.1	EST_HUMAN	601306848.F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
8250	21332	34849	0.6	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8250	21332	34850	0.6	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11695	21071	34582	1.56	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
12184	26059		3.54	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12898	25595		2.35	3.9E-02	U68081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV14S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, Mus musculus chromosome X contigB: X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmx28orf
13036	25979		64.89	3.9E-02	AL049866.2	NT	Human protein C gene, complete cds
5556	18754	31792	0.8	3.8E-02	M11228.1	NT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
6212	19387	32736	1.04	3.8E-02	P10284	SWISSPROT	Human sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
7471	20548	34018	1.72	3.8E-02	6005700	NT	Human von Willebrand factor gene, exons 23 through 34
8864	21943		1.51	3.8E-02	M60675.1	NT	Human sapiens PRO0514 protein (PRO0514), mRNA
10789	23822	37446	0.84	3.8E-02	7682563	NT	Human sapiens PELOTA (PELOTA) gene, complete cds
10888	23972	37603	1.71	3.8E-02	AF143952.2	NT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1016	14187	27248	4.05	3.7E-02	P19137	SWISSPROT	wrs568.xt NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2310	15442	28577	6.19	3.7E-02	A1984806.1	EST_HUMAN	Homo sapiens mRNA for KIAA0718 protein, partial cds
2645	18768	28853	0.97	3.7E-02	AB018261.1	NT	EOMESODERMIN
3115	18291	29306	1.13	3.7E-02	P79944	SWISSPROT	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
3117	16293	29307	4.33	3.7E-02	BF312963.1	EST_HUMAN	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
3543	16708		0.91	3.7E-02	6680541	NT	Aeropyrum pernix genome DNA, section 617
7226	26216		0.95	3.7E-02	AP000063.1	NT	Xyella fastidiosa, section 121 of 229 of the complete genome
7869	20923	34430	0.81	3.7E-02	AE003975.1	NT	ai55c09.s1 Soares_papillary thyroid tumor_NbHFA Homo sapiens cDNA clone 1360912 3'
10219	23255		1.01	3.7E-02	AA782516.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12227	25175	38837	7.41	3.7E-02	BF124874.1	EST_HUMAN	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
12961	25945	31764	3.71	3.7E-02	11418392	NT	Odontella sinensis chloroplast, complete genome
13069	25599		1.23	3.7E-02	11467432	NT	Fl. vulgare Ss1 gene for sucrose synthase
3744	18905	29909	0.82	3.6E-02	X73221.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
3752	16913	29916	0.9	3.6E-02	AL096806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5313	18430	31400	0.67	3.6E-02	AL096810.1	NT	C-glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5543	18740	31758	0.61	3.6E-02	X59403.1	NT	C-glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5543	18740	31774	0.61	3.6E-02	X59403.1	NT	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5617	18811	31880	0.66	3.6E-02	AF181722.1	NT	Homo sapiens RUSAS (RU2) mRNA, complete cds
6846	19959	33406	4.48	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-570 EN0013 Homo sapiens cDNA
6846	19959	33407	4.48	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-570 Homo sapiens cDNA
7234	20318	33761	1.79	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cx2 precursor (sgp2) gene, complete cds
7459	20534	34009	2.88	3.6E-02	AA714521.1	EST_HUMAN	nt20e05.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241024.3 similar to gb:J00314_rna2
7811	20866	34360	0.94	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
9591	22846	36216	2.16	3.6E-02	U20608.1	NT	MR0-HT0158-030200-003-508 HT0158 Homo sapiens cDNA
9591	22846	36217	2.16	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9812	22852	36431	0.94	3.6E-02	BF347586.1	EST_HUMAN	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
11466	24516	38183	1.48	3.6E-02	BF131609.1	EST_HUMAN	602020453F1 NCI CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4156116.5'
11456	24516	38184	1.46	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570.5'
918	14053	27158	0.99	3.5E-02	U09506.1	NT	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570.5'
1033	14202	27260	2.43	3.5E-02	AF253417.1	NT	Drosophila melanogaster igggrin mRNA, complete cds
1595	14748	27831	1.4	3.5E-02	BF678085.1	EST_HUMAN	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1595	14748	27832	1.4	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377.5'
4329	17472	30457	1.83	3.5E-02	AE001773.1	NT	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377.5'
4435	17575	30556	1.11	3.5E-02	P53790	SWISSPROT	Thermotoga maritima section 85 of 136 of the complete genome
6351	19521	32878	1.76	3.5E-02	J01238.1	NT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
8165	21247		0.91	3.5E-02	H29951.1	EST_HUMAN	Maize actin 1 gene (MAG1), complete cds
8824	21903	35443	2.53	3.5E-02	BE96870.1	EST_HUMAN	yp44a05.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190256.5 similar to contains Alu repetitive element
10224	23260	36848	0.94	3.5E-02	X79642.1	NT	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929737.3'
10270	23305	36902	0.51	3.5E-02	BE861042.1	EST_HUMAN	L. lactis MG1363 grpE and dnaK genes
11785	24775	38471	1.79	3.5E-02	AW861641.1	EST_HUMAN	601344661F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654.5'
11785	24775	38472	1.79	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-r03 CT0326 Homo sapiens cDNA
12876	25583		1.31	3.5E-02	AF009693.1	NT	PM1-CT0326-291299-002-r03 CT0326 Homo sapiens cDNA
12955	25691		2.71	3.5E-02	BE276948.1	EST_HUMAN	Homo sapiens T cell receptor beta locus, TCRBV8SGP to TCRBV21S2A2 region
592	13783	26802	47.29	3.4E-02	AK024424.1	NT	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833.5'
592	13783	26803	47.29	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
593	13783	26802	3.26	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
593	13783	26803	3.26	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1076	14242	27298	2.57	3.4E-02	AW274020.1	EST_HUMAN	xv26d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW: C211_HUMAN P63801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1233	14392		5.43	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2465	15592	28717	1.7	3.4E-02	T57160.1	EST_HUMAN	yc20a06.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3517	16683	29694	1.5	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3875	17034	30032	0.81	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-080700-071-d10 FN0155 Homo sapiens cDNA
4030	17186	30166	3.72	3.4E-02	AW794952.1	EST_HUMAN	RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4720	17855	30838	2.77	3.4E-02	X59789.1	NT	M.musculus S-antigen gene promoter region
5172	18294		1.9	3.4E-02	Q26487	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5189	18311	31277	1.81	3.4E-02	AJ012489.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6993	18512	31504	4.68	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8496	21537		3.15	3.4E-02	A1899629.1	EST_HUMAN	w189604.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2433031 3'
8947	22026	35567	1.18	3.4E-02	AA684886.1	EST_HUMAN	nt70708.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element contains element MER25 MER25 repetitive element ;
9118	22197		5.28	3.4E-02	AA194306.1	EST_HUMAN	zq0411.s1 Stragene muscle 937208 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
9880	23019		0.66	3.4E-02	A1092719.1	EST_HUMAN	IPISGKPLPKVTLSDGVPLKATMRFNTEITAEINLTKESVTADAGRYEITANSSGTTKAFINIVLDRP G
383	13591		6.8	3.4E-02	A399735.1	EST_HUMAN	PPT GPVWISDITEESVTLKWEPPKYDGGQVNTNLLKRETSVAVWTEVSATVARTMMKVMKL ... ;
1193	14355	27413	12.43	3.4E-02	AB035967.1	NT	oz96h08.x1 Soares_papillary tumor_NbHPA Homo sapiens cDNA clone IMAGE:1683519 3'
1659	14821	27804	1.23	3.4E-02	AF10763.1	NT	z175608.x1 Soares_lactis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1776	14927		1.37	3.4E-02	AE000700.1	NT	Grietus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
2149	15285		2.02	3.4E-02	R09112.1	EST_HUMAN	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3445	16613	29631	0.86	3.4E-02	H02389.1	EST_HUMAN	Aquifex aeolicus section 32 of 109 of the complete genome
4293	14821	27804	3.74	3.4E-02	AF110763.1	NT	y2509.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:127888 5'
4589	17726	30709	2.24	3.4E-02	BF245995.1	EST_HUMAN	y35h02.r1 Soares placenta NB21P Homo sapiens cDNA clone IMAGE:150771 5'
6560	19722	33099	25.73	3.4E-02	BF245995.1	EST_HUMAN	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
6560	19722	33100	25.73	3.4E-02	BF245995.1	EST_HUMAN	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
7677	19742	34223	0.63	3.4E-02	AF124162.1	NT	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9523	22588	36167	0.74	3.4E-02	BF115621.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9523	22588	36158	0.74	3.4E-02	BF115621.1	EST_HUMAN	Nicotiana plumbaginifolia methyltransferase synthase sulphurase (cnc6) gene, partial cds
9523	22588	36158	0.74	3.4E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9624	22879	36248	0.57	3.3E-02	AA488202.1	EST_HUMAN	ad0809.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN)
9624	22879	36249	0.57	3.3E-02	AA488202.1	EST_HUMAN	ad0809.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN)
11383	24444	38104	3.28	3.3E-02	BF691107.1	EST_HUMAN	ad0809.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN)
12428	25303		3.1	3.3E-02	T96545.1	EST_HUMAN	60224771F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
12557	25379		1.6	3.3E-02	AF289665.1	NT	ye49f11.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:121101 5'
12591	25398		1.85	3.3E-02	M81890.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
134	13360	26394	1.79	3.2E-02	AJ002005.1	NT	Human Interleukin 11 (IL11) gene, complete mRNA
1150	14314	27370	6.32	3.2E-02	AF098275.1	NT	Oryzabagus cuticularis gene encoding ileal sodium-dependent bile acid transporter
1150	14314	27371	6.32	3.2E-02	AF098275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1812	14961	28054	1.08	3.2E-02	AF128884.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2187	15322		1.09	3.2E-02	P28955	SWISSPROT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
2902	13360	26394	0.87	3.2E-02	AJ002005.1	NT	LARGE TEGUMENT PROTEIN
3204	16379	29369	13.21	3.2E-02	BE867353.1	EST_HUMAN	Oryzabagus cuticularis gene encoding ileal sodium-dependent bile acid transporter
3806	16966	29970	0.94	3.2E-02	AL163293.2	NT	601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
4334	17477		16.42	3.2E-02	X94768.1	NT	Homo sapiens chromosome 21 segment HS21C003
4890	18020	31005	3.85	3.2E-02	AF114182.1	NT	H. sapiens RP3 gene (XLRP gene 3)
5310	18427	31397	0.93	3.2E-02	AW850159.1	EST_HUMAN	Saxifraga nidifica maturase (matk) gene, chloroplast gene encoding chloroplast protein, partial cds
5352	18846	32127	1.49	3.2E-02	X68709.1	NT	IL3-CT0210-271099-022-C04 C10219 Homo sapiens cDNA
5652	18846	32128	1.49	3.2E-02	X68709.1	NT	S. griseocaneum whiG-Stv gene
5653	18812	33200	2.4	3.2E-02	M32497.1	NT	S. griseocaneum whiG-Stv gene
6656	19815		30.91	3.2E-02	T89367.1	EST_HUMAN	Rat polyomavirus left junction in cell line W98.14
6743	19898	33290	3.7	3.2E-02	AF173845.1	NT	yd33h12.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains Alu repetitive element; contains LTR1 repetitive element ;
7839	20989	34499	0.92	3.2E-02	11424048	NT	Sagittaria oedipus tissue kallikrein gene, complete cds
8498	21577	35113	8.04	3.2E-02	6680585	NT	Homo sapiens cytochrome P450, subfamily 1B (phenobarbital-inducible) (CYP2B), mRNA
9141	22220		0.87	3.2E-02	AF109718.1	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
9426	22500	36065	1.2	3.2E-02	A1278971.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
9426	22500	36066	1.2	3.2E-02	A1278971.1	EST_HUMAN	qim17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
10282	23297		4.51	3.2E-02	AA719795.1	EST_HUMAN	qim17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
10566	23601	37207	1.11	3.2E-02	U96762.1	NT	zg54b12.s1 Soares pineal gland N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to gb:L08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN); Macaca mulatta chemokine receptor COR5 mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1289	14445		1.92	3.1E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1333	14490	27559	1.46	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1940	15083	28184	1.28	3.1E-02	6871664	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5378	18580	31449	1.29	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5478	18875		2.6	3.1E-02	AA278478.1	EST_HUMAN	z881a06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
5764	18956	32259	0.77	3.1E-02	BF687742.1	EST_HUMAN	602066783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789 5'
8122	21204		0.58	3.1E-02	AV696088.1	EST_HUMAN	AV696088 GKC Homo sapiens cDNA clone GKCAVH09 5'
9142	22221	35784	0.48	3.1E-02	BE96092.2	EST_HUMAN	601658879R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886291 3'
9339	22415	35968	0.46	3.1E-02	AI872302.1	EST_HUMAN	wm57d09.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2440049 3'
10237	23272	36864	2.67	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1652	14905		2.41	3.0E-02	AF187125.1	NT	Platyketetes minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2852	15775	28888	1.08	3.0E-02	AA402242.1	EST_HUMAN	z63h03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3743	16804	28908	2.82	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3839	16938		0.93	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0298-150200-040-e09 ST0298 Homo sapiens cDNA
4058	17214		0.94	3.0E-02	AA364003.1	EST_HUMAN	EST74530 Pineal gland II Homo sapiens cDNA 5' end
5164	18266	31250	8.17	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5164	18286	31251	8.17	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5507	18706		3.21	3.0E-02	AB045793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6384	19553	32910	0.67	3.0E-02	N89615.1	EST_HUMAN	z339a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element
6384	19553	32911	0.67	3.0E-02	N99615.1	EST_HUMAN	z339a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element
6928	20244	33577	2.87	3.0E-02	AJ242806.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (NOS gene)
7047	20100	33516	2.9	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7047	20100	33517	2.9	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7218	20083	33497	1.92	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7218	20083	33498	1.92	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7380	20458	33921	1.22	3.0E-02	M86524.1	NT	Human dystrophin gene
8317	21399		0.48	3.0E-02	BF679706.1	EST_HUMAN	602154364F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295654 5'
8821	21900	35439	0.55	3.0E-02	BE152670.1	EST_HUMAN	601171626F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3545047 5'
8842	21921	35459	0.74	3.0E-02	BF353889.1	EST_HUMAN	IL5-HT0704-290600-108-c04 HT0704 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8953	22072		1.93	3.0E-02	AF275654.1	NT	Omithorhynchus anatinus coagulation factor X mRNA, complete cds
10677	23711	37519	2.03	3.0E-02	AE001797.1	NT	Thermotoga maritima section 108 of 136 of the complete genome
10770	23803	37425	0.47	3.0E-02	Z21211.1	EST_HUMAN	HSAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11508	24568	38243	2.26	3.0E-02	M81557.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11989	24974	38678	7.11	3.0E-02	AA483216.1	EST_HUMAN	ne87f04.s1 NCL_CGAP_Ki67 Homo sapiens cDNA clone IMAGE:311263
12538	26168	31556	1.96	3.0E-02	R32019.1	EST_HUMAN	yf63d04.s1 Soares placenta N22HP Homo sapiens cDNA clone IMAGE:134407 3'
12943	25621		11.62	3.0E-02	AW895665.1	EST_HUMAN	QV4-NN0038-270400-187-H05 NN0038 Homo sapiens cDNA
12989	26161			3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Galglucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
3650	16813	29826	0.9	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
4039	17195	30206	0.81	2.9E-02	H72805.1	EST_HUMAN	yu07610.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
6188	19364	32712	1.39	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6421	19590	32955	6.58	2.9E-02	BF032233.1	EST_HUMAN	G01452661F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:388658 5'
7398	20478	33943	9.95	2.9E-02	BE271437.1	EST_HUMAN	G01140728F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7584	20656	34133	0.65	2.9E-02	D29214.1	EST_HUMAN	HUMNK282 Human epidermal keratinocyte Homo sapiens cDNA clone 262
8187	21259	34793	0.82	2.9E-02	AF126279.1	NT	Buchnera aphidicola natural-host Schlechtendalla chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
8187	21269	34794	0.82	2.9E-02	AF126279.1	NT	Buchnera aphidicola natural-host Schlechtendalla chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
9859	22859	36482	2.14	2.9E-02	AW875979.1	EST_HUMAN	GM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9859	22859	36483	2.14	2.9E-02	AW875979.1	EST_HUMAN	GM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
10078	23116		0.65	2.9E-02	AW976597.1	EST_HUMAN	EST1388706 IMAGE resequences, MAGN Homo sapiens cDNA
10553	23588	37196	1.25	2.9E-02	AF000064.1	NT	Aeropyrum pernix genomic DNA, section 7/7
11303	16813	29826	1.44	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12538	26057		1.35	2.9E-02	AU135817.1	EST_HUMAN	AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002982 5'
579	13771		0.76	2.8E-02	AW970163.1	EST_HUMAN	EST382234 IMAGE resequences, MAGK Homo sapiens cDNA
3453	16620	29639	1.2	2.8E-02	AF060063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3453	16620	29840	1.2	2.8E-02	AF060063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
4430	17570		0.76	2.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5505	18800	31866	11	2.8E-02	BE741083.1	EST_HUMAN	G01594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5'
5948	20261	33689	1.08	2.8E-02	T78980.1	EST_HUMAN	yc21b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108655 5'
8523	21604	35142	1.67	2.8E-02	AJ005620.1	NT	Craterostigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
9219	22297	35840	0.75	2.8E-02	AA280762.1	EST_HUMAN	zs95c06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711486 5'
9409	22483	36047	1.41	2.8E-02	AF187872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9513	22578	36144	0.76	2.8E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
9674	22636	36207	0.47	2.8E-02	J05109.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds
9674	22636	36208	0.47	2.8E-02	J05109.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds
1518	14671	27753	0.96	2.7E-02	U66059.1	NT	Human gamma T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2P, TCRBV7S2A1N4T, TCRBV13S9/13S>
3518	16884	29695	1.99	2.7E-02	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4319	17462	30447	1.93	2.7E-02	N47258.1	EST_HUMAN	Y66H12.1 Soares multiple sclerosis 2/Nb-HMSP Homo sapiens cDNA clone IMAGE:280487 5'
4319	17462	30448	1.93	2.7E-02	N47258.1	EST_HUMAN	Y66H12.1 Soares multiple sclerosis 2/Nb-HMSP Homo sapiens cDNA clone IMAGE:280487 5'
5382	18565	31432	0.6	2.7E-02	BF245672.1	EST_HUMAN	601864811F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083075 5'
5567	18755	31793	1.43	2.7E-02	R12245.1	EST_HUMAN	Y33d09.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP_JC2284.JC2284 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6022	19205	32525	0.69	2.7E-02	XG1670.1	NT	T.aestivum pTTH20 mRNA for wheat type V thionin
6734	19880	33491	1.02	2.7E-02	X97560.1	NT	A.bisporus pgkA gene
7213	20078	33491	1.92	2.7E-02	AA893571.1	EST_HUMAN	ci66H03.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624661 3'
8549	21630	35434	1.36	2.7E-02	A1377036.1	EST_HUMAN	tc28g08.x1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to contains Alu repetitive element;
8816	21855	35434	0.55	2.7E-02	S43442.1	NT	transmembrane secretory component [human, leukocytes, Genomic, 657 nt, segment 4 of 11]
585	13776	26796	2.52	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1399	14553	28694	0.99	2.6E-02	AW850515.1	EST_HUMAN	IL3-CTD219-280100-062-C09.GT0219 Homo sapiens cDNA
2439	15567	28694	2.6	2.6E-02	AA490021.1	EST_HUMAN	eb02b02.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2441	15569	28696	4.45	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2441	15569	28697	4.45	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2982	16158		2.07	2.6E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and snRNP genes, complete cds; G7A gene, partial cds; and unknown genes
5025	18154	31131	3.89	2.6E-02	L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds
5176	18298	31261	1.22	2.6E-02	AE002014.1	NT	Delicatococcus radiodurans RT section 151 of 229 of the complete chromosome 1
5203	18324	31263	2.54	2.6E-02	AW241154.1	EST_HUMAN	Q13041 HYPOTHETICAL PROTEIN KIAA0069 ;
8011	19195		2.94	2.6E-02	AL161563.2	NT	xa52004.x1 NCI CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN
6349	19519		6.85	2.6E-02	AI206030.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6555	19717	33063	2	2.6E-02	BE621748.1	EST_HUMAN	cg27f11.x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
6966	20194	33619	0.83	2.6E-02	Z96064.1	NT	601468473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
						NT	Vaccinia virus ORF1L, strain Wyeth

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6966	20194	33620	0.83	2.6E-02	Z99064.1	NT	Vaccinia virus ORF1L, strain Wyeth
7050	20103	33620	5.63	2.6E-02	6081271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7449	20326	33999	0.65	2.6E-02	P21894	SWISSPROT	ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)
9703	21783	35316	0.73	2.6E-02	AA860946.1	EST_HUMAN	ak2204.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1406719 3'
9580	22702	36268	1.24	2.6E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
9915	22955	36541	0.78	2.6E-02	AF114952.1	NT	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9915	22955	36542	0.78	2.6E-02	AF114952.1	NT	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10514	23648	37257	5.37	2.6E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11670	24747	38547	1.59	2.6E-02	AA279351.1	EST_HUMAN	z88402.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704182 5'
11861	24849	38547	1.35	2.6E-02	AW500847.1	EST_HUMAN	UHF-BNO-alk-10-0-JL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
12480	26150	31553	1.43	2.6E-02	BF343827.1	EST_HUMAN	602015501F1 NCI_CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4160944 5'
12583	26392		1.32	2.6E-02	11422936	NT	Homo sapiens hypothetical protein FLJ10724 (FLJ10724), mRNA
12847	26699		1.39	2.6E-02	R43678.1	EST_HUMAN	yc8607.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22845 3' similar to contains DBR repetitive element;
545	13738	26762	1.75	2.5E-02	A1783130.1	EST_HUMAN	on26108.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
545	13738	26763	1.75	2.5E-02	A1783130.1	EST_HUMAN	on26108.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
832	14010	27066	9.54	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
892	14068	27133	5.83	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2821	15935		2.53	2.5E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
3021	16197	29219	2.95	2.5E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
3021	16197	29220	2.95	2.5E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4156	18488	30302	0.92	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-g12 NN0128 Homo sapiens cDNA
4156	18488	30303	0.92	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-g12 NN0128 Homo sapiens cDNA
4322	17485	30450	4.66	2.5E-02	AW592114.1	EST_HUMAN	h36108.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834015 3'
5530	19021	32327	0.72	2.5E-02	A1732776.1	EST_HUMAN	z6830.10.x5 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:810354 3'
6322	18494		4.88	2.5E-02	BE670128.1	EST_HUMAN	7e30e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1 t1 L1 repetitive element;
6338	19508		3.72	2.5E-02	BE746888.1	EST_HUMAN	601579393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
6466	19633	32984	0.8	2.5E-02	L29028.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7843	20898	34400	1.72	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4213406 5'
7843	20898	34401	1.72	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4213406 5'
8008	21058	34570	0.84	2.5E-02	AF129459.1	NT	Chlamydomonas reinhardtii class II DNA photolyase (PHF2) gene, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8167	21249	34768	0.5	2.5E-02	BE252469.1	EST_HUMAN	601108291F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3344278 5'
9025	22104	35645	0.92	2.5E-02	Q81713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
9164	22242	35785	0.57	2.5E-02	AW025821.1	EST_HUMAN	wt08c10.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2516370 3'
10271	23306		0.63	2.5E-02	X71303.1	NT	D.radicum 28S ribosomal RNA, 32 domain
10810	23843	37466	0.65	2.5E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares pregnant uterus Nib-IPU Homo sapiens cDNA clone IMAGE:1695982 3'
11048	24125	37759	1.71	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
11048	24125	37760	1.71	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IiAalpha) and major histocompatibility protein class II beta chain (IiEbata) genes, complete cds; butyrophilin-like (NG9), butyrophilin-lp
11120	24192		2.93	2.5E-02	AF050157.1	NT	Homo sapiens gene for LECT2, complete cds
12085	25046		1.87	2.5E-02	AB007546.1	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC86634), mRNA
12419	26072		2.17	2.5E-02	11420078	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12521	25934		1.29	2.5E-02	11433220	NT	Homo sapiens discoidin putative protein kinase MicaA (mkaA) gene, complete cds
12716	25476		1.83	2.5E-02	U80169.1	NT	Dicotyledon discoidin putative protein kinase MicaA (mkaA) gene, complete cds
12750	25497	32032	1.58	2.5E-02	BE973327.1	EST_HUMAN	6011652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
178	13401	28431	1.44	2.4E-02	AI378592.1	EST_HUMAN	tc72c07.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2070155 3'
1628	14790	27855	1.89	2.4E-02	H65884.1	EST_HUMAN	y75f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211149 5'
2102	16054	28363	1.38	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2102	16054	28364	1.38	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4488	17628	30609	1.69	2.4E-02	J05110.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
6344	19514	32871	0.86	2.4E-02	W86680.1	EST_HUMAN	zh63h04.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:416791 3'
7370	20449	33912	1.2	2.4E-02	Z20573.1	EST_HUMAN	HSAAAGKX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7386	20464	33928	1.11	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7386	20464	33929	1.11	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
8074	21156		0.76	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0186-230300-018-H06 ST0186 Homo sapiens cDNA
8129	21211		0.57	2.4E-02	M16780.1	NT	Human retrotansposon 3' long terminal repeat
8636	21716		0.57	2.4E-02	H78376.1	EST_HUMAN	y412c05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains
8728	21808	35344	11.69	2.4E-02	N69442.1	EST_HUMAN	Alu repetitive element; contains A3R repetitive element;
9187	22265	35906	0.78	2.4E-02	AE001125.1	NT	z435g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284595 3' similar to
							gbj02909JFATSR7K Rat (RNA); contains A3R, b1 A3R repetitive element;
							Borrelia burgdorferi (section 11 of 70) of the complete genome
							z491c08.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gbj04422 ISLET
9211	22285	35831	0.81	2.4E-02	AA825660.1	EST_HUMAN	AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9883	22933	36516	0.55	2.4E-02	AF124160.1	NT	Arabidopsis thaliana methylodiphenyl synthase sulphydrylase (cmt5) gene, complete cds
9893	22933	36517	0.55	2.4E-02	AF124160.1	NT	Arabidopsis thaliana methylodiphenyl synthase sulphydrylase (cmt5) gene, complete cds
10011	23049	36943	2.75	2.4E-02	AV682954.1	EST_HUMAN	AV682954 GK Hom sapiens cDNA clone GKCDSC03.5
10186	23223	36917	2.82	2.4E-02	AA493894.1	EST_HUMAN	h07b12.s1 NCL CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element contains element PTR5 repetitive element
10859	23872		0.5	2.4E-02	BE387111.1	EST_HUMAN	601274962F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3615902.5
11874	24862	38557	2.45	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11874	24862	38558	2.45	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
12210	25163		3.98	2.4E-02	9627909	NT	Bacteriophage b107, complete genome
12362	25260	32116	4.45	2.4E-02	6753635	NT	Mus musculus DmB homolog 1 (E. coli) (Dmb1), mRNA
12478	25330	32055	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12478	25330	32096	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12668	25445		10.87	2.4E-02	AB008569.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
12697	25464		1.28	2.4E-02	N42980.1	EST_HUMAN	y08a06.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270610.5
12883	25900	31858	1.25	2.4E-02	AA179693.1	EST_HUMAN	zp18h01.11 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609361.5
1921	15094		5.25	2.3E-02	W03340.1	EST_HUMAN	za84g08.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:269294.5
1936	15079		16.26	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT8 (INT8) gene, exon 4
2065	15205	28321	0.99	2.3E-02	AW797355.1	EST_HUMAN	CM2-UM0038-290400-172-b11 UM0038 Homo sapiens cDNA
2426	15554	28681	2.68	2.3E-02	Z74293.1	EST_HUMAN	S. cerevisiae chromosome IV reading frame ORF YDL245c
3773	16934	29940	7.02	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH P, Human fetal Brain Whole tissue Homo sapiens cDNA
3807	16987		0.67	2.3E-02	L23428.1	NT	Canis beta-galactosides-binding lectin (LGALS3) mRNA, 3' end
4267	17412	30398	1.17	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4267	17412	30399	1.17	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4540	17678	30660	1.08	2.3E-02	AW899107.1	EST_HUMAN	CM4-NN0080-290400-160-b04 NN0080 Homo sapiens cDNA
4571	17709	30689	0.6	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4571	17709	30690	0.6	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4572	18469	30691	1.2	2.3E-02	AW593893.1	EST_HUMAN	xs25d08.x1 NCL CGAP_U2 Homo sapiens cDNA clone IMAGE:2770671.3

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4572	18469	30692	1.2	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NC1_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4717	17852	30835	3.01	2.3E-02	BF028487.1	EST_HUMAN	601872279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4717	17852	30836	3.01	2.3E-02	BF028487.1	EST_HUMAN	601872279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
5144	18267	31237	0.9	2.3E-02	AW844307.1	EST_HUMAN	RC2-CN0051-290100-011-e07 CN0051 Homo sapiens cDNA
5265	18384	31349	0.62	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5265	18384	31350	0.62	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5491	18690	31707	3.86	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA
6365	19535	32894	0.62	2.3E-02	BF106464.1	EST_HUMAN	carboxylase beta chain (pcsb) homolog gene, partial cds
6755	19911	33306	4	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7119	18545	31456	0.69	2.3E-02	BE141475.1	EST_HUMAN	MRO-HT0080-011099-002-c08 HT0080 Homo sapiens cDNA
7619	20689	34164	0.63	2.3E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8060	21143	34661	4.52	2.3E-02	U63610.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8667	21747	35285	1.12	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8667	21747	35286	1.12	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8894	21973	35509	0.75	2.3E-02	AI685380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
8894	21973	35510	0.75	2.3E-02	AI685380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9338	22414	35967	0.84	2.3E-02	P41896	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
10063	23101	36704	0.94	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
10236	23271	36862	1.44	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10236	23271	36863	1.44	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
11022	24101	37739	2.38	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN
12338	25919		3.61	2.3E-02	BE278331.1	EST_HUMAN	GLUCOHYDROLASE)
12801	25535	32011	1.78	2.3E-02	BF528462.1	EST_HUMAN	601179958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
12801	25535	32012	1.78	2.3E-02	BF528462.1	EST_HUMAN	602043829F1 NC1_CGAP_Bin67 Homo sapiens cDNA clone IMAGE:4181454 5'
12919	25604	31974	2.47	2.3E-02	U39394.1	NT	602043829F1 NC1_CGAP_Bin67 Homo sapiens cDNA clone IMAGE:4181454 5'
12975	26195		1.88	2.3E-02	U11077.1	NT	Streptomyces sp. alpha-1,3/4-lucosidase precursor gene, complete cds
756	13937	26982	3.59	2.2E-02	AF018267.1	NT	Dichytellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
1786	14935		1.79	2.2E-02	4557443	NT	Columba livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein,
1800	14949	28042	2.94	2.2E-02	P07313	SWISSPROT	complete cds
1800	14949	28043	2.94	2.2E-02	P07313	SWISSPROT	Homo sapiens chromodomain helixase DNA binding protein 2 (CHD2) mRNA
							MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
							MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2072	15212	28329	2.17	2.2E-02	Z82001.1	NT	S. pneumoniae popA gene and open reading frames
3521	16687		2.03	2.2E-02	AA577765.1	EST_HUMAN	nm24g04.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3736	16897		4.09	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain L4 VP1 gene, complete cds
3956	17114	30110	0.98	2.2E-02	AW601317.1	EST_HUMAN	PM0-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
4029	17185	30195	0.99	2.2E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
5177	18299	31262	1.37	2.2E-02	Z73597.1	NT	S. cerevisiae chromosome XVI reading frame ORF YPL241c
7396	20474	33941	3.43	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
8666	21647	35188	1.41	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8568	21647	35189	1.41	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9009	22098	35630	0.82	2.2E-02	X79488.1	NT	P. vulgaris alpha tub 2 mRNA
9856	22898	36478	0.46	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9856	22898	36479	0.46	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9888	22928	36511	2.73	2.2E-02	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9888	22928	36512	2.73	2.2E-02	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10409	23444		1.26	2.2E-02	6678140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
12625	25421		6.8	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
432	13627		4.48	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
462	13657		0.62	2.1E-02	AF029726.1	NT	Dietosellum discoideum histidine kinase C (dhkC) mRNA, complete cds
1292	14448	27514	6.65	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), Codi (cotL), and spore coat protein CotM (cotM) genes, complete cds
1418	14571	27844	1.31	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1418	14571	27645	1.31	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1823	14972	28065	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1823	14972	28066	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1823	14972	28067	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2019	15159	28264	0.97	2.1E-02	AF190899.1	NT	Tegula aureolincta major acrosomal protein precursor (TMAP) mRNA, complete cds
2092	16232	28354	1.16	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0548-120100-001-f11 BT0548 Homo sapiens cDNA
2092	16232	28355	1.16	2.1E-02	BE072548.1	EST_HUMAN	PM2-BT0548-120100-001-f11 BT0548 Homo sapiens cDNA
2877	13980	27032	3.12	2.1E-02	N29268.1	EST_HUMAN	y43h07.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:264541 5'
3674	18837	29847	1.01	2.1E-02	AA461271.1	EST_HUMAN	z66b09.r1 Soares_fetus NB2HF8_9w Homo sapiens cDNA clone IMAGE:796121 5'
4249	17395	30384	0.68	2.1E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4427	17567	30549	0.89	2.1E-02	BF343656.1	EST_HUMAN	602016306F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4151161 5'
4667	17705	30685	2.14	2.1E-02	U4494.1	NT	Borrelia burgdorferi plasmid op32-2, erpC and erpD genes, complete cds; and unknown genes
4577	17714	30698	1.64	2.1E-02	A1768127.1	EST_HUMAN	wg81d11.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4631	17964	30953	5.95	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4852	17985	30973	0.75	2.1E-02	AA665737.1	EST_HUMAN	ag55g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
4940	18070	31048	0.89	2.1E-02	A1823432.1	EST_HUMAN	wh54a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
5315	18432	31402	0.91	2.1E-02	BF026405.1	EST_HUMAN	60167141F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954410 5'
5756	18948	32250	0.6	2.1E-02	AW379529.1	EST_HUMAN	CM4-HT0244-11199-040-h05 HT0244 Homo sapiens cDNA
7212	20077	33490	0.73	2.1E-02	BF086199.1	EST_HUMAN	QV3-GN0058-120900-328-e12 GN0058 Homo sapiens cDNA
8716	21786	35333	0.66	2.1E-02	9790238	NT	Mus musculus sorting nexin 1 (Snrx1), mRNA
9703	22752	36322	0.54	2.1E-02	AA984288.1	EST_HUMAN	am83e07.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
9831	22871	36453	2.49	2.1E-02	AJ243213.1	NT	Alu repetitive element; contains element MER11 repetitive element;
9831	22871	36454	2.49	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10189	23226	36820	1.15	2.1E-02	L29324.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10266	23301	36899	0.75	2.1E-02	AA984288.1	EST_HUMAN	Streptococcus pneumoniae integrase, excisionase, repressor, protein, relaxase, UmuC MucB homolog, and
10856	23880	37508	0.49	2.1E-02	AF001519.1	NT	UmuD MucA homolog genes, complete cds; and unknown genes
11787	24777	38474	1.48	2.1E-02	6754255	NT	am83e07.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
12063	25044	38752	1.42	2.1E-02	AW844320.1	EST_HUMAN	Alu repetitive element; contains element MER11 repetitive element;
12602	18493	26556	11.16	2.1E-02	Y19213.1	NT	Bacillus halodurans genomic DNA, section 13/14
12847	25915	31862	1.22	2.1E-02	L34170.1	NT	Mus musculus heat shock protein, 74 kDa, A (Hsp89a), mRNA
13091	25712	31938	3.82	2.1E-02	AF183913.1	NT	RC4-CN0050-130200-012-h04. 1 CN0050 Homo sapiens cDNA
19	13287	26257	1.28	2.0E-02	BF002832.1	EST_HUMAN	Homo sapiens putative psithba pseudogene for hair keratin, exons 2 to 7
20	13288	26258	14.95	2.0E-02	AW895665.1	EST_HUMAN	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
269	13488	26518	5.03	2.0E-02	6753635	NT	Azospirillum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds
306	13622	26556	2.95	2.0E-02	AA456538.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER11.3
821	14000	27054	3.63	2.0E-02	6753635	NT	MER1 repetitive element;
1111	14276	27333	0.98	2.0E-02	AL098805.1	NT	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
1226	14388	27448	0.91	2.0E-02	8922391	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
							art5b10.r1 Soares NIH-MPU_S1 Homo sapiens cDNA clone IMAGE:813307 5'
							Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
							Homo sapiens genomic region containing hypervariable minisatellites chromosome 1 [p36.33] of Homo sapiens
							Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1286	14386	27449	0.91	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1922	15065	28168	1.84	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1922	15065	28169	1.84	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2859	15973		2.09	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3148	13257	26257	1.56	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3309988 3' similar to contains MER1.13
3213	16387		1.13	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
3299	16473		1.99	2.0E-02	AF095588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
4113	17267	30267	1.57	2.0E-02	M18096.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
5219	18341		0.74	2.0E-02	A1271995.1	EST_HUMAN	qj83a03.x1 NCI_CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1896076 3'
6018	19201	32520	0.59	2.0E-02	L35321.2	NT	Dicotyledonous discoidium class VII unconventional myosin (myo) gene, complete cds
7723	20787	34275	0.95	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (417)
7723	20787	34276	0.95	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (417)
10081	23119		2.39	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10570	23605	37210	1.84	2.0E-02	A1640342.1	EST_HUMAN	wat7502.x1 NCI_CGAP_K1d1 Homo sapiens cDNA clone IMAGE:2298315 3'
10879	23964	37692	1.85	2.0E-02	Z73986.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162
11653	24732	38423	1.91	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
11978	24963	38694	2.04	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
11978	24963	38695	2.04	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12149	18499	31535	1.8	2.0E-02	AA456538.1	EST_HUMAN	aaf15b10.x1 Scores: NhlMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12844	15973		2.26	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
13186	25771		5.63	2.0E-02	T80037.1	EST_HUMAN	yd04c09.1 Scores infant brain INIB Homo sapiens cDNA clone IMAGE:24675 5'
711	13893	26929	2.42	1.9E-02	AA572764.1	EST_HUMAN	nf19a07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:314196 similar to contains L.1.11 L.1
2097	15237	28358	4.85	1.9E-02	AL163303.2	NT	repetitive element;
2097	15237	28359	4.85	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2970	16146	29164	9.15	1.9E-02	AA713556.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
3018	16194	29217	1.92	1.9E-02	AV848669.1	EST_HUMAN	nm04f05.s1 NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1238337 3'
3332	16505		0.72	1.9E-02	AB033611.1	NT	A1648669 GLC Homo sapiens cDNA clone GLCBLH07 3'
3699	16860		1.12	1.9E-02	N52250.1	EST_HUMAN	Utrichus talpoides mitochondrial gene for cytochrome b, complete cds
3793	16954		8.1	1.9E-02	BE738088.1	EST_HUMAN	y28b02.s1 Scores_multiple_sclerosis_2NhlMSP Homo sapiens cDNA clone IMAGE:284331 3'
3808	16968	29971	0.83	1.9E-02	AI301183.1	EST_HUMAN	801572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
							q104c07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4158	17309	30306	1.3	1.9E-02	AF141940.1	NT	Mycoplasma imitans VlnA1 precursor (vlnA1) and VlnA2 precursor (vlnA2) genes, partial cds
4310	17453	30440	1.58	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4310	17453	30441	1.58	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4863	17798	30785	2.79	1.9E-02	AK452999.1	EST_HUMAN	94804.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
5125	15701	28822	4.22	1.9E-02	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5431	18031	31609	0.96	1.9E-02	AF037552.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5585	18780	31825	1.25	1.9E-02	L47572.1	NT	Meleagris gallopavo paraxonase-2 (PON2) mRNA, complete cds
5908	19097		0.93	1.9E-02	AB019507.1	NT	Drosophila kankoi gene for glyceral-3-phosphate dehydrogenase, complete cds
7250	20333	33780	1.1	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7250	20333	33781	1.1	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8769	21648		1.33	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 3/7
9532	22597	36169	1.21	1.9E-02	BF316129.1	EST_HUMAN	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126462 5'
9814	22854	36540	0.67	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
10251	23268	36882	1.24	1.9E-02	BF685832.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
10458	23493	37104	0.67	1.9E-02	D64001.1	NT	Synechocystis sp. PCC6803 complete genome, 2027, 2539000-2644794
11021	24100	37738	1.91	1.9E-02	AF008938.1	NT	Vibrio cholerae V86 phage putative replication protein gene, complete cds
12372	25924	31865	4.41	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament gllarin mRNA, complete cds
13006	25890		1.46	1.9E-02	L11068.1	NT	Candida albicans lambda Csa3/5 fragment
358	13567	26595	1.67	1.8E-02	AW771104.1	EST_HUMAN	hm52c06.x1 NCI CGAP Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
703	13886	26918	1.81	1.8E-02	BF308122.1	EST_HUMAN	MER29 repetitive element;
1186	14348	27406	1.43	1.8E-02	X17664.1	NT	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1467	14621	27704	1.38	1.8E-02	AF243382.1	NT	H. francisci mRNA for myelin basic protein (MBP)
2743	16860	28972	1.74	1.8E-02	AE004544.1	NT	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds
3282	16456		0.94	1.8E-02	AI806829.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3993	17160	30156	1.09	1.8E-02	AW879122.1	EST_HUMAN	te52a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090286 3'
3993	17150	30157	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4197	17347		1.01	1.8E-02	AA861446.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4550	17688	30689	1.52	1.8E-02	AW936363.1	EST_HUMAN	al24h04.x1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:1406935 3'
5068	18197	31171	2.02	1.8E-02	O60810	SWISSPROT	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA
6949	20282	33700	4.44	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
7624	20694	34170	2.3	1.8E-02	BF125690.1	EST_HUMAN	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
7650	20694	34170	0.61	1.8E-02	BF125690.1	EST_HUMAN	601783268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
							601783268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8322	21404	34931	0.88	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
8663	21743	35283	0.46	1.8E-02	AW905327.1	EST_HUMAN	QV2-NN1073-220400-159-009 NN1073 Homo sapiens cDNA
8710	21790	35326	0.76	1.8E-02	6878943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
9683	22742	36311	0.57	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9693	22742	36312	0.57	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9842	22882		2.23	1.8E-02	AA897543.1	EST_HUMAN	aj62109.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb:L11672 ZINC
10268	23303	36900	1.7	1.8E-02	BE778274.1	EST_HUMAN	FINGER PROTEIN 81 (HUMAN);
10431	23466	37072	1.29	1.8E-02	XG6633.1	NT	601463545F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3866963 5'
11721	23907	37530	1.76	1.8E-02	AB002337.2	NT	L. stagnalis mRNA for myomodulin neuropeptide precursor
11721	23907	37531	1.76	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11912	24899	38602	1.55	1.8E-02	AP000006.1	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11926	24912	39613	2.45	1.8E-02	U62749.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (677)
13096	25894		1.78	1.8E-02	AF202180.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
929	14104	27167	1.34	1.7E-02	BE394869.1	EST_HUMAN	Plasmodium falciparum erythrocyte membrane-associated giant protein antigen 332 (Ag332) gene, partial cds
1831	14979	28075	2.12	1.7E-02	AW573183.1	EST_HUMAN	601310628F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1831	14979	28076	2.12	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.t1 L1 repetitive element;
1920	15063		2.85	1.7E-02	AL163204.2	NT	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.t1 L1 repetitive element;
2181	15316		13.13	1.7E-02	AB0004816.1	NT	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.t1 L1 repetitive element;
2705	15823		1.36	1.7E-02	7667495	NT	Homo sapiens chromosome 21 segment HS21C004
3062	16238	29259	0.89	1.7E-02	A1147615.1	EST_HUMAN	Oryctolagus cuniculus mRNA for mitogenin29, complete cds
3602	16766		4.64	1.7E-02	AW827368.1	EST_HUMAN	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
3716	16877		0.83	1.7E-02	P04929	SWISSPROT	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
4284	17429		1.23	1.7E-02	AA668618.1	EST_HUMAN	hm45a04.x1 NCI_CGAP_LU5 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains
4317	17460		2.02	1.7E-02	R02506.1	EST_HUMAN	MER19.b1 MER19 repetitive element;
4576	17713	30687	0.74	1.7E-02	A1305279.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4649	17785	30768	1.32	1.7E-02	AW573183.1	EST_HUMAN	act1604.s1 Stratagene ovary (#837217) Homo sapiens cDNA clone IMAGE:856827 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
							ye6608.r1 Soares_fetal_liver_spleen_1NLS Homo sapiens cDNA clone IMAGE:124647 5'
							qm08g07.x1 NCI_CGAP_LU5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X62369 ZINC
							FINGER PROTEIN 30 (HUMAN);
							h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.t1 L1 repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4836	17869	30857	1.91	1.7E-02	V06441.1	NT	Messenger RNA for anglerfish (<i>Lophius americanus</i>) somatostatin II
4934	18064		5.98	1.7E-02	AI015076.1	EST_HUMAN	ov51602.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
6253	19427	32773	1.99	1.7E-02	AI769247.1	EST_HUMAN	wg33f09.x1 Soares NSF_F8_GW_OT_PA_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
6709	19867	33256	1.23	1.7E-02	AI038280.1	EST_HUMAN	cy85h03.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672601 3'
7195	20060	33471	1.26	1.7E-02	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7353	20432	33894	1.9	1.7E-02	8400716	NT	Homo sapiens nebulin (NEB), mRNA
7513	20587	34080	1.08	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7513	20587	34081	1.08	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7921	20872		1.71	1.7E-02	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
9636	21079	34591	0.89	1.7E-02	U21854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
9900	22940	35526	1.28	1.7E-02	AL040554.1	EST_HUMAN	DKFZp434j0314_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434j0314 5'
12093	25073	39760	1.66	1.7E-02	5902007	NT	Homo sapiens serum constituent protein (MSE56), mRNA
12991	26111	31687	2.35	1.7E-02	AW903482.1	EST_HUMAN	QMA-NN1030-0400-130-106 NN1030 Homo sapiens cDNA
13166	25757	31928	1.46	1.7E-02	AA846926.1	EST_HUMAN	ce08d04.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385287 similar to contains element MSR1 repetitive element;
524	13717		4.05	1.6E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1989	14841	27826	1.37	1.6E-02	Y18889.1	NT	Treponema mallophilum flaB2, flaB3 and flid genes for flagellin subunit proteins and CAP protein homologue
2323	15455	28586	1.81	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2323	15455	28587	1.81	1.6E-02	Q84176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2631	15754	28869	0.97	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQ17 gene
2708	15826	28941	1.75	1.6E-02	AA494872.1	EST_HUMAN	ne81d05.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2758	15875		1.01	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3614	16778	29793	5.33	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
4291	17436		1.96	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4415	17556	30543	2.04	1.6E-02	AW875407.1	EST_HUMAN	QV2-PT0012-140100-030-407 PT0012 Homo sapiens cDNA
5367	18570	31438	0.59	1.6E-02	AI281385.1	EST_HUMAN	qu42b08.x1 NCL_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:1967417 3'
5741	18934	32234	1.42	1.6E-02	6671715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6780	19935	33331	2.18	1.6E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
7071	20124	33539	1.14	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7071	20124	33540	1.14	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7888	20940	34446	0.96	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8312	21394	34919	0.74	1.6E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8372	21453		3.37	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
10246	23281		2.97	1.6E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10633	23667	37276	1.61	1.6E-02	AA572818.1	EST_HUMAN	m19g03.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29294 TELOKIN. [1]:
10633	23667	37277	1.61	1.6E-02	AA572818.1	EST_HUMAN	m19g03.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29294 TELOKIN. [1]:
11149	25968	37848	2.9	1.6E-02	Z84828.1	NT	G.gallus microsatellite DNA (LEID260 (=T1611E11))
11488	24547	38219	2.11	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11488	24547	38220	2.11	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11801	24791	38488	2.16	1.6E-02	AL373558.1	EST_HUMAN	q286610.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3'
12348	15455	28586	3.49	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
12348	15455	28587	3.49	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
770	13951		9.38	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2209	15343	28469	3.58	1.5E-02	N39521.1	EST_HUMAN	y27507.s1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:243926 3'
2244	15377	28505	1.6	1.5E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3128	16304	29317	1.04	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3128	16304	29318	1.04	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3818	16978	29982	1.14	1.5E-02	BF092942.1	EST_HUMAN	MR4-TN0115-080900-201-512 TN0115 Homo sapiens cDNA
4590	17727	30710	0.72	1.5E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
6423	19592	32957	2.07	1.5E-02	Q09711	SWISSPROT	HYPOPHOSPHATE CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7472	20547		1.69	1.5E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
7561	20633	34108	1.57	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
8058	21141	34690	1.38	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8065	21147	34698	3.08	1.5E-02	11417739	NT	Homo sapiens vally-rRNA synthetase 2 (VARS2), mRNA
9030	22106	35650	1.42	1.5E-02	BF343554.1	EST_HUMAN	602019135F1 NC1_CGAP_Brn07 Homo sapiens cDNA clone IMAGE:4154504 5'
9668	22630		0.58	1.5E-02	AF096774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9770	22766	36337	1.59	1.5E-02	D44606.1	NT	Saccharomyces cerevisiae chromosome VI plasmid CapC
10016	23054	36849	1.3	1.5E-02	R32667.1	EST_HUMAN	yf54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
10016	23054	36650	1.3	1.5E-02	R32667.1	EST_HUMAN	yf54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
10860	23893	37614	0.46	1.5E-02	T92196.1	EST_HUMAN	yf17f10.s1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:118027 3'
11056	24133		1.78	1.5E-02	D26547.1	NT	Ribe gene for thiodoxin h, complete cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11442	24503	38171	2.21	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
12576	25970		2.38	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
430	13626		1.54	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome
1142	14307	27363	3.81	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51226), mRNA
1285	14441		2.12	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1326	14483		2.49	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
3284	16458	29478	1.83	1.4E-02	AF160969.2	NT	Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosamine-6-phosphate repressor protein (nagCxyR) gene, partial cds
3485	16653	29668	1.23	1.4E-02	AW074212.1	EST_HUMAN	x090909.x1 NCI_CGAP GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3573	16738	29753	6.9	1.4E-02	AL161686.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3573	16738	29754	6.9	1.4E-02	AL161686.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3608	16772	29787	0.75	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3748	16907	29911	12.14	1.4E-02	6986918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-B), mRNA
4612	17749	30729	9.97	1.4E-02	AW962688.1	EST_HUMAN	EST374761: MAGG Homo sapiens cDNA
4612	17749	30730	9.97	1.4E-02	AW962688.1	EST_HUMAN	EST374761: MAGG Homo sapiens cDNA
4998	18127	31102	6.22	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3842280 5'
4998	18127	31103	6.22	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3842280 5'
5911	26210		0.74	1.4E-02	X91338.1	NT	H. sapiens La/SS-B pseudogene 3
6545	19707	33083	4.52	1.4E-02	AA559030.1	EST_HUMAN	nl11c04 s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
6545	19707	33084	4.52	1.4E-02	AA559030.1	EST_HUMAN	nl11c04 s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
8333	21416		1.55	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 88/162
9098	22178	35722	1.44	1.4E-02	M81702.1	NT	Candida boidinii melanol oxidase (AOD1) gene, complete cds
9366	22431	35989	1.41	1.4E-02	AJ272285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9600	22655	36227	1.96	1.4E-02	BE644561.1	EST_HUMAN	601078239F1 NIH_MGC 12 Homo sapiens cDNA clone IMAGE:3464241 5'
10780	23813		0.89	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
12268	25194	38358	8.95	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12640	25430		1.84	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21 J9.2 mRNA, complete cds
12859	25625		1.45	1.4E-02	11426968	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
13075	25704		1.51	1.4E-02	AF238059.2	NT	Rheum x cultum NADH dehydrogenase subunit F (ndhF) gene, partial cds; chloroplast gene for chloroplast product

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1913	15056		1.19	1.3E-02	BE739283.1	EST_HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5'
2010	15150	28254	2.13	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2612	15638	28759	0.98	1.3E-02	AE002445.1	NT	Neisseria meningitidis serogroup B strain MC58 section 87 of 206 of the complete genome
3285	16459	29479	2.41	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
3285	16459	29480	2.41	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
4076	17232		1.22	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
5275	18394		3.02	1.3E-02	D26547.1	NT	Rice gene for thiredoxin h, complete cds
5360	18563	31478	1.81	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 276, Zinc finger protein 92, mmxq2borf
5360	18563	31479	1.81	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 276, Zinc finger protein 92, mmxq2borf
6293	19466	32819	1.2	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
6327	19469	32856	1.05	1.3E-02	M62962.1	NT	C reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7101	18528	31481	1.3	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7101	18528	31482	1.3	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7752	20812	34303	4.9	1.3E-02	AI031593.1	EST_HUMAN	ow06g05.x1 Soares_parathyroid_tumor_NBHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element
8678	21758	35294	1.67	1.3E-02	AF158961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10411	23446	37051	1.89	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10485	23520	37129	0.95	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
11239	24308	37944	3.35	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GEC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
11239	24308	37945	3.35	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GEC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
12645	26127		1.7	1.3E-02	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
12753	25499		2.56	1.3E-02	9633069	NT	Human herpesvirus 8B, complete genome
12985	25885		30.16	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
219	13441		0.82	1.2E-02	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, iPP2, LMP2, TAP1, LMP7, DOB, DQB2 and RING8, 9, 13 and 14 genes
365	13575	26606	4.38	1.2E-02	AA059299.1	EST_HUMAN	zfb5g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element;
465	13660	26696	1.43	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR53REGION
757	13938	26983	2.67	1.2E-02	AI183522.1	EST_HUMAN	q66a12.x1 Soares_besit_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.t1 L1 repetitive element;
2246	15379	28507	2.03	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2614	15640	28762	1.02	1.2E-02	AW172350.1	EST_HUMAN	xj37e09.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2701	15640	28762	1.43	1.2E-02	AW172350.1	EST_HUMAN	xj37e09.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3170	16346		7.3	1.2E-02	AA075418.1	EST_HUMAN	zm88e03.r1 Stratiogene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:645020 5'
3369	16531	29545	2.05	1.2E-02	RC2805.1	EST_HUMAN	y11h08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
3362	16534	29548	0.59	1.2E-02	AI688694.1	EST_HUMAN	zb68a07.x5 Soares_Tetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:308532 3' similar to contains element MER22 repetitive element;
5035	18163	31139				NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP T3) gene, complete cds
5154	18276		1.97	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster OpluqT mRNA, partial cds
5195	18317	31288	1.31	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5871	19061	32368	1.78	1.2E-02	D78589.1	NT	Rana rugosa mRNA for cathecolin, complete cds
6243	19417	32765	0.72	1.2E-02	AF045555.1	NT	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7147	20282	33724	8.67	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7443	20520	33993	1.42	1.2E-02	H02197.1	EST_HUMAN	y34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150696 3'
7465	20640	34014	8.54	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBJC09 5'
7729	20791	34280	0.68	1.2E-02	BF216850.1	EST_HUMAN	601882949F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095253 5'
8186	21263	34792	2.3	1.2E-02	Q11205	SWISSPROT	GMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B)
8321	21403	34929	0.56	1.2E-02	R68831.1	EST_HUMAN	y43f06.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8321	21403	34930	0.56	1.2E-02	R68831.1	EST_HUMAN	y43f06.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8386	21467	34993	1.22	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8386	21467	34994	1.22	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
9091	22170		1	1.2E-02	T76967.1	EST_HUMAN	yf72c08.s1 Soares fetal liver spleen tNFLS Homo sapiens cDNA clone IMAGE:113774 3'
9839	22879	36461	2.54	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9872	22912	36487	1.24	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12757	25986		1.16	1.2E-02	P17139	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
12974	26634		6.24	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-557/006 5'
1298	14454	27520	1.22	1.1E-02	AA070364.1	EST_HUMAN	zm69e11.s1 Stratiogene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1743	14852	27986	1.48	1.1E-02	X75491.1	NT	H.sapiens LIPA gene, exon 4
1743	14852	27987	1.48	1.1E-02	X75491.1	NT	H.sapiens LIPA gene, exon 4
2096	15236	28357	5.35	1.1E-02	BF345283.1	EST_HUMAN	602018037FT NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153808 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2942	16119		5.31	1.1E-02	N99523.1	EST_HUMAN	zr40a05.t1 Soares fetal liver spleen TNF α Homo sapiens cDNA clone IMAGE:295040 5'
3612	16776	20792	3.59	1.1E-02	AI653508.1	EST_HUMAN	ig85b10.x1 NCI CGAP_OV23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XP_F_HUMAN
4222	17370		0.68	1.1E-02	AW813786.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;
4951	18081	31057	1.27	1.1E-02	AL048383.2	EST_HUMAN	RC3-STO197-120200-015-g11 ST0197 Homo sapiens cDNA
							DKFZ586E0924_s1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZ586E0924
							Bacillus subtilis SpoVK (spoVK), YnaA (ybaA), YnaB (ybaB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ybaA), YnaB (ybaB), YnaC (ybaC), YnaD (ybaD), YnaE (ybaE), YnaF (ybaF), YnaG (ybaG), YnaH (ybaH), YnaI (ybaI), YnaJ (ybaJ), xylan beta-1,4-xylosyl>
6277	19451	32800	0.89	1.1E-02	U66480.1	NT	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
7773	20830	34321	2.19	1.1E-02	BE149611.1	EST_HUMAN	Melanoplus sanguinipes entomopoxvirus, complete genome
7989	21039	34551	1.25	1.1E-02	9631294	NT	METALLOTHIONEIN (MT-1/MT-2)
8451	21532	35061	0.46	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8451	21532	35062	0.46	1.1E-02	P80394	SWISSPROT	QV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA
8841	21920	35458	0.69	1.1E-02	AW986160.1	EST_HUMAN	QC4803 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NH-4040
9022	22101	35641	0.7	1.1E-02	C04803.1	EST_HUMAN	NEUROGENIC LOCUS NOTCH 3 PROTEIN
9103	22182	35727	7.44	1.1E-02	Q51982	SWISSPROT	
10133	23171	36769	2.02	1.1E-02	AA082576.1	EST_HUMAN	zr24a01.t1 Stralagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
10299	23334	36939	4.06	1.1E-02	AA314665.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
11224	24293	37934	2.41	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
							ab77111.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
12195	25182		4.01	1.1E-02	AA669239.1	EST_HUMAN	Alu repetitive element
7	13245	26247	8.82	1.0E-02	AW846120.1	EST_HUMAN	MR3-CT0176-111058-003-a10 CT0176 Homo sapiens cDNA
1562	14705	27785	0.97	1.0E-02	AW368128.1	EST_HUMAN	CM2-HT0177-041099-017-H12 HT0177 Homo sapiens cDNA
2838	15761		1.71	1.0E-02	AA806389.1	EST_HUMAN	cc22h08.s1 NCI CGAP_GC81 Homo sapiens cDNA clone IMAGE:1350495 3'
3159	16334	26344	2.88	1.0E-02	BE835556.1	EST_HUMAN	RC0-FN0025-250500-021-402 FN0025 Homo sapiens cDNA
3336	16509	29529	1.24	1.0E-02	BE969999.1	EST_HUMAN	601648667R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
3598	16762		0.7	1.0E-02	AW845621.1	EST_HUMAN	MRO-CT0060-081099-003-h10 CT0060 Homo sapiens cDNA
3988	17143	30148	0.85	1.0E-02	AI060086.1	EST_HUMAN	HA0821 Human fetal liver cDNA library Homo sapiens cDNA
4002	17159	30165	0.59	1.0E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4899	18029	31017	5	1.0E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4969	18098	31074	4.14	1.0E-02	R96567.1	EST_HUMAN	yt54h01.t1 Soares fetal liver spleen TNF α Homo sapiens cDNA clone IMAGE:199633 5'
5116	18243	31208	0.83	1.0E-02	AL161593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
5242	18364	31332	1.96	1.0E-02	P06599	SWISSPROT	EXTENSIN PRECURSOR
5632	18729	31745	0.81	1.0E-02	H52681.1	EST_HUMAN	yj36h11.t1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235941 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5885	19055	32362	0.66	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6242	19416	32764	1.29	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (Syx2) gene, complete cds
6310	19482	32836	2.78	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6310	19482	32837	2.78	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6901	20216	33646	1.69	1.0E-02	Z29842.1	NT	Z.mays U5snRNA pseudogene
9593	22648	36219	6.34	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3863177 5'
9593	22648	36220	6.34	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3863177 5'
11542	24598		2.12	1.0E-02	AF157559.1	NT	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11573	24628		1.7	1.0E-02	AI417961.1	EST_HUMAN	ig55h07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:X15163_cds1
11849	24728	38420	1.95	1.0E-02	AV760016.1	EST_HUMAN	HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); contains Alu repetitive element; contains element MER5 repetitive element
12278	26208		1.76	1.0E-02	D62203	SWISSPROT	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
12339	25941	31762	3.58	1.0E-02	AW635521.1	EST_HUMAN	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) [SPLICING FACTOR 3A SUBUNIT 2] (SF3A66)
12355	26002		4.31	1.0E-02	S70330.1	NT	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
12764	25974		1.4	1.0E-02	AJ276505.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12949	26060		2.91	1.0E-02	X62654.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
916	14091	27156	5.69	9.0E-03	AI796126.1	EST_HUMAN	H.sapiens gene for Me491/GD63 antigen
1293	14449		1.66	9.0E-03	BE781889.1	EST_HUMAN	WH4209.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
2469	15593	28721	2.64	9.0E-03	AL161559.2	NT	MER22 MER22 repetitive element
2971	16147	29165	0.81	9.0E-03	AI251744.1	EST_HUMAN	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2971	16147	29166	0.81	9.0E-03	AI251744.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
3758	16919	29921	0.66	9.0E-03	J05184.1	NT	q180f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
5931	19117		1.19	9.0E-03	AB09792.1	EST_HUMAN	q180f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
6766	19922		4.01	9.0E-03	BE745988.1	EST_HUMAN	S.acidocalcarius thermopsis gene, complete cds
7823	20693	34169	0.61	9.0E-03	AI242218.1	EST_HUMAN	wf77604.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'
7840	20709	34188	0.91	9.0E-03	8922570	NT	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834762 5'
8059	21142		0.8	9.0E-03	AL039991.1	EST_HUMAN	q187c12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
8443	21524		0.54	9.0E-03	AF223391.1	NT	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
10050	23088	36690	0.54	9.0E-03	P26011	SWISSPROT	DKFZp434L0412.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0412 5'
10068	23104	36707	1.47	9.0E-03	P20908	SWISSPROT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M280 IEL ANTIGEN)
							COLLAGEN ALPHA 1(V) CHAIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11232	24301		1.68	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
11951	24937	38638	1.31	9.0E-03	L11144.1	NT	Homo sapiens preprogalactin (GAL1) gene, exons 1, 2, and 3
11951	24937	38639	1.31	9.0E-03	L11144.1	NT	Homo sapiens preprogalactin (GAL1) gene, exons 1, 2, and 3
12494	26208		2.07	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
12722	26200		37.58	9.0E-03	BE348385.1	EST_HUMAN	hw17609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
12838	25558	32016	1.21	9.0E-03	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
13074	25703		17.6	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
514	13708		3.15	8.0E-03	AA723007.1	EST_HUMAN	z330e03 at Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains
1013	14185	27246	12.69	8.0E-03	AF108896.1	NT	Alu repetitive element
2226	15360	28489	1.87	8.0E-03	AL163283.2	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2617	15741	28853	3.05	8.0E-03	P10268	SWISSPROT	Homo sapiens chromosome 21 segment HS21C083
3442	16610	29628	1.02	8.0E-03	AJ131016.1	NT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
3766	16927	29630	1.81	8.0E-03	P32844	SWISSPROT	Homo sapiens SCL gene locus
3766	16927	29931	1.91	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4372	17515	30495	1.15	8.0E-03	BE940049.1	EST_HUMAN	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4502	17642	30627	5.73	8.0E-03	BF363327.1	EST_HUMAN	QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4839	17972	30961	0.83	8.0E-03	P03181	SWISSPROT	CM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
4839	17972	30962	0.83	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
5271	18360	31358	0.94	8.0E-03	AJ140261.1	EST_HUMAN	HYPOTHETICAL BHLF1 PROTEIN
5640	18834	31911	2.8	8.0E-03	AF110520.1	NT	AU140261 PLACE2 Homo sapiens cDNA clone PLACE200223 5'
6328	25823	32857	1.27	8.0E-03	AP000002.1	NT	Mus musculus major histocompatibility complex region NC27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and
6889	20041	33450	4.4	8.0E-03	P55577	SWISSPROT	RPS18 genes, complete cds; Sacm21 gene, partial>
7059	20112		1.06	8.0E-03	V01109.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (2/7)
7367	20436	33898	1.43	8.0E-03	M17197.1	NT	PROBABLE PEPTIDASE Y4NA
7714	20779		1.8	8.0E-03	AB038267.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
9084	22163	35707	0.64	8.0E-03	P98160	SWISSPROT	A. californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end
9111	22190	35734	3.53	8.0E-03	AW808692.1	EST_HUMAN	Tursiops truncatus mRNA for p40-phox, complete cds
9180	22258	35801	0.68	8.0E-03	9789956	NT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
10154	23191		4.75	8.0E-03	BE086509.1	EST_HUMAN	PRECURSOR (HSPG) (PERLECAN) (PLC)
							MR1-ST0111-111199-011-H06 ST0111 Homo sapiens cDNA
							Mus musculus fusion 2 (human) (Fus2), mRNA
							QV1-BT0577-040400-131-g03 BT0577 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11005	24084	37721	2.01	8.0E-03	BE788441.1	EST_HUMAN	601475819F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
11231	24300		2.78	8.0E-03	Z49952.1	NT	S.cerevisiae chromosome X reading frame ORF YJR152w
11663	24742	38433	1.39	8.0E-03	AA828817.1	EST_HUMAN	0480a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11663	24742	38434	1.39	8.0E-03	AA828817.1	EST_HUMAN	0480a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
12015	24989	38701	4.37	8.0E-03	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-G1) gene, complete cds
12205	25159		1.89	8.0E-03	M69035.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
12252	25191		7.14	8.0E-03	AB038181.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
13145	25959		1.16	8.0E-03	A1277808.1	EST_HUMAN	qtr85a09.x1 Soares_placenta_8y6weeks_2NbpP8tc9W Homo sapiens cDNA clone IMAGE:1892762 3'
712	13894	26930	12.35	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
998	14170	27231	3.26	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1140	14305	27361	3.55	7.0E-03	AV731742.1	EST_HUMAN	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1395	14549		1.03	7.0E-03	Q61080	SWISSPROT	AV731742 HTF Homo sapiens cDNA clone HTFAZF10 5'
1426	14580	27653	3.39	7.0E-03	AA668298.1	EST_HUMAN	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1532	14685	27764	3.28	7.0E-03	AW303599.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)
2332	16060	28568	2	7.0E-03	P04929	SWISSPROT	ab79b09.s1 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
2695	15815		0.98	7.0E-03	AW772132.1	EST_HUMAN	x121b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
3648	16811	29824	0.85	7.0E-03	A1150273.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3863	17023	30022	0.71	7.0E-03	AW44463.1	EST_HUMAN	hm67r07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3032989 3' similar to contains Alu repetitive element
3914	17073	30071	1.13	7.0E-03	AF166344.1	NT	q324f02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
4128	17023	30022	0.77	7.0E-03	AW44463.1	EST_HUMAN	U1-H-B13-akb- α -10-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4721	17856		0.98	7.0E-03	AW630988.1	EST_HUMAN	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
5103	18231		6.54	7.0E-03	AL163278.2	NT	h189a05.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968936 5'
5940	19126		0.72	7.0E-03	H71106.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6238	25821		4.42	7.0E-03	AW861059.1	EST_HUMAN	y62g01.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to gb:U4723 CLUSTERIN PRECURSOR (HUMAN);
6444	19611	32974	1.67	7.0E-03	W68251.1	EST_HUMAN	RC1-C10286-050400-018-c08 CT0286 Homo sapiens cDNA
6667	18826	33213	2.92	7.0E-03	AA327129.1	EST_HUMAN	z633f10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 5'
							EST30674 Colon I Homo sapiens cDNA 5' end

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6695	19853	33243	1.05	7.0E-03	BE957385.1	EST_HUMAN	7634b10.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
7228	20133	33550	1.93	7.0E-03	BE928133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 384D8_2, contains TAR1;2 TAR1 TAR1 repetitive element ;
7686	20754	34238	4.76	7.0E-03	Z35838.1	NT	CML2-CT0476-230800-347-b11 CT0478 Homo sapiens cDNA
7689	20754	34239	4.76	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
8031	21114	34632	0.59	7.0E-03	AJ228043.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
8031	21114	34633	0.59	7.0E-03	AJ228043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3f3
8302	21384	34905	2.48	7.0E-03	BE175687.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3f3
8302	21384	34905	2.48	7.0E-03	BE175687.1	EST_HUMAN	RC5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
8813	21892	35433	0.58	7.0E-03	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
9597	22652		0.64	7.0E-03	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
9794	22834	36414	0.68	7.0E-03	N52378.1	EST_HUMAN	y49c10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246068 3' similar to contains
9921	22961	36548	2.72	7.0E-03	P48882	SWISSPROT	Alu repetitive element
9921	22961	36549	2.72	7.0E-03	P48882	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10513	23548		1.34	7.0E-03	AV687379.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10704	29737		0.82	7.0E-03	AJ789734.1	EST_HUMAN	AV687379 GKC Homo sapiens cDNA clone GKACFC07 5'
10800	29833	37456	0.47	7.0E-03	BE164643.1	EST_HUMAN	wc37e09.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2320840 3'
11065	24141	37776	2.41	7.0E-03	AB008852.1	NT	PM3-HT0344-181199-002-g06 HT0344 Homo sapiens cDNA
11140	24212	37838	1.55	7.0E-03	AJ004862.1	NT	Bos taurus mRNA for NDP52, complete cds
11140	24212	37839	1.55	7.0E-03	AJ004862.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
12782	26189		1.95	7.0E-03	H84065.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12800	25634		1.46	7.0E-03	BE263253.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12908	25601		1.76	7.0E-03	Y17455.1	NT	Homo sapiens chromosome 21 segment HS21C100
13058	26186		1.68	7.0E-03	AL163300.2	NT	Alu repetitive element
1269	14427	27494	8.76	6.0E-03	AW511148.1	EST_HUMAN	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160478 5'
1269	14427	27495	8.76	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens LSF2 gene, penultimate exon
2831	15645	28054	0.94	6.0E-03	AF112374.1	NT	Homo sapiens LSF2 gene, penultimate exon
2956	16133	29147	3.29	6.0E-03	AA7569135.1	EST_HUMAN	hcd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
2956	16133	29148	3.29	6.0E-03	AA7569135.1	EST_HUMAN	SW:PXK_HUMAN_078469 ORPHAN NUCLEAR RECEPTOR PXR ;
3318	16491		2.27	6.0E-03	H75690.1	EST_HUMAN	SW:PXK_HUMAN_078469 ORPHAN NUCLEAR RECEPTOR PXR ;
			2.27	6.0E-03	H75690.1	EST_HUMAN	Danio rerio odorant receptor gene cluster
			2.27	6.0E-03	H75690.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
			2.27	6.0E-03	H75690.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
			2.27	6.0E-03	H75690.1	EST_HUMAN	y77H04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3378	16550		0.63	6.0E-03	AF190338.1	NT	Nicotinic sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3469	10336	29655	1.25	6.0E-03	U00880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3469	16636	29655	1.25	6.0E-03	U00880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3536	16800		1.11	6.0E-03	W37985.1	EST_HUMAN	zz13a11.1 Scarses, parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3750	16911	29914	3.73	6.0E-03	BF510986.1	EST_HUMAN	UI-H-814-apm-c-08-0-UI.s1 NCJ CGAP Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3877	17036	30034	1.31	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA
4032	17188	30199	0.6	6.0E-03	AW847284.1	EST_HUMAN	RCO-CT0204-240989-021-b10 CT0204 Homo sapiens cDNA
4067	17223		1.28	6.0E-03	BE280108.1	EST_HUMAN	600942804F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2858513 5'
4484	17624		1.54	6.0E-03	A1016833.1	EST_HUMAN	ov33c11.x1 Scarses, testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4817	17650	30935	7.9	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5305	18422	31392	0.8	6.0E-03	AA880972.1	EST_HUMAN	q95g09.s1 Scarses, parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404256 3'
6281	25822	32803	0.68	6.0E-03	9627521	NT	Varicella virus, complete genome
6956	20269	33707	0.8	6.0E-03	O14994	SWISSPROT	SYNAPSIN III
6984	18513	31505	0.97	6.0E-03	BE253748.1	EST_HUMAN	601112353F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7399	20477	33944	0.65	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7399	20477	33945	0.65	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7824	20879	34380	0.8	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
8042	21125	34643	6.71	6.0E-03	A1033980.1	EST_HUMAN	ov13a04.x1 Scarses, parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element
8161	21243	34763	2.78	6.0E-03	AW799337.1	EST_HUMAN	RCO-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
8236	21318		1.65	6.0E-03	BF038198.1	EST_HUMAN	601454815F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858626 5'
9754	22692	36262	7.03	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
10249	23284		2.49	6.0E-03	AI-32681.1	EST_HUMAN	i22c02.x1 NCJ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10365	23400	37011	0.75	6.0E-03	AJ011849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A ;
10603	23538		0.91	6.0E-03	AF084555.1	NT	Bacillus subtilis ftnD gene
10616	23649	37258	0.64	6.0E-03	X68366.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10661	23685		0.54	6.0E-03	AF245505.1	NT	M.thermofilicium complete plasmid pSV1 DNA
10983	24062	37697	1.56	6.0E-03	AW962164.1	EST_HUMAN	Homo sapiens adican mRNA, complete cds
11049	24128		1.94	6.0E-03	11546814	NT	EST374237 MAGE sequences, MAGG Homo sapiens cDNA
							Homo sapiens hypodermal zinc finger protein FLJ14011 (FLJ14011), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11228	24297		4.1	6.0E-03	U14558.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
11229	24298	37938	2.68	6.0E-03	BE737895.1	EST_HUMAN	601572746F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:3839747 5'
12321	25232		2.04	6.0E-03	AF010496.1	NT	Rhomboid capulatus strain SB1003, partial genome
12425	25998		1.3	6.0E-03	BF671185.1	EST_HUMAN	602151024F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4292212 5'
12451	25926		4.65	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450298 (section 39 of 148) of the complete genome
12532	25993		2.49	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12590	25397		1.63	6.0E-03	Q62209	SWISSPROT	SYNAPTOMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
12944	26622		2.41	6.0E-03	AJ245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
13095	26018		1.61	6.0E-03	X74907.1	NT	R.norvegicus VEGP2 gene
13147	25746		1.19	6.0E-03	BF110298.1	EST_HUMAN	7n35b1.1 x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565564 3'
686	13871	26903	1.59	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and gprE- like protein, complete cds
686	13871	26904	1.59	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and gprE- like protein, complete cds
687	13871	26903	3.08	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and gprE- like protein, complete cds
687	13871	26904	3.08	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and gprE- like protein, complete cds
1136	14301	27357	1.47	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
1601	14754	28974	1.08	5.0E-03	A1138977.1	EST_HUMAN	qd79d05 x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1735989 3'
2746	15863	28974	2.43	5.0E-03	AB033008.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
3206	16381	29392	3.87	5.0E-03	T87623.1	EST_HUMAN	ye81f09 s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3223	16397		2.72	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3235	16409	29423	1.17	5.0E-03	R71794.1	EST_HUMAN	y88g02 s1 Soares breast 2N5HBst Homo sapiens cDNA clone IMAGE:155666 3'
3351	16523		0.84	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3790	16951	29957	5.28	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (pbpB) gene, complete cds
3854	17014	30014	0.81	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4079	17235		1.64	5.0E-03	AA298675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4241	17387	30374	0.65	5.0E-03	AJ002125.1	NT	Natrix domestica Zfx type gene
4421	17562	30549	0.71	5.0E-03	H78355.1	EST_HUMAN	y179g10 r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:240066 5'
4423	17014	30014	0.76	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4731	17866	30848	0.92	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4841	17974	30964	1.56	5.0E-03	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC.cn15c02 random
5286	18405		1.9	5.0E-03	4758747	NT	Homo sapiens myosin-binding protein C, fast-type (MYBPC2) mRNA
5916	19104	32417	5.4	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
							PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
6169	19345	32891	2.82	5.0E-03	Q00507	SWISSPROT	Chlamydomonas reinhardtii AR39, section 82 of 84 of the complete genome
6204	19379		0.88	5.0E-03	AE002234.2	NT	6009445641.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960871 3'
6726	19882		7.34	5.0E-03	BE300091.1	EST_HUMAN	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6986	18505	31520	7.22	5.0E-03	AB025024.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7185	20050		0.85	5.0E-03	AB038287.1	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahe11), mRNA
7237	20321	33765	0.61	6.0E-03	6753651	NT	EST03012 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBRC93 similar to EST containing Alu repeat
7654	20722	34198	0.7	5.0E-03	T05124.1	EST_HUMAN	RC3-CT0255-031099-011-f07 CT0255 Homo sapiens cDNA
7774	20831		1.21	5.0E-03	AW654327.1	EST_HUMAN	Homo sapiens MASL1 mRNA, complete cds
7944	20994	34505	7.18	5.0E-03	AB018816.1	NT	RC8-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8415	21498	35027	0.81	5.0E-03	AW655907.1	EST_HUMAN	RC8-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8415	21498	35028	0.81	5.0E-03	AW655907.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8433	21514	35045	1.99	5.0E-03	P48982	SWISSPROT	Mouse complement receptor (CR2) mRNA, 3' end
8817	21890		5.83	5.0E-03	M01132.1	NT	Escherichia coli genomic DNA, (19.1 - 19.4 min)
9007	22086	35629	1.21	5.0E-03	D90723.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
9140	22219	35763	0.52	5.0E-03	M25090.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
10044	23082	36684	1.03	5.0E-03	L21710.1	NT	RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10176	23213	36805	0.74	5.0E-03	AW821888.1	EST_HUMAN	1146h10.s1 NCL_CGAP_P16 Homo sapiens cDNA clone IMAGE:995587
10360	23395	37008	0.66	5.0E-03	AA533143.1	EST_HUMAN	Homo sapiens PRO0471 protein (PRO0471), mRNA
10539	23574	37181	0.47	5.0E-03	7682567	NT	ag49c10.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126290 3'
10696	23729		0.47	5.0E-03	AA53281.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
10959	24040		4.79	5.0E-03	T19586.1	EST_HUMAN	xr59g05.x1 Soares_NHCCo_cervical_tumor Homo sapiens cDNA clone IMAGE:26980/40 3' similar to contains L1 L2 L1 repetitive element
11181	24250	37884	2.39	5.0E-03	AW170334.1	EST_HUMAN	xr59g05.x1 Soares_NHCCo_cervical_tumor Homo sapiens cDNA clone IMAGE:26980/40 3' similar to contains L1 L2 L1 repetitive element
11181	24250	37885	2.39	5.0E-03	AW170334.1	EST_HUMAN	contains L1 L2 L1 repetitive element
11297	24363	38004	1.76	5.0E-03	T49153.1	EST_HUMAN	y09e04.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70586 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11615	24666		3.41	5.0E-03	BE048055.1	EST_HUMAN	tz46c04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2281622 5'
12070	25051	38759	1.4	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12070	25051	38760	1.4	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12467	26144		11.86	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12616	25414		21.79	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12718	25478		2.03	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12760	25504		1.94	5.0E-03	AA456597.1	EST_HUMAN	z675a03.s1 Scores ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:809548 3' similar to SW:DXA2_MOUSE P14885 PROBABLE DIPHENOL OXIDASE A2 COMPONENT ;
12802	25936		5.96	5.0E-03	BF572332.1	EST_HUMAN	60207774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
13002	26851	31951	2.66	5.0E-03	AW449109.1	EST_HUMAN	U1H-B13-akf4-08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
242	13464	26493	1.54	4.0E-03	AW500156.1	EST_HUMAN	U1HF-BND-ako-h-04-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
331	13545	26575	1.75	4.0E-03	R46482.1	EST_HUMAN	y651e04.s1 Scores infant brain T1NB Homo sapiens cDNA clone IMAGE:35988 3'
456	13651	26689	1.36	4.0E-03	P54675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)
616	13805	26825	4.37	4.0E-03	AA836039.1	EST_HUMAN	cn75g12.s1 Scores infant brain T1NB Homo sapiens cDNA clone IMAGE:1562566 3'
900	14075	27142	1.65	4.0E-03	R46482.1	EST_HUMAN	y651e04.s1 Scores infant brain T1NB Homo sapiens cDNA clone IMAGE:35988 3'
934	14109		2.85	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-011 B T0333 Homo sapiens cDNA
1174	14337	27393	34.06	4.0E-03	AA059777.1	EST_HUMAN	2181a08.r1 Stralagene colon (#637204) Homo sapiens cDNA clone IMAGE:510998 5'
1196	14358	27417	1.83	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1331	14488	27556	1.48	4.0E-03	AA284374.1	EST_HUMAN	zs59a01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1783	14932	28026	2.69	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-imbic associated protein AT1-46 mRNA, complete cds
2075	15215	28334	17.33	4.0E-03	AA099777.1	EST_HUMAN	2181a08.r1 Stralagene colon (#637204) Homo sapiens cDNA clone IMAGE:510998 5'
2321	15463		2.06	4.0E-03	BE410555.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2352	15483	28615	1.53	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2639	15762	28875	1.95	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adreno-leukodystrophy protein >
2639	15762	28876	1.95	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adreno-leukodystrophy protein >
2755	15872	28980	2.97	4.0E-03	AJ27365.1	NT	CDM protein (CDM), adreno-leukodystrophy protein >
2755	15872	28981	2.97	4.0E-03	AJ27365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2761	15877	28984	0.97	4.0E-03	AL163284.2	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
3297	16471	29491	1.09	4.0E-03	BE154134.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3297	16471	29492	1.09	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-H08 HT0340 Homo sapiens cDNA
3619	16783	29798	0.83	4.0E-03	AW188426.1	EST_HUMAN	X9804.x1 NCI CGAP Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3619	16783	29798	0.83	4.0E-03	AW188426.1	EST_HUMAN	X9804.x1 NCI CGAP Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3714	16875	29880	0.84	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4021	16875	29880	0.85	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4040	17186	30207	0.72	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tg101) gene, complete cds
4102	17256		2.18	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
5339	18452	31420	0.98	4.0E-03	AW500547.1	EST_HUMAN	UHF-BND-ak-e-10-q-UJ.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
5390	18592	31564	1.58	4.0E-03	AF003658.1	NT	Drosophila melanogaster anan2D7 (anan2D7) mRNA, complete cds
5515	18713	31726	27.24	4.0E-03	AF169825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5914	19102	32416	3.1	4.0E-03	P04196	SWISSPROT	(HPRG)
5918	19106	32418	1.8	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELED TROPHOBLAST ANTIGEN PRECURSOR
6003	19188	32507	0.8	4.0E-03	AL133871.1	EST_HUMAN	DKFZp7611014.1 T761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7611014 5'
6209	19384		4.18	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
6363	19533	32892	0.97	4.0E-03	AW590572.1	EST_HUMAN	hg48c07.x1 NCI CGAP Co6 Homo sapiens cDNA clone IMAGE:2948852 3'
6439	19606	32989	1.78	4.0E-03	BE548453.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461864 5'
6809	19983	33397	1.07	4.0E-03	AA813222.1	EST_HUMAN	a32f11.s1 Soares_Jeslis_NHT Homo sapiens cDNA clone 1392045 3'
6914	20228	33682	1.41	4.0E-03	U76408.1	NT	Lycopodium obscurum knotted 3 protein (TKn3) mRNA, complete cds
7217	20082	33495	1.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7217	20082	33496	1.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7348	20428	33898	3.73	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7589	20660	34136	0.96	4.0E-03	AI681483.1	EST_HUMAN	h37g12.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7591	20662	34138	0.62	4.0E-03	BE670170.1	EST_HUMAN	7e31b02.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7693	20758		0.85	4.0E-03	X92109.1	NT	H. sapiens hglX gene
8128	21210	34791	0.57	4.0E-03	Q9T792	SWISSPROT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5)
8238	21320	34838	4.61	4.0E-03	AF11944.1	NT	(ADAMTS-5) (ADAM-TS5) (AGGREGANASE-2) (ADMP-2) (ADAM-TS 11)
8398	21479	35006	2	4.0E-03	7662067	NT	Dicotyledon discoidium AX4 development protein DG1122 (DG1122) gene, partial cds
8665	21745	35284	0.67	4.0E-03	AF139827.1	NT	Homo sapiens KIA00345 gene product (KIA00345), mRNA
8781	21840	35381	0.51	4.0E-03	Y12855.1	NT	Plasmodium falciparum replication factor C subunit 1 (rfc1) gene, complete cds
						NT	Homo sapiens P2X7 gene, exon 12 and 13
						NT	h49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element
8911	21990	35529	7.06	4.0E-03	AI553983.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
9080	22169		3.24	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C078
9100	22179	35723	3.76	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9825	22855	36447	0.47	4.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9825	22855	36448	0.47	4.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10131	23160	36766	0.63	4.0E-03	H30664.1	EST_HUMAN	yp42g12.r1 Soares retina N2bHR Homo sapiens cDNA clone IMAGE:190150 5'
10587	23622	37229	1.35	4.0E-03	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
11283	24349	37898	1.36	4.0E-03	4759101	NT	Homo sapiens splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot, Drosophila homolog) (SFRS8) mRNA
11394	24455	38117	5	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
12072	25053	38762	1.57	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
12434	26153	39153	5.84	4.0E-03	BE15173.1	EST_HUMAN	PM4-BN0138-180600-002-508 BN0138 Homo sapiens cDNA
12457	25321	39280	1.35	4.0E-03	BE28280.1	EST_HUMAN	801118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12541	25367		1.95	4.0E-03	AW504273.1	EST_HUMAN	UHF-BND-4p-g04-q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12814	25543		3.33	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3080622 5' element; contains element MER31 repetitive element ;
12858	26053		2.18	4.0E-03	AW614596.1	EST_HUMAN	h102c07.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR5 repetitive element ;
12871	25581		1.34	4.0E-03	AW819141.1	EST_HUMAN	RC3-ST0281-240400-015-f03 ST0281 Homo sapiens cDNA
13202	25784	31918	1.23	4.0E-03	11436955	NT	Homo sapiens Gib2-associated binder 2 (KIAA0571), mRNA
382	13580	26828	1.25	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
902	14077	27143	4.87	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1694	14846	27030	3.65	3.0E-03	AA458110.1	EST_HUMAN	nc73c05.s1 NCI_CGAP_P2 Homo sapiens cDNA clone IMAGE:782884 similar to contains Alu repetitive element;
2367	15498		6.37	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2368	15496	28624	1.14	3.0E-03	U48858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2368	15499	28625	1.14	3.0E-03	U48858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3056	16232		0.77	3.0E-03	Y06006.1	NT	Arabidopsis thaliana ipm1 gene
3152	16327	28338	3.55	3.0E-03	BE379286.1	EST_HUMAN	801237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609833 5'
3220	16394	29405	2.63	3.0E-03	AW802687.1	EST_HUMAN	IL2-UM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3504	16671	29681	2.16	3.0E-03	U34808.1	NT	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exon 1 and 2
3513	16679		7.5	3.0E-03	Y12500.1	NT	C.elegans samdc gene
4086	17241	30248	7.76	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4086	17241	30249	7.76	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4147	17289	30291	1.67	3.0E-03	AI792278.1	EST_HUMAN	ah04f09.y5 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4515	17654	30642	5.53	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4641	17777	30756	4.62	3.0E-03	AI536141.1	EST_HUMAN	xu8.P10.H3 conoform Homo sapiens cDNA 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4858	17991	30978	0.69	3.0E-03	AL119067.1	EST_HUMAN	DKFZp761B0712.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B0712.5
4955	18085	31061	2.06	3.0E-03	A1732754.1	EST_HUMAN	ab18a08.x6 Stragelene lung (#337210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4978	18107	31083	5.53	3.0E-03	BE787946.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5255	18375	31341	0.9	3.0E-03	4508414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5255	18375	31342	0.9	3.0E-03	4508414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5262	18381	31347	1.75	3.0E-03	A1193860.1	EST_HUMAN	q80b10.x1 Soares fetal lung_NbHL-19W Homo sapiens cDNA clone IMAGE:1748275 3' similar to SW:AP17_MOUSE Q00380 CLATHRIN COAT ASSEMBLY PROTEIN AP17 ;contains MSR1.12 MER22 repetitive element
5380	18582	31451	3.36	3.0E-03	8922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5673	18867	32153	1.09	3.0E-03	AJ249991.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5744	18937	32237	0.83	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6683	19841	33231	9.72	3.0E-03	AA456701.1	EST_HUMAN	aat310.11 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7168	20301	33744	0.75	3.0E-03	D37977.1	NT	Fugu rubripes mRNA for sodium channel alpha subunit, partial cds
7354	20433	33895	1.38	3.0E-03	AJ011419.1	NT	Kluyveromyces marxianus pop3 gene for purine-cytosine permease
7691	20756	34241	3.71	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
8124	21206	34726	0.9	3.0E-03	BF333058.1	EST_HUMAN	RC00-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8124	21206	34727	0.9	3.0E-03	BF333058.1	EST_HUMAN	RC00-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8350	21431	34955	1.4	3.0E-03	N62580.1	EST_HUMAN	zb27104.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3'
8490	21571	35108	0.47	3.0E-03	A186028.1	EST_HUMAN	w12409.x1 NCI_CGAP_U01 Homo sapiens cDNA clone IMAGE:2425841 3'
8510	21691		0.83	3.0E-03	M63498.1	NT	S.cerevisiae UGA35 gene, complete cds
8655	21735	35276	1.34	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8679	21759	35295	1.5	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
8788	21865		1.45	3.0E-03	Q9QMB1	SWISSPROT	NONSTRUCTURAL PROTEIN V
9192	22270		10.8	3.0E-03	AW613774.1	EST_HUMAN	h18010.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968131 3' similar to contains L.11 L.1 repetitive element
9245	22322	35866	4.28	3.0E-03	AL161599.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
9269	22345	35886	9.86	3.0E-03	A1016731.1	EST_HUMAN	ov03d12.x1 NCI_CGAP_K48 Homo sapiens cDNA clone IMAGE:1836247 3' similar to gb:X57138_mai
9280	22356	35906	0.53	3.0E-03	BF33078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9609	22664		0.78	3.0E-03	D90901.1	NT	602036980F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:418938 5'
9646	21089	34604	0.77	3.0E-03	BE154670.1	EST_HUMAN	Synchoecysis sp. PCC6803 complete genome, 3/27, 271600-402289
9836	22876		0.96	3.0E-03	P03355	SWISSPROT	PM3-HT0344-071299-003-007 HT0344 Homo sapiens cDNA POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9908	22948		6.51	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
10099	23137	38738	2.31	3.0E-03	P11389	SWISSPROT	RETROVIRUS-RELATED POL POLYPYRROLINE (CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
10200	23237	36827	1.44	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10344	23378	36990	3.89	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11085	24159		2.67	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11458	20756	34241	1.45	3.0E-03	AB021786.1	NT	Oryza sativa gene for bZIP protein, complete cds
11722	23908	37832	1.47	3.0E-03	P22631	SWISSPROT	SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)
11732	23918	37943	1.9	3.0E-03	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11770	24762	38457	2.52	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11770	24762	38458	2.52	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11849	24838	38532	1.36	3.0E-03	P11389	SWISSPROT	RETROVIRUS-RELATED POL POLYPYRROLINE (CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
12077	25057		1.46	3.0E-03	AW294812.1	EST_HUMAN	UI-H-B12-ant-d-06-0-UJ.st NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726842 3'
12199	25948		1.62	3.0E-03	AI525058.1	EST_HUMAN	promoter-5.E07.1 btkmuror Homo sapiens cDNA 5'
12235	25179	38346	1.24	3.0E-03	AA993154.1	EST_HUMAN	α77b10.st Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.13 MER26 repetitive element;
12266	26090		1.78	3.0E-03	AB003668.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
12481	25333	32057	1.23	3.0E-03	AJ298282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
528	13721	26746	0.87	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
528	13721	26747	0.87	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
808	16023	27624	11.88	2.0E-03	T70874.1	EST_HUMAN	yt15h03.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108341 5'
1394	14548	27624	2.08	2.0E-03	IM20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1397	14551	27626	1.42	2.0E-03	AA861605.1	EST_HUMAN	nu8601.st NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217593
1406	14660	27634	20.85	2.0E-03	AF284448.1	NT	Homo sapiens tumor-related protein DR02 (DRC2) gene, complete cds
1519	14672	27754	1.1	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1546	14698	27776	2.26	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1546	14698	27777	2.26	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1621	14773		6.17	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
1811	14960	28053	1.27	2.0E-03	AA450138.1	EST_HUMAN	z42af10.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1928	15071		1.09	2.0E-03	BE144808.1	EST_HUMAN	CM2-HT0183-061099-01B-003 HT0183 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2051	15192	28305	1.59	2.0E-03	AF302891.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2324	15456	28588	0.97	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2847	15770		4.93	2.0E-03	AW137782.1	EST_HUMAN	UI-H-B11-adj-g-10-0-UI.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3503	16670	29680	4.92	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares fetal_fetus_Nb2HF8 9w Homo sapiens cDNA clone IMAGE:789114 5'
3510	16678	29686	0.96	2.0E-03	BF588955.1	EST_HUMAN	6021836071 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3756	16917	29919	5.48	2.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
4082	17218	30228	0.62	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4229	17378	30364	2.39	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP62; COAT PROTEIN GP36]
4290	17435	30423	1.02	2.0E-03	AA176693.1	EST_HUMAN	zp13h01.r1 Stratagene fetal telina 937202 Homo sapiens cDNA clone IMAGE:609361 5'
4336	17479		13.93	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4632	17870		1.99	2.0E-03	L35079.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4547	17885		1.22	2.0E-03	AW297380.1	EST_HUMAN	UI-H-BW0-adj-g-03-0-UI.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2730413 3'
4551	17889	30670	1.05	2.0E-03	A064746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4668	17803	30780	2.11	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4668	17803	30791	2.11	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4828	17961	30949	1.02	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4832	17965		1.57	2.0E-03	R87773.1	EST_HUMAN	yc45602.s1 Soares adult brain N2b4fB55Y Homo sapiens cDNA clone IMAGE:180850 3'
4982	18091	31067	1.07	2.0E-03	P11000	SWISSPROT	WALL-ASSOCIATED PROTEIN PRECURSOR
5132	18257	31223	0.84	2.0E-03	AF003528.1	NT	Homo sapiens X-linked arylidic beta-dermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5604	18799	31849	1.57	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5745	25810	32238	1.83	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5828	19019	32325	2.08	2.0E-03	U63711.1	NT	Xenopus laevis xefilin mRNA, complete cds
6236	19411	32758	3.83	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6236	19411	32759	3.93	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6476	19643	33004	2.28	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XP II) (CA-XI)
6476	19643	33005	2.28	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XP II) (CA-XI)
6478	19845	33007	7.55	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6514	19679	33049	2.16	2.0E-03	Q9UKP4	SWISSPROT	ADAMTS 7 PRECURSOR (A-Disintegrin and Metalloproteinase with Thrombospondin Motifs 7) (ADAMTS-7) (ADAM-TS7)
6515	19680	33050	0.75	2.0E-03	AV709075.1	EST_HUMAN	AV709075 ADC Homo sapiens cDNA clone ADCAEF09 5'
6544	19706	33082	1.45	2.0E-03	X94451.1	NT	L. esculentum mRNA for lysyl-tRNA synthetase (LysRS)

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6736	19882		1.36	2.0E-03	AI991089.1	EST_HUMAN	wu36h09.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2622177 3' similar to SW_RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29; contains element MSRI repetitive element;
6775	19930	33326	0.7	2.0E-03	AA677831.1	EST_HUMAN	z13a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430692 3'
7098	18525	31517	1.35	2.0E-03	AS038502.1	NT	Caenorhabditis elegans mRNA for glectin LEC-11, complete cds
7231	20136	33564	3.3	2.0E-03	BE057886.1	EST_HUMAN	CM4-BT0366-061289-054-d01 BT0366 Homo sapiens cDNA
7294	20376	33683	0.55	2.0E-03	AI298883.1	EST_HUMAN	qm59a11.x1 NCJ_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896885 3'
7444	20521	33994	0.8	2.0E-03	T86588.1	EST_HUMAN	W77g10.r1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:114306 5'
7794	20860	34342	1.41	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
							h37b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834035 3' similar to TR:Q60976
8241	21323	34840	2.97	2.0E-03	AW592004.1	EST_HUMAN	Q60976_JERKY.;
8412	21493	35023	5.49	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares_melanocyte_2N5b1M_Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2.L1 repetitive element;
8412	21493	35024	5.49	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares_melanocyte_2N5b1M_Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2.L1 repetitive element;
8459	21540	35069	0.84	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C6G9.05 IN CHROMOSOME 1
8481	21562	35037	1.09	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8536	21617	35153	1.04	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8536	21617	35154	1.04	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8561	21642	35181	1.03	2.0E-03	AU136679.1	EST_HUMAN	AU136679 PLACE1 Homo sapiens cDNA clone PLACE104839 5'
8614	21694		0.9	2.0E-03	AJ400877.1	NT	Homo sapiens ASOL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
9396	19018	32323	0.79	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9396	19018	32324	0.79	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9441	22515	36079	1.07	2.0E-03	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9726	22791	36362	0.71	2.0E-03	H50632.1	EST_HUMAN	yp89a09.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:194296 3'
9726	22791	36363	0.71	2.0E-03	H50632.1	EST_HUMAN	yp89a09.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:194296 3'
							TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEIN) (J1) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
9758	22696	36264	3.33	2.0E-03	P24821	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9868	22908	36493	1.22	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9868	22908	36494	1.22	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9924	22964	36552	0.6	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9924	22834	36553	0.6	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
10119	23157	36755	0.96	2.0E-03	AW884269.1	EST_HUMAN	QV3-OT0084-060400-144-e01 OT0084 Homo sapiens cDNA
10248	23293		6.26	2.0E-03	AA251376.1	EST_HUMAN	Zs10a06.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684764 3'
10828	23682	37270	0.49	2.0E-03	BF367386.1	EST_HUMAN	MR2-IGN030-140900-001-e05 GN0030 Homo sapiens cDNA
11265	24334		2.14	2.0E-03	M86524.1	NT	Human dystrophin gene
11778	20850	34342	3.79	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11836	24825		2.36	2.0E-03	BF330908.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11844	24833	38528	9.64	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
12180	25140		3.37	2.0E-03	A1625745.1	EST_HUMAN	ty65h03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE
12198	25155	38833	4.31	2.0E-03	AF157516.2	NT	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ; Homo sapiens SEL1L (SEL1L) gene, partial cds
12222	25171	38836	1.71	2.0E-03	A084325.1	EST_HUMAN	oy43g08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668834 3' similar to TR:P97535 P97535 PS-PLA1 PRECURSOR ;
12245	18497		4.98	2.0E-03	AJ245167.1	NT	Camelus dromedarius cwhp19 gene for immunoglobulin heavy chain variable region
12462	26140		4	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGX005 5'
12581	26383	32039	1.29	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
12897	25594		1.38	2.0E-03	AF128756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, ApoM, BAT3, BAT2, AIF-1, C7, LST-1, LTB, TNF, and LTA genes, complete cds
13090	25927		2.46	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGX005 5'
452	13648	26684	1.38	1.0E-03	H96471.1	EST_HUMAN	y98c08.r1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
852	14029	27091	1.55	1.0E-03	A1720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENYOYL-COA HYDRATASE ;
852	14029	27092	1.55	1.0E-03	A1720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENYOYL-COA HYDRATASE ;
1119	14284	27339	2.61	1.0E-03	A1865788.1	EST_HUMAN	wk86a06.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
1139	14304	27360	1.51	1.0E-03	A1954572.1	EST_HUMAN	wx33e10.x1 NCL CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
1192	14354	27412	0.85	1.0E-03	A1692816.1	EST_HUMAN	wd86a01.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
2084	16224	28346	3.42	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMWI)
2222	15356	28486	9.52	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3044	16220	29241	1.37	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
3280	16434	28451	2.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3260	16434	29452	2.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3374	16546	29560	0.75	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
3632	16798	29813	0.94	1.0E-03	U68081.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3632	16798	29814	0.94	1.0E-03	U68081.1	NT	Human MUC2 gene, promoter region
3755	16916		1.43	1.0E-03	AB044400.1	NT	Human MUC2 gene, promoter region
4034	17190	30200	0.98	1.0E-03	AW170552.1	EST_HUMAN	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4044	17200	30211	0.91	1.0E-03	Z49648.1	NT	contains TAR1.1 TAR1 repetitive element ;
4556	17694	30673	2.34	1.0E-03	BE939162.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR149w
4598	17735	30715	4.99	1.0E-03	BE246536.1	EST_HUMAN	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4785	17920	30908	0.81	1.0E-03	U29449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4945	18075	31050	2.54	1.0E-03	A1073485.1	EST_HUMAN	cy45c04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4945	18075	31051	2.54	1.0E-03	A1073485.1	EST_HUMAN	cy45c04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4946	18076		6	1.0E-03	BE164087.1	EST_HUMAN	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5188	18310	31276	15.5	1.0E-03	O46409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5324	18437	31407	4.73	1.0E-03	BE219340.1	EST_HUMAN	hV3102.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178955 3'
5423	18624	31600	2	1.0E-03	AA280951.1	EST_HUMAN	zs44101.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5518	18716	31730	3.57	1.0E-03	AJ009345.1	NT	Homo sapiens KVLQ11 gene
5572	18768	31809	1.64	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5572	18768	31810	1.94	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5680	18884	32176	0.95	1.0E-03	BE786491.1	EST_HUMAN	601589841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5'
5696	18890	32181	1.77	1.0E-03	Q02398	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5751	18943	32244	0.8	1.0E-03	N41974.1	EST_HUMAN	yy07106.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element ;
5751	18943	32245	0.8	1.0E-03	N41974.1	EST_HUMAN	yy07106.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element ;
6033	19216		0.58	1.0E-03	BF541639.1	EST_HUMAN	602088042F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068907 5'
6144	19322		2.75	1.0E-03	X07699.1	NT	Mouse nucleolin gene
6184	19360	32708	0.85	1.0E-03	BE663939.2	EST_HUMAN	601657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3675638 3'
6321	19493		8.77	1.0E-03	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6464	19631	32992	1.11	1.0E-03	T87761.1	EST_HUMAN	yc93a1.1.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:115712 5'
6539	19702		1.68	1.0E-03	AW902585.1	EST_HUMAN	QY3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6895	20046	33455	1.41	1.0E-03	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric and
7302	20384	33843	2.81	1.0E-03	D16826.1	NT	Human gene for fourth somatostatin receptor subtype
7656	20724		1.12	1.0E-03	AJ228042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
7817	20872	34370	1.98	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7885	20937	34443	3.44	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7934	20984	34492	0.79	1.0E-03	BE880044.1	EST_HUMAN	601491081F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893276 5'
8073	21155	34674	0.66	1.0E-03	AF274981.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
8136	21218	34739	5.02	1.0E-03	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
8337	21418	34944	1.95	1.0E-03	AA122720.1	EST_HUMAN	zK97c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490788 3' similar to contains L1.1 L1 repetitive element;
8438	21519	35048	2.35	1.0E-03	AF153980.1	NT	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8625	21705	35241	0.75	1.0E-03	U29397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
9144	22223		1.48	1.0E-03	Y11204.1	NT	V. carteri gene encoding valvexoplin
9170	22248	35791	0.65	1.0E-03	AW840353.1	EST_HUMAN	CM3-LT0079-170200-092-e07 LT0079 Homo sapiens cDNA
9281	22357		0.65	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
9319	22395	35947	3.89	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9319	22395	35948	3.89	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9796	22836		0.47	1.0E-03	AJ247482.1	EST_HUMAN	qf56d01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1848673 3' similar to gbtM97388 TATA-BINDING PROTEIN-ASSOCIATED PHOSPHOPROTEIN (HUMAN);
9807	22847	36424	2.06	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aga1A) gene, complete cds
9807	22847	36425	2.06	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aga1A) gene, complete cds
10025	23063	36560	0.88	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10366	23401	37012	9.37	1.0E-03	AF003528.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
10372	23407		0.75	1.0E-03	AF087485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10522	23557	37165	1.08	1.0E-03	AJ024350.1	EST_HUMAN	ov7508.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39.b1
10823	23858	37478	0.5	1.0E-03	AE004782.1	NT	MER39 MER39 repetitive element;
10823	23858	37479	0.5	1.0E-03	AE004782.1	NT	Pseudomonas aeruginosa PAO1, section 323 of 529 of the complete genome
							Pseudomonas aeruginosa PAO1, section 323 of 529 of the complete genome

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10830	23863		0.53	1.0E-03	AA706202.1	EST_HUMAN	ag93f12.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:1142063 3' similar to contains Alu repetitive element;
10902	23866	37617	2.01	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0278-181088-011-a09 CT0279 Homo sapiens cDNA
10902	23869	37618	2.01	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0278-181088-011-a09 CT0279 Homo sapiens cDNA
10969	24068	37702	2.46	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
11062	24138		2.03	1.0E-03	AI583947.1	EST_HUMAN	tf73e12.x1 NCL_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q28198 Q28195 PVA1 GENE.:
11425	24486		2.63	1.0E-03	AV759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
11858	24846	38543	2.17	1.0E-03	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
11858	24846	38544	2.17	1.0E-03	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
11924	24910	38611	1.53	1.0E-03	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY)
11924	24910	38612	1.53	1.0E-03	P13002	SWISSPROT	(TRANSCRIPTION FACTOR NTF-1)
12176	25136	38831	5.51	1.0E-03	BE894488.1	EST_HUMAN	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY)
12679	26118		7.37	1.0E-03	AI347355.1	EST_HUMAN	601468878F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12812	26142	31551	3.83	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
12889	25590		1.17	1.0E-03	11465934	NT	Nicotiana tabacum chloroplast complete genome
5327	18440	31409	0.7	9.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5789	18937		2.08	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6615	19775	33166	0.88	9.0E-04	AJ008345.1	NT	Homo sapiens KVLQ11 gene
9843	22883		1.27	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
1517	14670		1.46	9.0E-04	AB037203.1	NT	Glycerhiza glabra GgBAS1 mRNA for beta-amylin synthase, complete cds
4296	17439		1.07	8.0E-04	X06469.1	NT	X. laevis mRNA for C4SR protein
4887	18017	31002	4.4	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11412	24473		2.5	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11576	24631		2.59	8.0E-04	AA777084.1	EST_HUMAN	224c10.s1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:377874 3'
1874	15018	28127	1.87	8.0E-04	AI571098.1	EST_HUMAN	b95a08.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
2472	15599	28724	1.11	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' and
2778	15894	29004	1.45	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
3363	18526	29540	1.33	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
			1.4	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6221	19398	32745	0.93	7.0E-04	AA516212.1	EST_HUMAN	ng65g12.s1 NCI CGAP_Lip2 Homo sapiens cDNA clone IMAGE:339718 similar to contains L1 b3 L1 L1 repetitive element;
6642	19801		2.33	7.0E-04	A1769331.1	EST_HUMAN	wg56109.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
7376	20455		0.72	7.0E-04	AK024446.1	NT	Homo sapiens mRNA for FLJ00335 protein, partial cds
10008	23046	36639	0.65	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10008	23046	36640	0.65	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11865	24853		1.7	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
11883	24881	38578	3.76	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12723	25481		9.28	7.0E-04	BE077941.1	EST_HUMAN	CM1-BT0814-110300-142-b12 BT0814 Homo sapiens cDNA
13001	25650		2.68	7.0E-04	R17336.1	EST_HUMAN	y913c06.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32298 5'
13038	25682		5.43	7.0E-04	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
2760	15876		0.97	6.0E-04	BF341380.1	EST_HUMAN	602013339F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4146297 5'
4069	17225	30232	1.64	6.0E-04	A1862525.1	EST_HUMAN	w115811.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
4201	17350	30341	0.65	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4201	17350	30342	0.65	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4301	17444	30430	3.91	6.0E-04	U45883.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
4565	17703	30683	0.89	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-009 HT0560 Homo sapiens cDNA
4565	17703	30684	0.89	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-009 HT0560 Homo sapiens cDNA
8050	21133		4.58	6.0E-04	P46408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
8205	21287		0.51	6.0E-04	H92947.1	EST_HUMAN	y94c11.s1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231956 3' similar to contains LOR1 repetitive element;
10185	23222		3.26	6.0E-04	AL048507.2	EST_HUMAN	DKFZp568M2024_r1 588 (synonym: huter1) Homo sapiens cDNA clone DKFZp568M2024
10215	23251		0.53	6.0E-04	A1858286.1	EST_HUMAN	w135g02.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2426830 3'
10285	23320	36922	2.28	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
10547	23582		0.84	6.0E-04	AF287478.1	NT	Lytechinus variegatus embryonic blastocoel extracellular matrix protein precursor (ECM3) mRNA, complete cds
11774	24766	38462	2.07	6.0E-04	AJ228042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11866	24854	38549	2.47	6.0E-04	AW013647.1	EST_HUMAN	UHH-B10-aa6-09-0-UI.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
11837	24923		1.62	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
12363	26007		3.31	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0269-261189-012-088 HT0269 Homo sapiens cDNA
13226	25797		14.14	6.0E-04	A1817088.1	EST_HUMAN	w176g11.x1 NCI CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element;
668	13654	26982	7.88	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF92)

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1531	14684		2.03	5.0E-04	AW861844.1	EST_HUMAN	QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA
3500	16667	29677	1.6	5.0E-04	AA548931.1	EST_HUMAN	nk27e11.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element
3809	16969	28972	0.94	5.0E-04	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5589	18764	31830	2.51	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8765	19921	33317	7.06	5.0E-04	AA156080.1	EST_HUMAN	zp33b08.r1 Stragene colon (#937204) Homo sapiens cDNA clone IMAGE:589863 5'
7534	20607	34082	9.01	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
							qdl1306.x1 Soares_placenta_8to9weeks_2NHP80c9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602.cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element
8143	21225	34745	5.58	5.0E-04	AI188382.1	EST_HUMAN	cb386d02.s1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1339228 3' similar to contains element MER22 repetitive element
8488	21679	35115	0.95	5.0E-04	AA814519.1	EST_HUMAN	af55h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9477	22534	36098	1.87	5.0E-04	AA846545.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
9671	22713	36281	0.58	5.0E-04	N83765.1	EST_HUMAN	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYL4 PRECURSOR
9718	22783	36354	0.84	5.0E-04	P29128	SWISSPROT	xs06e02.x1 NCI_CGAP_Ki611 Homo sapiens cDNA clone IMAGE:2788858 3'
9809	22849	36428	4.78	5.0E-04	AW270938.1	EST_HUMAN	Human familial Alzheimer's disease (STM2) gene, complete cds
10484	23519		0.8	5.0E-04	U50871.1	NT	DKFZp686M2024_r1 588 (synonym: hule1) Homo sapiens cDNA clone DKFZp586M2024
11220	24289		1.9	5.0E-04	AL048607.2	EST_HUMAN	
12012	18784	31830	15	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12301	25936		2.39	5.0E-04	AA568513.1	EST_HUMAN	nf15h02.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:913875
12872	25961		1.33	5.0E-04	U63834.1	NT	Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cds
403	13600		0.75	4.0E-04	BF241482.1	EST_HUMAN	601876534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
660	13874	26907	1.36	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
870	14046	27111	1.55	4.0E-04	AI720293.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
870	14046	27112	1.55	4.0E-04	AI720293.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENYOL-COA HYDRATASE ;
1493	14646	27728	5.58	4.0E-04	AW793386.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
2148	15284	28410	1.87	4.0E-04	AL163278.2	NT	RC3-CT0254-130100-023-r01 CT0254 Homo sapiens cDNA
2202	15337		1.1	4.0E-04	AL046704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
							DKFZp434D059_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2691	15811	28927	2.04	4.0E-04	O96615	SWISSPROT	SERPIN-2 (SILK GUM PROTEIN 2)
3233	16407	29420	2.78	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3397	16597	29583	0.60	4.0E-04	AF20263.1	EST_HUMAN	as70608.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
3443	16611	29629	0.6	4.0E-04	AF696624.1	EST_HUMAN	Q13825 AL-BINDING PROTEIN ENOYL-COA HYDRATASE.1
4443	17583	30561	3.24	4.0E-04	AA578331.1	EST_HUMAN	AV636624 GKC Homo sapiens cDNA clone GKCFFH07 5'
4443	17583	30562	3.24	4.0E-04	AA578331.1	EST_HUMAN	nt10a10.s1 NCL_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL
4659	17795	30781	2.33	4.0E-04	AA088324.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5199	18320	31289	3.62	4.0E-04	BE560660.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
7418	20496	33965	1.55	4.0E-04	P48442	SWISSPROT	zn61c08.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562670 3'
7706	20770		0.95	4.0E-04	AL161568.2	NT	601345895F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3878910 5'
7896	20948	34456	0.8	4.0E-04	AU122079.1	EST_HUMAN	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL
8733	21813	35348	3.64	4.0E-04	BF240712.1	EST_HUMAN	CALCIUM-SENSING RECEPTOR
8741	21820	35354	1.68	4.0E-04	N25507.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 66
9892	22932	36515	3.37	4.0E-04	A025699.1	EST_HUMAN	AU122079 MAMMA1 Homo sapiens cDNA clone MAMMA1001620 5'
10045	23083		1.12	4.0E-04	AF022855.1	NT	601876985F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4099700 5'
12691	25908		1.56	4.0E-04	AF254822.1	NT	yc89612.1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:264142 5'
160	13365	26415	3.21	3.0E-04	AL119426.1	EST_HUMAN	ov67h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3'
200	13423	26454	1.7	3.0E-04	P49259	SWISSPROT	Mus musculus neuropilin-2(al7) mRNA, alternatively spliced, complete cds
803	14078	27144	1.63	3.0E-04	U83991.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
1886	15030	28137	1.7	3.0E-04	A1282100.1	EST_HUMAN	DKFZp761J22T11 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5'
1901	15044		0.97	3.0E-04	A1399674.1	EST_HUMAN	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
3383	16554	29568	4.35	3.0E-04	P25147	SWISSPROT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
4071	17227	30234	4.94	3.0E-04	P49448	SWISSPROT	q228d03.y1 NCL_CGAP_Kkl11 Homo sapiens cDNA clone IMAGE:2028197 5'
4167	17317		1.36	3.0E-04	AJ271735.1	NT	nt23a02.x1 NCL_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2119082 3'
4205	17354		1.06	3.0E-04	BE140603.1	EST_HUMAN	INTERNALIN B PRECURSOR
4635	17771		1.16	3.0E-04	BE148546.1	EST_HUMAN	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4937	18067		5.2	3.0E-04	BE153778.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
5004	18133	31107	0.65	3.0E-04	AW937723.1	EST_HUMAN	RCO-HT0014-310599-028 HT0014 Homo sapiens cDNA
6271	19445		5.58	3.0E-04	AL163281.2	NT	MP0-HT10241-030200-008-c01 HT0241 Homo sapiens cDNA
6959	20187	33611	1.54	3.0E-04	AL163278.2	NT	PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
							QV3-DT0045-221299-048-d09 DT0045 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C081
							Homo sapiens chromosome 21 segment HS21C078

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7130	18556	31471	0.87	3.0E-04	AW893991.1	EST_HUMAN	RC4-NN0027-060400-011-b08 NN0027 Homo sapiens cDNA
7765	20824	34316	0.73	3.0E-04	P23488	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8454	21535	35055	2.16	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
10124	23162	36790	1.26	3.0E-04	AA454055.1	EST_HUMAN	zx48408.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:785471 5' similar to gb:M62762
10381	23416	37025	0.46	3.0E-04	AI992139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN); wt75a11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:2513276 3'
10676	23710	37318	1.96	3.0E-04	AA781201.1	EST_HUMAN	ai24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); nc38e04.t1 NCI CGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.L2 L1 repetitive element;
12249	26164	31555	2.39	3.0E-04	AA228301.1	EST_HUMAN	Homo sapiens mRNA for KIAA0749 protein, partial cds
12646	25987	31799	2.54	3.0E-04	AB018282.1	NT	DKFZp547L185.t1 547 (synonym: hifar1) Homo sapiens cDNA clone DKFZp547L185 5'
13114	25727		4.81	3.0E-04	AL134483.1	EST_HUMAN	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
180	13403	26432	1.33	2.0E-04	AF217796.1	NT	Human dystrophin gene
491	13685	26719	2.67	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
930	14105	27168	5.02	2.0E-04	M86524.1	NT	Human dystrophin gene
930	14105	27168	5.02	2.0E-04	M86524.1	NT	Human dystrophin gene
1206	14368		2.78	2.0E-04	AI286021.1	EST_HUMAN	qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
1213	14374		2.6	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1879	15023		1.71	2.0E-04	AF224268.1	NT	Mus musculus 5' flanking region of Plb3 gene
2257	15390		1.21	2.0E-04	AA478980.1	EST_HUMAN	zx38b05.s1 Soares ovary tumor NbhOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2641	15764	28878	6.42	2.0E-04	U66061.1	NT	Human germ-line T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV16S1, TCRBV15S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
3052	16228	29248	1.23	2.0E-04	AI124529.1	EST_HUMAN	anf58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3415	16584	29500	0.82	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3622	16698	29697	2.58	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0036-070500-194-b07 BT0636 Homo sapiens cDNA
4022	17178	30187	0.98	2.0E-04	AW978441.1	EST_HUMAN	EST390950 IMAGE resequences, MAGP Homo sapiens cDNA
4261	17406		5.5	2.0E-04	U01029.1	NT	Phasodius vulgaris nitrate reductase (PNR2) gene, complete cds
4791	17926	30914	1.76	2.0E-04	H96265.1	EST_HUMAN	yu01e11.t1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4791	17926	30915	1.76	2.0E-04	H96265.1	EST_HUMAN	yu01e11.t1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4916	18046		1.22	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5171	18293	31258	1.47	2.0E-04	AB037997.1	NT	Danio rerio hagaromo gene, exons 1 to 6, partial cds
5216	18337	31310	0.92	2.0E-04	AF037019.1	NT	Dicotyledon discoidium intercalin (ebpD) gene, complete cds
5631	18653	32138	1.11	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLC010.3'
5674	18663	32154	1.83	2.0E-04	AI690862.1	EST_HUMAN	IQ03b11.x1 NCI_CGAP_U3 Homo sapiens cDNA clone IMAGE:2207709.3'
5868	19059	32365	0.93	2.0E-04	AA296852.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' and similar to EST containing O family repeat
6088	19250	32578	0.92	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6388	19538	32897	1.01	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7378	20457		2.57	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798.5'
7478	20553		0.84	2.0E-04	AW860963.1	EST_HUMAN	QV0-CT0387-180300-167-a10 CT0387 Homo sapiens cDNA
7798	20854		13.66	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7808	20863	34357	1.45	2.0E-04	P64296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
8142	21224	34743	1.02	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8142	21224	34744	1.02	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8479	21560	35094	1.24	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL4 genes, complete cds)
8479	21560	35095	1.24	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL4 genes, complete cds)
8783	21842	35383	2.14	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
8941	22020	35561	0.67	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
9535	22800	36173	0.58	2.0E-04	AA725700.1	EST_HUMAN	al22a12.s1 Soares testis NHT Homo sapiens cDNA clone 1343518.3'
9619	22674	36244	0.47	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLOGF26.1
10180	23217	36808	1.16	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0254-151099-011-b05 HT0254 Homo sapiens cDNA
10223	23259	36847	2.06	2.0E-04	AA405777.1	EST_HUMAN	zu65c11.1 Soares testis NHT Homo sapiens cDNA clone IMAGE:742864.5'
11088	24162	37798	3.98	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA01.5'
11585	24638	38318	2.68	2.0E-04	AI440282.1	EST_HUMAN	tt01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269.3' similar to contains Alu repetitive element
11710	24750	38443	2.30	2.0E-04	AW136740.1	EST_HUMAN	UHH-B11-adm-c-04-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190.3'
11859	24847		2.71	2.0E-04	BE066781.1	EST_HUMAN	RC2-BT0317-150200-011-h04 BT0317 Homo sapiens cDNA
12108	25086	38790	32.04	2.0E-04	P21733	SWISSPROT	HYPOTHETICAL 29.1 KD PROTEIN IN CRYB1 5'REGION (ORF2)
12121	25101	38806	2.05	2.0E-04	L19248.1	NT	Caenorhabditis elegans homeodomain protein (lin-39) mRNA, complete cds
13191	26179		1.29	2.0E-04	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
788	13987	27018	0.98	1.0E-04	H99646.1	EST_HUMAN	yx26c09.s1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.1 L1 repetitive element;
1100	14285	27322	2.86	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
1138	14303	27358	3.79	1.0E-04	AW013947.1	EST_HUMAN	UJ-H-B10-aab-e-09-Q.U1 s1 NCI CGAP Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1138	14303	27358	3.79	1.0E-04	AW013947.1	EST_HUMAN	UJ-H-B10-aab-e-09-Q.U1 s1 NCI CGAP Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1363	14517		2.65	1.0E-04	U62918.1	NT	Arginella anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1657	14810	27894	4.23	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphatibosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1657	14810	27895	4.23	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphatibosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1909	15052	28164	2.02	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY38
2752	15869	28978	1.08	1.0E-04	BE218833.1	EST_HUMAN	hva5c08.x1 NCI CGAP L124 Homo sapiens cDNA clone IMAGE:3176366 3'
2752	15869	28979	1.08	1.0E-04	BE218833.1	EST_HUMAN	hva5c08.x1 NCI CGAP L124 Homo sapiens cDNA clone IMAGE:3176366 3'
3356	16528	29543	1.18	1.0E-04	Q82203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 92 (SAP 92) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A68)
3829	16989	29992	0.88	1.0E-04	A1440282.1	EST_HUMAN	tp0111.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
4171	17321	30314	1.72	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4192	17342	30335	1.12	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBB04 3'
5207	18328	31298	1.24	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5207	18328	31299	1.24	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5980	19185	32485	1.35	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6569	19731	33109	0.95	1.0E-04	AA177111.1	EST_HUMAN	hnd2e12.s1 NCI CGAP Pr3 Homo sapiens cDNA clone IMAGE:252
6977	20205	33883	0.88	1.0E-04	AA564561.1	EST_HUMAN	h25a04.s1 NCI CGAP AA1 Homo sapiens cDNA clone IMAGE:993486 3' similar to gb.M97252
7336	20417	33879	12.52	1.0E-04	A1251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN) contains Alu repetitive element;
7744	20417	33879	13.49	1.0E-04	A1251980.1	EST_HUMAN	q157d10.x1 NCI CGAP O32 Homo sapiens cDNA clone IMAGE:1985683 3'
8184	21266	34789	1.02	1.0E-04	AA630453.1	EST_HUMAN	q157d10.x1 NCI CGAP O32 Homo sapiens cDNA clone IMAGE:1985683 3'
9538	22603	36175	2.75	1.0E-04	A1806220.1	EST_HUMAN	ab94g08.s1 Straglene tung (#937210) Homo sapiens cDNA clone IMAGE:954664 3'
9548	22613	36182	1.54	1.0E-04	O68969	SWISSPROT	wf26d08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9625	22880		0.76	1.0E-04	T77153.1	EST_HUMAN	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9846	22886	35466	1.06	1.0E-04	10863876	NT	y472c08.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 5'
							Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10382	23417		3.59	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10420	23455	37060	1.12	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10775	23808	37431	0.46	1.0E-04	P51786	SWISSPROT	ZINC FINGER PROTEIN 157
11622	24673		2.3	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11950	24636	38637	1.81	1.0E-04	AB032968.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
11991	24976	38980	1.94	1.0E-04	AW269061.1	EST_HUMAN	xx49g12.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2816518 3'
12024	25008	38709	1.57	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12024	25008	38710	1.57	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
716	13898	26336	2.44	9.0E-05	AA718933.1	EST_HUMAN	af45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1282468 3'
4198	17346	30338	1.13	9.0E-05	AI762209.1	EST_HUMAN	wf54c11.x1 NCL_CGAP_Cot6 Homo sapiens cDNA clone IMAGE:2394068 3' similar to contains MER6.t1
6094	19266	32595	1.37	9.0E-05	Q07016	SWISSPROT	MER6 repetitive element;
7751	20811	34301	2.44	9.0E-05	AW204958.1	EST_HUMAN	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7751	20811	34302	2.44	9.0E-05	AW204958.1	EST_HUMAN	UI-H-B1-aer-d-05-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9877	22639		3.03	9.0E-05	D85608.1	NT	UI-H-B1-aer-d-05-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9879	22841	36211	3.3	9.0E-05	AF120982.1	NT	Homo sapiens gene for cholesterylkinin type-A receptor, complete cds
11402	24463	38127	2.31	9.0E-05	AW073078.1	EST_HUMAN	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11518	24574	38251	1.61	9.0E-05	AI287878.1	EST_HUMAN	xa34g05.x1 NCL_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1
11916	19266	32595	3.41	9.0E-05	Q07016	SWISSPROT	repetitive element;
							qv2306.x1 NCL_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
							MIR repetitive element;
							PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12469	26016		3.37	9.0E-05	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G8b, G8c, G8d, G8e, G8f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, TC7, LST-1, LTB, TNF, and LTA genes, complete cds
844	14022	27080	1.22	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
887	14063		3.11	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
3015	18191		1.01	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4604	17741	30719	0.78	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
8948	22027	35568	0.51	8.0E-05	Y11668.1	NT	Mus musculus gene for hexokinase II, exon 1 (and joined CDS)
11419	24480	38146	2.58	8.0E-05	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
13169	26011		1.78	8.0E-05	AA279333.1	EST_HUMAN	zs8810.1.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu
357	13568	26596	3.16	7.0E-05	AW847445.1	EST_HUMAN	repetitive element; contains element MSR1 repetitive element;
357	13568	26597	3.16	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220699-011-E04 CT0208 Homo sapiens cDNA
							RC3-CT0208-220699-011-E04 CT0208 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
561	13773	26793	1.14	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
561	13773	26794	1.14	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1080	14246	27303	1.07	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2763	15899	29008	5.16	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3227	16401	29413	3.9	7.0E-05	AB009090.1	NT	Dictyostelium discoideum gene for TRFA, complete cds
4168	17318		0.85	7.0E-05	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4492	17832	30614	1.88	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5041	18169	31144	0.68	7.0E-05	9845300	NT	Rat cytomegalovirus Maastricht, complete genome
8420	21501	35033	1.24	7.0E-05	AA503582.1	EST_HUMAN	h33g01.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:368096 3'
9753	22691	36261	3.6	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBED60
11430	24491		5.87	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2083	15223	28344	1.59	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2083	15223	28345	1.59	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2655	15778	28892	1.56	6.0E-05	AI655241.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:2308631 3' similar to gb.J03250 DNA TOPOISOMERASE I (HUMAN);
2876	13880	26912	2.54	6.0E-05	AF033630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
6034	19217	32538	3.26	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6034	19217	32539	3.26	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
9533	19697	33070	1.5	6.0E-05	N72829.1	EST_HUMAN	y50g11.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:249212 5'
7073	20126	33542	0.74	6.0E-05	AA897680.1	EST_HUMAN	q380a03.s1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1504588 3'
8276	21358	34876	1.03	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
8276	21358	34877	1.03	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
8638	21718	35255	0.62	6.0E-05	AA150482.1	EST_HUMAN	208c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MER28 repetitive element ;
8643	21723	35260	2.92	6.0E-05	AW896829.1	EST_HUMAN	PM4-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA
8780	21859	35402	2.93	6.0E-05	Q60401	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR
9452	22588	36134	1.59	6.0E-05	P08807	SWISSPROT	CAB-BINDING PROTEIN PRECURSOR (C4BP)
9452	22588	36135	1.59	6.0E-05	P08807	SWISSPROT	CAB-BINDING PROTEIN PRECURSOR (C4BP)
9721	22786	36357	1.77	6.0E-05	T94149.1	EST_HUMAN	y28c12.11 Strategene lung (8937210) Homo sapiens cDNA clone IMAGE:119062 5'
9922	22962	36550	0.69	6.0E-05	AW627986.1	EST_HUMAN	hi37a03.s1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2874444 3'
10987	24066	37701	2.42	6.0E-05	R75639.1	EST_HUMAN	y69a08.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element contains LTR7 repetitive element ;

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11807	24797	38495	2.7	6.0E-05	AA044015.1	EST_HUMAN	z68f02.r1 Soares_pregant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12699	25959	31773	9.37	6.0E-05	AW890110.1	EST_HUMAN	MRO-NT0038-250400-001-699 NT0038 Homo sapiens cDNA
1435	14598	27661	20.87	5.0E-05	AW392086.1	EST_HUMAN	QV4-S10234-241199-040-h11 ST0234 Homo sapiens cDNA
1912	15055		1.07	5.0E-05	8923991	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
2924	16102	28116	0.84	5.0E-05	AJ251058.1	NT	Homo sapiens MESP1A gene, promoter region and exon 1
4088	17243	30250	3.16	5.0E-05	AJ251894.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5642	18836	31913	11.81	5.0E-05	X58855.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
6115	19255	32630	3.58	5.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCDMA06 3'
6297	19470	32825	0.97	5.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7485	20560		1.4	5.0E-05	AB037984.1	NT	Mus musculus gene for calretinin, exon 1
12466	25503		5.26	6.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12759	25503		6.9	5.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2868	13457		2.73	4.0E-05	U12821.1	NT	Human retin (REN) gene, 5' flanking region
4605	17742	30720	0.76	4.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4605	17742	30721	0.76	4.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4997	18126		0.95	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
5131	18256	31222	0.73	4.0E-05	AF212313.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, complete cds
9723	22788		8.75	4.0E-05	AF202835.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
10517	23651	37260	0.54	4.0E-05	P23780	SWISSPROT	Homo sapiens PP1200 mRNA, complete cds
11007	24086	37723	4.14	4.0E-05	AW627946.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (AGID BETA-GALACTOSIDASE)
12343	25248	32113	3.27	4.0E-05	AL163252.2	NT	Hi86c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element;
12426	25302		1.47	4.0E-05	AW117580.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C062
13189	25773		1.16	4.0E-05	AA417756.1	EST_HUMAN	Homo sapiens x99e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192 3'
698	13881	28914	0.8	3.0E-05	AJ248061.1	EST_HUMAN	z01e11.st NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746252 3'
1084	14250	27307	1.16	3.0E-05	AW273851.1	EST_HUMAN	q164c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
1550	14702	27781	3.73	3.0E-05	BE169211.1	EST_HUMAN	x24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1550	14702	27782	3.73	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
3365	16537		0.7	3.0E-05	AJ288919.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4501	17641	30625	7.91	3.0E-05	BE169211.1	EST_HUMAN	q161g11.x1 Soares_NhlHMPu_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:O08632
4501	17641	30626	7.91	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4598	17725	30707	1.11	3.0E-05	AA388679.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
							EST79996 Placenta Homo sapiens cDNA similar to similar to p53-associated protein

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4598	17725	30708	1.11	3.0E-05	AA368679.1	EST_HUMAN	EST78686 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4741	17876	30859	0.93	3.0E-05	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4959	13881	26014	0.7	3.0E-05	AJ248061.1	EST_HUMAN	q164c10.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element.
5975	18869	32155	1.72	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Myo2p), mRNA
6897	20047	33456	1.21	3.0E-05	AJ25782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6897	20047	33457	1.21	3.0E-05	AJ25782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
8082	21164	34681	2.26	3.0E-05	BE735167.1	EST_HUMAN	6071567.451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5'
8547	21628	35166	1.55	3.0E-05	AA284049.1	EST_HUMAN	zs60605.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
9094	22173	35718	1.56	3.0E-05	AW77082.1	EST_HUMAN	H94608.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
9096	22177	35721	1.63	3.0E-05	6912431	NT	Homo sapiens interleukin-1 receptor antagonist homolog 1 (L1HY1), mRNA
9102	22181	35726	0.59	3.0E-05	P43361	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9331	22407		0.51	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9521	22588	36154	1.4	3.0E-05	AA372582.1	EST_HUMAN	EST8475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
9863	22903		3.62	3.0E-05	AI769331.1	EST_HUMAN	wg36709.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10755	23788	37403	0.92	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10756	23788	37404	0.92	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12353	25255		1.61	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
12561	25374		1.37	3.0E-05	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12913	26196		1.29	3.0E-05	AW518889.1	EST_HUMAN	xs89d08.x1 NCI_CGAP_UJ2 Homo sapiens cDNA clone IMAGE:2776811 3'
2400	15531	28658	1.49	2.0E-05	AJ286021.1	EST_HUMAN	q108e11.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2650	15773	28886	14.63	2.0E-05	M13792.1	NT	MER3.b2 MER3 repetitive element;
2777	15893		6.99	2.0E-05	AA160562.1	EST_HUMAN	Human adenosine deaminase (ADA) gene, complete cds
3207	16382	29393	1.29	2.0E-05	BE068036.1	EST_HUMAN	zq48a12.r1 Stralagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:832734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3429	16597	29613	1.04	2.0E-05	AF184614.1	NT	RC3-BT0319-120200-014-h08 BT0319 Homo sapiens cDNA
3455	16822	29643	1.12	2.0E-05	X89211.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3583	16748		0.87	2.0E-05	X95485.1	NT	H.sapiens DNA for endogenous retroviral like element
3909	17088		0.81	2.0E-05	AL039107.1	EST_HUMAN	S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
6003	18132	31106	0.6	2.0E-05	AJ131016.1	NT	DKFZ5661064_11 566 (synonym: hfk42) Homo sapiens cDNA clone DKFZ5661064 5'
5878	18098	32376	1.84	2.0E-05	AJ011712.1	NT	Homo sapiens SCL gene locus
6039	19222		0.87	2.0E-05	AF028308.1	NT	Homo sapiens TNNI1 gene, exons 1-11 (and joined CDS)
							Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6092	19273	32601	0.91	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6092	19273	32602	0.91	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6266	19459	32811	0.79	2.0E-05	AH149272.1	EST_HUMAN	similar to contains L1, b3 L1 repetitive element.
6760	19913	33311	2.11	2.0E-05	AA714330.1	EST_HUMAN	nm05d12.s1 NCJ CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
7042	20065	33511	1.69	2.0E-05	Y08926.1	NT	P. falciparum mRNA for AARP1 protein, partial
7054	20107	33523	1	2.0E-05	AI492980.1	EST_HUMAN	q247b06.x1 NCJ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:O02711
7062	20115		7.24	2.0E-05	AI991025.1	EST_HUMAN	vc35n07.x1 Soares_Dieckgraefe_color_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7303	20385	33844	2	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7303	20385	33845	2	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7524	20557		0.77	2.0E-05	AF128847.1	NT	Homo sapiens indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
8069	21151	34671	1.58	2.0E-05	A1381040.1	EST_HUMAN	ig20h05.x1 NCJ CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109369 3'
9467	22524	36087	0.56	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9467	22524	36088	0.56	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10127	23165	36794	0.6	2.0E-05	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10339	23374	36884	0.94	2.0E-05	BF055839.1	EST_HUMAN	7175g09.y1 NCJ CGAP_Bm20 Homo sapiens cDNA clone IMAGE:3340576 5'
10817	23850	37472	3.53	2.0E-05	N41751.1	EST_HUMAN	ww91a06.r1 Soares_placenta_8tc9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:259570 5'
10817	23850	37473	3.53	2.0E-05	N41751.1	EST_HUMAN	ww91a06.r1 Soares_placenta_8tc9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:259570 5'
10861	20115		2.66	2.0E-05	AI991025.1	EST_HUMAN	ww35n07.x1 Soares_Dieckgraefe_color_NHCD Homo sapiens cDNA clone IMAGE:2622077 3'
11738	23824	37549	1.55	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
11981	24966	38668	5.74	2.0E-05	AI912713.1	EST_HUMAN	ww21b05.x1 NCJ CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340921 3'
12477	25921		3.7	2.0E-05	BE348228.1	EST_HUMAN	hw21b03.x1 NCJ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183632 3' similar to TR:Q12832
12592	26104		8.13	2.0E-05	AW074604.1	EST_HUMAN	Q12832 GLYCOPHORIN HEP2 ; x889a03.x1 NCJ CGAP_Cot17 Homo sapiens cDNA clone IMAGE:2573932 3' similar to contains L1, b3 L1 repetitive element ;

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12850	25905		3.24	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12825	25951	32014	2.01	2.0E-05	AU131513.1	EST_HUMAN	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
13206	25787		1.84	2.0E-05	AU20970.1	EST_HUMAN	qf68g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755236 3'
2759	16071	28983	1.86	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3740	16901	29905	1.71	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lambda 120 Suppressor of Hairless (Su(H)) gene, partial cds
3915	17074		0.97	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4074	17230	30236	11.86	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4288	17433	30420	1.45	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4392	17635	30514	2.14	1.0E-05	AA431119.1	EST_HUMAN	zlv99g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781484 5'
4975	18104	31080	2.24	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_L1034.1 Homo sapiens cDNA clone IMAGE:2855548 3'
5079	18207	31179	0.86	1.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5084	18212	31185	0.64	1.0E-05	Z18943.1	NT	H. sapiens repeat region
6891	20043	33451	1.13	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
7230	20135	33553	4.24	1.0E-05	AA641846.1	EST_HUMAN	rs19g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.11 L1
7232	20316	33769	5.19	1.0E-05	4505844	NT	L1 repetitive element;
7837	20892	34394	0.73	1.0E-05	BF222646.1	EST_HUMAN	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7956	21006		2.03	1.0E-05	P19474	SWISSPROT	7p57d01.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3648945 3' similar to contains MER10 b3
9116	22195		2.39	1.0E-05	AL163227.2	NT	MER10 repetitive element;
9260	22337	35887	2.59	1.0E-05	AA452578.1	EST_HUMAN	52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9487	22544	36107	12.29	1.0E-05	AA238110.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9566	22708	36275	0.81	1.0E-05	AV732190.1	EST_HUMAN	z35h12.s1 Soares_testis_NCI_HF8_9v Homo sapiens cDNA clone IMAGE:788519 3' similar to
10043	23081	36682	0.79	1.0E-05	AW510902.1	EST_HUMAN	gbL02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
10043	23081	36683	0.79	1.0E-05	AW510902.1	EST_HUMAN	z505e11.11 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu
10120	23158	36756	1.18	1.0E-05	AW291521.1	EST_HUMAN	repetitive element/contains element TART1 repetitive element;
10120	23158	36757	1.18	1.0E-05	AW291521.1	EST_HUMAN	AV732190 HTF Homo sapiens cDNA clone HTFB1H01 5'
10387	23422		2.04	1.0E-05	AW466995.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812043 3' similar to contains
							OFR.t1 OFR repetitive element;
							hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains
							OFR.t1 OFR repetitive element;
							UIH-B12-egk-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724388 3'
							UIH-B12-egk-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724388 3'
							hd07c10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1
							repetitive element;

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11159	24230	37860	2.22	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11159	24230	37861	2.22	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
13023	28096	31663	1.4	1.0E-05	AL163503.2	NT	Human sapiens chromosome 21 segment HS21C103
2737	15854	28968	5.83	9.0E-06	AF583811.1	EST_HUMAN	h73a08.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3166	16340	29348	6.11	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1759191 3'
3698	16859		2.56	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6026	19208	32528	2.48	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
7003	20139	33557	0.82	9.0E-06	BC065042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7598	20668	34144	2.82	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7963	21003	34515	12.35	9.0E-06	AI034370.1	EST_HUMAN	cx20g01.x1 Soares_fetal_liver_infls_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element
8659	21739	35280	1.17	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9183	22261	35803	3.3	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9183	22261	35804	3.3	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9423	22497	36063	4.43	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
11180	24249	37883	3.61	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2596	16065	28839	2.01	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201189-011-h11 CT0283 Homo sapiens cDNA
6728	19884	33276	2.75	8.0E-06	AA284847.1	EST_HUMAN	z22c05.s1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:713865 3' similar to contains MER9.t1 MER9 repetitive element
10751	23784	37397	0.93	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10751	23784	37398	0.93	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
1002	14173		1.73	7.0E-06	AA669729.1	EST_HUMAN	ab93010.s1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.t1 MER20 repetitive element
1470	14624	27708	3.12	7.0E-06	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2936	16113		10.58	7.0E-06	AI368252.1	EST_HUMAN	qw16g09.x1 NCI_CGAP_UJ3 Homo sapiens cDNA clone IMAGE:1991286 3' similar to contains Alu repetitive element
3654	16817		0.85	7.0E-06	AA385542.1	EST_HUMAN	EST198205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5813	19003		5.49	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0062-250400-173-h01 OT0062 Homo sapiens cDNA
5925	19112	32424	0.93	7.0E-08	N88645.1	EST_HUMAN	y95c07.r1 Soares_multiple_sclerosis_2kbHMSP Homo sapiens cDNA IMAGE:278412 5'
8989	22088	35608	0.83	7.0E-08	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E), mRNA
10104	23142		0.52	7.0E-06	Q61147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
12202	26131	31547	1.83	7.0E-06	BF215972.1	EST_HUMAN	601881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4093972 5'
2984	16180	29177	1.17	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
3784	16945	29952	1.02	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
4876	16183	29206	2.13	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
							cd08e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element:
4883	18013	30997	2.19	6.0E-06	A1040099.1	EST_HUMAN	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5465	18665	31644	2.29	6.0E-06	AF167441.1	NT	PROTEIN XE7
5525	18722	31739	1.16	6.0E-06	Q02040	SWISSPROT	IL5JUN0070-110400-063-g02 UM0070 Homo sapiens cDNA
10060	23098		1.99	6.0E-06	AW801912.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
13142	25742	31948	2.39	6.0E-06	11418157	NT	
6186	19362	32710	3.74	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6467	19634	32995	1.94	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Mat protein (M8604 Met) gene, complete cds
7382	20460	33923	1.18	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
8654	21734	35274	0.58	5.0E-06	AW856872.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
8654	21734	35275	0.58	5.0E-06	AW856872.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10307	23342	36947	6.96	5.0E-06	AA313620.1	EST_HUMAN	EST185486 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
10731	23764	37372	0.51	5.0E-06	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
13011	25666	31957	5.49	5.0E-06	A1065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
664	13850	26877	5.47	4.0E-06	R16267.1	EST_HUMAN	ye48c03.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element:
869	14045	27110	4.73	4.0E-06	AW103354.1	EST_HUMAN	xc69g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element:
1365	14519	27593	3.18	4.0E-06	A1334928.1	EST_HUMAN	ib33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1365	14519	27594	3.18	4.0E-06	A1334928.1	EST_HUMAN	ib33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1503	14556	27738	1.45	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA
2339	15470	28605	1.56	4.0E-06	AW015401.1	EST_HUMAN	U1-H-B10-eat1-05-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3131	16307	29321	0.89	4.0E-06	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4000	17157	30163	0.99	4.0E-06	AW848293.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4929	18059	31041	1.89	4.0E-06	AI886939.1	EST_HUMAN	wl94c10.x1 NCI_CGAP_Brm26 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element;
8696	21776	35308	0.68	4.0E-06	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9000	22079	35620	4.49	4.0E-06	AF09660.1	NT	Homo sapiens T cell receptor beta locus, TORBV73A2 to TORBV12S2 region
9809	22949	36535	1.28	4.0E-06	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
11735	23921	37546	3.99	4.0E-06	AB007955.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
13149	26152		1.33	4.0E-06	AW289734.1	EST_HUMAN	xs53a01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773368 3'
2232	15366	28494	1.31	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.11 L1 repetitive element;
2232	15366	28495	1.31	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.11 L1 repetitive element;
2340	15471		1.48	3.0E-06	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2988	16164	29180	0.84	3.0E-06	AA68218.1	EST_HUMAN	ek48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 LTR1 repetitive element;
3339	16512		2.67	3.0E-06	AI857779.1	EST_HUMAN	wl22a05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN ;contains L1; L2 L1 repetitive element;
3883	17042	30040	1.47	3.0E-06	BE047094.1	EST_HUMAN	hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3883	17042	30041	1.47	3.0E-06	BE047094.1	EST_HUMAN	hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4597	17734	30714	0.8	3.0E-06	T50266.1	EST_HUMAN	yp78b10.r1 Straigene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4684	17819	30807	5.52	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N- terminus.)
6289	19462	32814	0.82	3.0E-06	AU159412.1	EST_HUMAN	AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
7377	20456		2.14	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8274	21356	34874	0.81	3.0E-06	BE562864.1	EST_HUMAN	801338213F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690314 5'
8883	21982	35496	0.75	3.0E-06	P07743	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
12656	25435		12.07	3.0E-06	AW386282.1	EST_HUMAN	RCOL T0001-261199-011-A03 LT0001 Homo sapiens cDNA
207	13430		2.22	2.0E-06	P64366	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1599	14752		6.39	2.0E-06	P21414	SWISSPROT	POLY(POLY)PROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2451	15579	28707	2.58	2.0E-06	AI672138.1	EST_HUMAN	ysa04a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297088 3' similar to contains MER30.b1 MER30 repetitive element;
2537	15662	28785	1.66	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2632	15755	28870	1.81	2.0E-06	P08719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3607	16771	28786	0.9	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFD805 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3858	17018	30017	1.54	2.0E-06	AA173518.1	EST_HUMAN	zp02a05.t1 Stratagene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:595232 5'
3858	17027	30026	0.68	2.0E-06	AW450215.1	EST_HUMAN	UIH-B13-aky-g-05-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'
3876	17035	30033	1.7	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
6214	19389		0.92	2.0E-06	AA974932.1	EST_HUMAN	on34h01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558609 3' similar to contains Alu repetitive element;
6246	19420	32768	0.62	2.0E-06	AF539448.1	EST_HUMAN	te51f05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR:Q13537
6571	19733	33112	5.64	2.0E-06	AB19424.1	EST_HUMAN	Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7635	20704	34183	0.63	2.0E-06	AA688423.1	EST_HUMAN	w90b04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
8102	21184	34882	1.02	2.0E-06	AW869223.1	EST_HUMAN	nv59c08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1234090 3' similar to contains L1 L3 L1 repetitive element;
8281	21363	34882	0.76	2.0E-06	T12238.1	EST_HUMAN	MR3-SN0067-120400-002-02 SN0067 Homo sapiens cDNA
9036	22115		1.05	2.0E-06	AA772497.1	EST_HUMAN	AA47R Heart Homo sapiens cDNA clone A447
9049	22128	35872	1.59	2.0E-06	H62051.1	EST_HUMAN	zh7c11.s1 Soares_pineal_gland_NbHPG Homo sapiens cDNA clone IMAGE:413300 3' similar to TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
9417	22491	36056	0.9	2.0E-06	AF003529.1	NT	y437c04.t1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929
9417	22491	36057	0.9	2.0E-06	AF003529.1	NT	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
9436	22510		0.46	2.0E-06	AI473450.1	EST_HUMAN	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
9902	22942	36527	0.86	2.0E-06	N30576.1	EST_HUMAN	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
10123	23161		0.7	2.0E-06	AV748969.1	EST_HUMAN	h18g10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730 3'
12548	26135	31549	1.34	2.0E-06	P23249	SWISSPROT	yw68a03.s1 Soares_placenta_8to8weeks_2NbHP8to8w Homo sapiens cDNA clone IMAGE:257212 3'
12711	25473		5.94	2.0E-06	BE328232.1	EST_HUMAN	AV748969 NPC Homo sapiens cDNA clone NPCAXD05 5'
34	13272	26276	1.16	1.0E-06	O76082	SWISSPROT	PROTEIN MOV-10
674	13860	26801	1.8	1.0E-06	AF084384.1	NT	hs92f02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1 L2 L1 repetitive element ;
1482	14635	27719	1.8	1.0E-06	P09125	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
1563	14706	27766	1	1.0E-06	AL163278.2	NT	Mus musculus D6Mm5E protein (D6Mm5e) mRNA, complete cds
1603	14766	27837	1.19	1.0E-06	AA034141.1	EST_HUMAN	MEROZOITE SURFACE PROTEIN CMZ-8
1603	14766	27838	1.19	1.0E-06	AA034141.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
							206a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429882 3' similar to contains Alu repetitive element;
							206a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429882 3' similar to contains Alu repetitive element;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1615	14768		0.99	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2050	15191	28303	4.49	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2050	15191	28304	4.49	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4499	17629	30610	16.97	1.0E-08	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5215	18336	31308	1.18	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5215	18336	31309	1.18	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5342	18455	31422	0.72	1.0E-06	N65946.1	EST_HUMAN	za27e03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:293750 3'
5405	18607	31579	6.14	1.0E-08	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
5430	18630	31607	0.94	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5430	18630	31608	0.94	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5592	18787	31834	1.04	1.0E-03	C60813	SWISSPROT	15 kDa SELENOPROTEIN PRECURSOR
6915	19103		0.72	1.0E-06	BE063527.1	EST_HUMAN	CM0-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
7012	20148	33569	7.53	1.0E-06	P02871	SWISSPROT	FIBRINOGEN ALPHA1-CHAIN PRECURSOR
7923	26223		0.73	1.0E-06	BE185330.1	EST_HUMAN	IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
8160	21272		0.99	1.0E-06	AA912823.1	EST_HUMAN	q26c08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3'
8488	21549	35079	1.12	1.0E-06	AI347010.1	EST_HUMAN	qp54e02.x1 NCL CGAP_C08 Homo sapiens cDNA clone IMAGE:1926842 3'
8685	21765	35297	1.31	1.0E-06	AI287878.1	EST_HUMAN	q23f06.x1 NCL CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element
9504	22770	36341	0.91	1.0E-06	N74635.1	EST_HUMAN	za55e01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296472 3'
9579	22721	36281	0.61	1.0E-06	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9884	22924	36507	3.47	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9884	22924	36508	3.47	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9929	22969	36558	5.22	1.0E-06	AA132611.1	EST_HUMAN	z017e08.f1 Strataene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 6'
9991	23030		3.55	1.0E-06	AA449257.1	EST_HUMAN	z04411.s1 Soares_fetal_fetus_Nb2HF8_0w Homo sapiens cDNA clone IMAGE:785493 3' similar to
10705	23738		2.19	1.0E-06	AL163203.2	NT	gbcD26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
11949	24935		3.1	1.0E-06	AW890941.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12589	25396	32041	8.24	1.0E-06	L78810.1	NT	RC4-NT0054-120500-012-b03 NT0054 Homo sapiens cDNA
371	13680	26613	1.95	9.0E-07	AF003529.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
371	13680	26614	1.95	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8602	21683		0.69	9.0E-07	AL163280.2	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
11525	24581	38257	1.83	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C080
4893	18023	31008	4.23	8.0E-07	AI288666.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
							q182g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878878 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4883	18023	31009	4.23	8.0E-07	AI288596.1	EST_HUMAN	q182g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
6007	19192		8.17	8.0E-07	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8191	21273		8.44	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11021	24907		5.84	8.0E-07	T07770.1	EST_HUMAN	EST05660 Fetal brain, Strabagene (cat#893020) Homo sapiens cDNA clone HFBEN89
12183	25143		6.1	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1914	15057	28167	0.97	7.0E-07	AF167341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5636	18830	31908	0.86	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5636	18830	31907	0.86	7.0E-07	6006700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1962	15105	28205	3.47	6.0E-07	AW855558.1	EST_HUMAN	CM3-CT0277-221059-024-e11 CT0277 Homo sapiens cDNA
2561	16866	28812	2.43	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
4080	17236		1.74	6.0E-07	P41479	SWISSPROT	HYPOPHOSPHATASE 2, HPP2, IN LEF4-P33 INTERGENIC REGION
9342	22418	35972	1.31	6.0E-07	BF001867.1	EST_HUMAN	7g9407.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 4FSL...
12115	25098	38800	1.45	6.0E-07	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
12444	26087		1.72	6.0E-07	AW903222.1	EST_HUMAN	CM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA
13229	25992		1.32	6.0E-07	BE222390.1	EST_HUMAN	hu11h05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166329 3' similar to contains L1.b2 L1 L1 repetitive element
336	13649		1.04	5.0E-07	AB31893.1	EST_HUMAN	wh64f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1082	14248		2.39	5.0E-07	AA380630.1	EST_HUMAN	EST193816 Supt cells Homo sapiens cDNA 5' and
3096	16272		0.73	5.0E-07	AB31893.1	EST_HUMAN	wh64f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
4789	17904	30886	0.97	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
6247	19421	32767	1.33	5.0E-07	U85067.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
7210	20076	33487	1.71	5.0E-07	AI933981.1	EST_HUMAN	tg06805.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
7210	20075	33488	1.71	5.0E-07	AI933981.1	EST_HUMAN	tg06805.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
7503	20578	34050	16.93	5.0E-07	AW070885.1	EST_HUMAN	xe31a02.x1 NCL_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb.X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA LIVER (HUMAN);
8470	21551	35081	1.02	5.0E-07	Q9WUQ1	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
8687	21767		0.88	5.0E-07	P09593	SWISSPROT	ADAM-TS 1 (ADAMTS-1) (ADAM-TS1)
							S-ANTIGEN PROTEIN PRECURSOR

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10577	23612	37217	5.47	5.0E-07	AI90887.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA
11805	24795	38493	5.69	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11880	24808		2.08	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12256	25908		1.2	5.0E-07	AL103285.2	NT	Homo sapiens chromosome 21 segment HS21C085
12818	25956		3.06	5.0E-07	AW862537.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
4108	17260	30261	1.66	4.0E-07	AW009002.1	EST_HUMAN	ws94h05.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504697.3
7328	20410		0.8	4.0E-07	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor; exons 1-8
7417	20495	33983	0.97	4.0E-07	Q9Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7417	20495	33984	0.97	4.0E-07	Q9Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
8107	21189	34709	0.51	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9251	22328	35875	4.9	4.0E-07	AW419134.1	EST_HUMAN	xy49g11.x1 NCL_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2855548.3
10332	23367	36976	0.53	4.0E-07	BE901975.1	EST_HUMAN	601876748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651.5
10332	23367	36977	0.53	4.0E-07	BE901976.1	EST_HUMAN	601876748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959651.5
10531	23566	37174	0.58	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11179	24248	37881	3.88	4.0E-07	A1765528.1	EST_HUMAN	w81b08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703.3
11179	24248	37882	3.88	4.0E-07	A1765528.1	EST_HUMAN	w81b08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703.3
11495	24553		1.69	4.0E-07	BE001828.1	EST_HUMAN	PM1-BND083-030300-003-e12 BND083 Homo sapiens cDNA
11919	24905		1.32	4.0E-07	BE987557.1	EST_HUMAN	601649083F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932924.5
13207	25788		1.71	4.0E-07	11437071	NT	Homo sapiens deleted in lymphocytic leukemia, 1 (DLEU1), mRNA
454	13650	26886	5.38	3.0E-07	U19719.1	NT	Human microfilament-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
596	13786	26808	3.59	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1405	14559	27633	1.43	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
1655	14908		3.62	3.0E-07	M64857.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
2104	15243		2.32	3.0E-07	AA528763.1	EST_HUMAN	ni56b09.e1 NCL_CGAP_Oy2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element contains L1.13 L1 repetitive element
2361	15492	28621	1.14	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2540	15665	28789	4.99	3.0E-07	BE005077.1	EST_HUMAN	MRO-BND0115-020300-001-f11 BND0115 Homo sapiens cDNA
2540	15665	28790	4.99	3.0E-07	BE005077.1	EST_HUMAN	MRO-BND0115-020300-001-f11 BND0115 Homo sapiens cDNA
3099	16275	29289	0.97	3.0E-07	T84704.1	EST_HUMAN	yds012.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:111695.6
3228	16402	29414	1.78	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4802	17937		0.64	3.0E-07	P20740	SWISSPROT	OVOSTATIN PRECURSOR (OVONACROGLOBULIN)
4849	17982	30970	8.04	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCDD01.3
4885	18015	30959	0.7	3.0E-07	A1797236.1	EST_HUMAN	we86b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347967.3

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
5175	18297	31259	1.43	3.0E-07	EST_HUMAN	yc14h09.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5175	18297	31260	1.43	3.0E-07	EST_HUMAN	yc14h09.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5783	18975	32281	12.39	3.0E-07	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6095	19276	32605	0.7	3.0E-07	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6842	19995	34224	5.09	3.0E-07	EST_HUMAN	WNT-14 PROTEIN PRECURSOR
7678	20743	34224	3.53	3.0E-07	EST_HUMAN	cc04c10.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
7841	20896		1.3	3.0E-07	EST_HUMAN	QV1-UM0036-200300-118-g02 UM0036 Homo sapiens cDNA
9330	22406	35959	0.48	3.0E-07	SWISSPROT	hw28f11.x1 NCL CGAP_Ov45 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element ;
9330	22406	35960	0.48	3.0E-07	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
13194	25777	26270	4.26	3.0E-07	NT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
29	13267	26270	7.32	2.0E-07	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
158	13383	26413	6.06	2.0E-07	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
158	13383	26414	6.06	2.0E-07	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
186	13408	26437	35.88	2.0E-07	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
767	13948	26995	1.48	2.0E-07	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
767	13948	26996	1.48	2.0E-07	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
779	13959		1.36	2.0E-07	SWISSPROT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
						RETROVIRUS-RELATED POL POLYPROTEIN[CONTAINS: REVERSE TRANSCRIPTASE ;
						ENDONUCLEASE]
866	14139	27200	2.32	2.0E-07	EST_HUMAN	zr08b07.s1 Stragene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:950869 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element
967	14140	27201	2.02	2.0E-07	EST_HUMAN	yc15g04.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element ;
1189	14351	27409	1.55	2.0E-07	SWISSPROT	I/g AUTOANTIGEN
1530	14782	27898	2.06	2.0E-07	SWISSPROT	HYPOPHYSICAL 72.5 KD PROTEIN C27.10 IN CHROMOSOME 1
3708	18869	29946	0.63	2.0E-07	EST_HUMAN	601818018F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3770	18940	29946	21.71	2.0E-07	NT	Homo sapiens cavellin 1 (CAV1) gene, exon 3 and partial cds
5238	18360		0.6	2.0E-07	EST_HUMAN	QV3-NN1023-260400-168-h11 NN1023 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5480	18660	31838	1.52	2.0E-07	AW68066.1	EST_HUMAN	RC3-NIN0066-260400-021-g11 NN0066 Homo sapiens cDNA
6681	25829	33229	0.73	2.0E-07	AW44968.1	EST_HUMAN	UIH-B13-ake-b-01-0-UI.s1 NCI CGAP Sub56 Homo sapiens cDNA clone IMAGE:2794008 3'
6802	19667	33857	3.39	2.0E-07	AI208716.1	EST_HUMAN	qg56d05.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8684	21744		3.87	2.0E-07	AV729390.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAE G02 5'
8893	21972	35508	1.11	2.0E-07	AA035188.1	EST_HUMAN	z127g09.s1 Soares pregnant_uterus_NbHPJ Homo sapiens cDNA clone IMAGE:471808 3'
9863	23002		1.44	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10474	23509	37122	6.34	2.0E-07	AW992507.1	EST_HUMAN	GM4-NN0003-280300-124-e08 NN0003 Homo sapiens cDNA
10706	23739	37342	1.01	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/G5 CONVERTASE) (PROPERDIN FACTOR B)
10706	23739	37343	1.01	2.0E-07	P00751	SWISSPROT	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
12138	26665		2.96	2.0E-07	BE153717.1	EST_HUMAN	COMPLEMENT FACTOR B PRECURSOR (C3/G5 CONVERTASE) (PROPERDIN FACTOR B)
12226	25967		2.38	2.0E-07	AI732462.1	EST_HUMAN	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
1126	14291		0.76	1.0E-07	AL163282.2	NT	PM0-HT0339-280100-006-H07 HT0339 Homo sapiens cDNA
2888	14704	27784	2.08	1.0E-07	P09256	SWISSPROT	z185h11.x5 Stratiogene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:505029 3' similar to contains THR.b2 THR repetitive element
3838	14291		1.24	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4408	17550	30534	2.91	1.0E-07	AV718682.1	EST_HUMAN	GLYCOPROTEIN GPV
4408	17550	30535	2.91	1.0E-07	AV718682.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
							Homo sapiens chromosome 21 segment HS21C082
6832	19791	33180	0.8	1.0E-07	U82671.2	NT	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
7006	20142	33560	4.69	1.0E-07	BE047871.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
7006	20142	33561	4.69	1.0E-07	BE047871.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
7882	20729	34205	7.6	1.0E-07	N55081.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
7826	20881	34382	0.69	1.0E-07	BF375909.1	EST_HUMAN	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
7826	20881	34383	0.69	1.0E-07	BF375909.1	EST_HUMAN	(MAGEA12), melanoma antigen family A2a (MAGEA2A), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
7854	20909	34413	1.24	1.0E-07	AL163281.2	NT	tz43d06.y1 NCI CGAP Brn62 Homo sapiens cDNA clone IMAGE:2291339 5'
8410	21491	35020	2.76	1.0E-07	P97435	SWISSPROT	tz43d06.y1 NCI CGAP Brn62 Homo sapiens cDNA clone IMAGE:2291339 5'
8410	21491	35021	2.76	1.0E-07	P97435	SWISSPROT	yw43c07.s1 Soares fetal liver spleen NFSL Homo sapiens cDNA clone IMAGE:245484 3'
9155	22233	35778	2.7	1.0E-07	AA693576.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
							PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C081
							ENTEROPEPTIDASE (ENTEROKINASE)
							ENTEROPEPTIDASE (ENTEROKINASE)
							z151e10.e1 Soares fetal_liver_spleen_NFSL Homo sapiens cDNA clone IMAGE:434346 3'
							ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
9470	22527	36090	1.05	1.0E-07	P57110	SWISSPROT	MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9816	22856	36436	0.6	1.0E-07	BE327843.1	EST_HUMAN	hu28h06.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
10140	23178	36776	2.35	1.0E-07	BF674524.1	EST_HUMAN	MER18 repetitive element;
10149	23187	36784	1.23	1.0E-07	AA386311.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
10682	23716		1.22	1.0E-07	AL163282.2	NT	EST185054 Brain IV Homo sapiens cDNA
12085	25065	38771	2.35	1.0E-07	A341136.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
12506	25539	31761	3.37	1.0E-07	BE048770.1	EST_HUMAN	q88903.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:095722 095722
12869	25438		1.45	1.0E-07	X84467.1	NT	h53c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12
12852	25566		2.1	1.0E-07	X51755.1	NT	DJ1163J1.1;
7433	20510	33962	0.75	9.0E-08	AI59362.1	EST_HUMAN	H. sapiens ALAD gene for porphobilinogen synthase
10091	23129	36732	2.04	9.0E-08	AV734819.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
11457	24517	38185	1.92	9.0E-08	AI891052.1	EST_HUMAN	te51b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'
11965	24950	38656	2.38	9.0E-08	AL163301.2	NT	AV734819 cda Homo sapiens cDNA clone cdABF806 5'
12456	25320		2.51	9.0E-08	AJ251973.1	NT	wr30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12
622	16017		2.09	8.0E-08	AI911352.1	EST_HUMAN	OFR repetitive element;
1075	14241		1.01	8.0E-08	BE785469.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
3634	16798		1.57	8.0E-08	BE785469.1	EST_HUMAN	Homo sapiens partial stefin-1 gene
8937	22016	35557	5.35	8.0E-08	AI752367.1	EST_HUMAN	wc16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
8937	22016	35558	5.35	8.0E-08	AI752367.1	EST_HUMAN	601590133FT NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
9827	22867	36449	3.03	8.0E-08	AW970893.1	EST_HUMAN	601590133FT NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
10788	23821	37445	0.48	8.0E-08	AF111167.2	NT	crn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_crn15c02 random
11523	24579		1.73	8.0E-08	AF253417.1	NT	crn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_crn15c02 random
82	13317	26345	3.91	7.0E-08	Q02357	SWISSPROT	EST382776 IMAGE resequences, MAGK Homo sapiens cDNA
1392	14546	27622	19.51	7.0E-08	X04809.1	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3666	16829	29839	0.88	7.0E-08	P15305	SWISSPROT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
3686	16825	29840	0.88	7.0E-08	P15305	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
5332	18445	31413	0.82	7.0E-08	T65891.1	EST_HUMAN	Rat mRNA for ribosomal protein L31
11052	24129		1.73	7.0E-08	AI535743.1	EST_HUMAN	DYNEIN HEAVY CHAIN (DYHC)
11970	24955	38658	4.1	7.0E-08	U24070.1	NT	DYNEIN HEAVY CHAIN (DYHC)
							yc11a12.r1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:80398 5'
							cong3 P11 A5 conom Homo sapiens cDNA 3'
							Rattus norvegicus Munc13-1 mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12978	16829	29839	1.84	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12978	16829	29840	1.84	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
840	14018	27073	3.3	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
840	14018	27074	3.3	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2436	15564	28693	1.77	6.0E-08	BE144398.1	EST_HUMAN	MR0-H10166-191189-004-009 H10166 Homo sapiens cDNA
3129	16305	29319	0.68	6.0E-08	7662473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4363	17808	30487	1.15	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8137	21219		0.59	6.0E-08	P08947	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8529	22594		0.55	6.0E-08	AA827075.1	EST_HUMAN	cb56c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains MER12.b3 MER12 repetitive element ;
11701	24998	38390	2.16	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11823	24812		1.43	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
87	13322	26350	2.17	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2309	16441	28576	3.93	5.0E-08	AA493851.1	EST_HUMAN	rh03b09.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element;
12185	25144		4.55	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12382	25271	32077	1.77	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131089-034-a12 CT0225 Homo sapiens cDNA
1799	14948	28040	1.03	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1799	14948	28041	1.03	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2950	16127		1.06	4.0E-08	AL079581.1	EST_HUMAN	DKFZp434J0426.t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434J0426 5'
3132	16308		1.01	4.0E-08	AI078417.1	EST_HUMAN	ca25e02.x1 Soares_fetal_liver_spleen_TNFLS_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to contains Alu repetitive element;
4024	17180	30189	0.65	4.0E-08	U62688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6635	19898	33071	1.07	4.0E-08	P52824	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
6998	22077	35917	0.9	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9340	22416	35969	1.13	4.0E-08	L42571.1	NT	Grieculus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
9845	22885		1.56	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10598	23571		0.85	4.0E-08	AI016342.1	EST_HUMAN	cd78d12.s1 Soares_fetal_liver_spleen_TNFLS_S1 Homo sapiens cDNA clone IMAGE:1622903 3'
10597	23632	37241	4.75	4.0E-08	AI050027.1	EST_HUMAN	an22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
11328	24391	38037	5.16	4.0E-08	AA393627.1	EST_HUMAN	z17b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579 G505579 NA/CA,K-EXCHANGER ;

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11328	24391	36038	5.16	4.0E-08	AA393627.1	EST_HUMAN	z476508.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11349	24411	36084	11.86	4.0E-08	BF692493.1	EST_HUMAN	G505579 NAYCA_K-EXCHANGER. ;
11349	24411	36085	11.89	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
12190	26108		1.93	4.0E-08	W76159.1	EST_HUMAN	z465g03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1t1 L1 repetitive element ;
12504	25598		2.01	4.0E-08	AI343383.1	EST_HUMAN	U595a11.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3
5728	18921	32215	2.27	3.0E-08	BE018348.1	EST_HUMAN	MER18 MER18 repetitive element ;
7115	18541	31498	6.01	3.0E-08	AI792737.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z188 Q9Z188
7711	20776	34262	1.43	3.0E-08	AL163246.2	NT	cs76f11.y5 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:1944045 5'
7928	20978		3.32	3.0E-08	AI436352.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
10102	23140		0.63	3.0E-08	AF055066.1	NT	tr93h09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
11276	24343	37983	1.64	3.0E-08	AI218001.1	EST_HUMAN	Homo sapiens MHC class 1 region
11957	24942	38646	1.32	3.0E-08	AF111167.2	NT	qh21a04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845294 3'
12156	25125		33.85	3.0E-08	R18420.1	EST_HUMAN	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
211	13434		4.16	2.0E-08	AW302996.1	EST_HUMAN	yg02704.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element ;
236	13458		5.76	2.0E-08	AA425598.1	EST_HUMAN	xr87f06.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767139 3'
509	13703	26732	4.46	2.0E-08	AF198349.1	NT	z448f07.r1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element/contains element MER18 repetitive element ;
677	13863	26893	9.7	2.0E-08	AW886438.1	EST_HUMAN	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
677	13863	26894	9.7	2.0E-08	AW886438.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1014	14186		7.75	2.0E-08	BE280477.1	EST_HUMAN	MRQ-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1373	14528	27602	1.46	2.0E-08	AL163247.2	NT	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1774	14923	28017	0.98	2.0E-08	AW841890.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
1780	14929		2.08	2.0E-08	BE794871.1	EST_HUMAN	IL5-CN0024-030300-026-C01 CN0024 Homo sapiens cDNA
1902	15045		6.7	2.0E-08	AW270271.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3945199 5'
2808	15732		1.86	2.0E-08	K00216.1	NT	xp43f11.x1 NCI_CGAP_JH11 Homo sapiens cDNA clone IMAGE:2743149 3'
3279	16453	29474	5.61	2.0E-08	O42280	SWISSPROT	Sheep His-4RNA-GUG
							WNT-14 PROTEIN PRECURSOR

Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3278	16453	28475	5.61	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3962	17120		1.63	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161099-012-b03 ST0197 Homo sapiens cDNA
4189	17339	30332	0.62	2.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4529	17664		1.48	2.0E-08	AA459040.1	EST_HUMAN	aa28c07.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element;
5072	18200		3.5	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element;
5753	18945	32247	0.85	2.0E-08	AA813204.1	EST_HUMAN	ab04111.s1 Soares testis_NHT1 Homo sapiens cDNA clone 1377189 3'
5955	19141	32457	1	2.0E-08	AW088924.1	EST_HUMAN	xx32c04.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.b3 MER18 MER18 repetitive element;
8193	21275	34798	1.11	2.0E-08	P10272	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8301	21383	34904	1.5	2.0E-08	AA490121.1	EST_HUMAN	eb02g06.s1 Strabagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
9286	22362		0.89	2.0E-08	AU139978	EST_HUMAN	AU139978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'
10738	23771	37381	0.83	2.0E-08	N78097.1	EST_HUMAN	yw72f02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
10738	23771	37382	0.83	2.0E-08	N78097.1	EST_HUMAN	yw72f02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
12476	25329		1.77	2.0E-08	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
13065	26159		1.8	2.0E-08	11431678	NT	Homo sapiens hypothetical protein FLJ11342 (FLJ11342), mRNA
1539	16041	27770	1.05	1.0E-08	P31792	SWISSPROT	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1872	14824	27607	1.33	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY)
1872	14824	27608	1.33	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY)
1816	14965	28058	1.56	1.0E-08	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
2110	15248		2.97	1.0E-08	BE141959.1	EST_HUMAN	PM2-HT0130-150999-001-f12 HT0130 Homo sapiens cDNA
3261	16435	29453	0.95	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D6232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
3261	16435	29454	0.95	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D6232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
5716	18909	32204	4.51	1.0E-08	AJ010770.1	NT	Homo sapiens hyperon gene, exons 1-50
7948	20996	34507	0.94	1.0E-08	P19474	SWISSPROT	52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8224	21306	34826	0.62	1.0E-08	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8320	21402	34927	0.54	1.0E-08	AF224698.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8320	21402	34928	0.54	1.0E-08	AF224698.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8744	21823	35359	2.27	1.0E-08	A015304.1	EST_HUMAN	alpha35a05.s1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:1618736 3'
9405	22479		0.56	1.0E-08	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
9406	22480	36043	0.85	1.0E-08	BE072572.1	EST_HUMAN	PM2-BT0546-210100-004-d02 BT0546 Homo sapiens cDNA
10171	23208	36801	0.84	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
10776	23811	37434	0.87	1.0E-08	P98063	SWISSPROT	(TRICARBOXYLATE CARRIER PROTEIN)
11595	24848	38332	3.55	1.0E-08	AF044083.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12681	25391		3.06	1.0E-08	X51755.1	NT	Homo sapiens major histocompatibility locus class II region
13137	25925		1.26	1.0E-08	BF375398.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
4357	17500	30481	4.17	9.0E-09	AL163279.2	NT	MR4-ST0240-240700-013-g04 ST0240 Homo sapiens cDNA
4357	17500	30482	4.17	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
10287	23302		0.63	9.0E-09	T97950.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
7414	20492	33950	8.1	8.0E-09	AI183500.1	EST_HUMAN	yes8a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
8189	21271	34796	2.54	8.0E-09	AW900159.1	EST_HUMAN	qp42a07.x1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1 t1 MSR1 repetitive element
9189	22267		2.53	8.0E-09	AA938892.1	EST_HUMAN	CM0-NN1004-100300-279-s06 NN1004 Homo sapiens cDNA
3695	16856		1.98	7.0E-09	D86842.1	NT	op74d08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1882575 3'
4115	17269		0.98	7.0E-09	U50871.1	NT	Homo sapiens DNA for 3-ketoacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3 Human familial Alzheimer's disease (STM2) gene, complete cds
8086	21168		0.58	7.0E-09	BF108755.1	EST_HUMAN	745e10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element
8237	21319		0.99	7.0E-09	AA256200.1	EST_HUMAN	zr60c05.r1 Soares_NHRMPu_S1 Homo sapiens cDNA clone IMAGE:881992 5' similar to contains L1.12 L1 repetitive element
9460	22517	36080	2.96	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10386	23421	37028	1.95	7.0E-09	BE254850.1	EST_HUMAN	60111173F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3351834 5'
10554	23589		0.76	7.0E-09	AA058626.1	EST_HUMAN	zr58c07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.12 L1 repetitive element
10910	23993		2.01	7.0E-09	T97950.1	EST_HUMAN	yes8a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
2221	18355		0.96	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0514 5'
5095	18223	31195	6.2	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-h05 HT0527 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6496	18696	31711	9.33	6.0E-09	AW195784.1	EST_HUMAN	xn85h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8775	21854	35396	1.11	6.0E-09	BE161653.1	EST_HUMAN	MR3-HT0446-260300-201-h12 HT0446 Homo sapiens cDNA
9377	22452	36014	2.18	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10483	23518		3.4	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TKS) gene, complete cds
10969	24049	37682	1.66	6.0E-09	BF108765.1	EST_HUMAN	745e10.x1 Soares_NSF_F8_OW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to
12089	25069	38776	1.37	6.0E-09	C01803.1	EST_HUMAN	contains MER29.b2 MER28 repetitive element;
1447	14600	27577	3.47	5.0E-09	BE149284.1	EST_HUMAN	HUMGS0003762 Human adult (K. Okubo) Homo sapiens cDNA
1900	15043	28154	7.4	5.0E-09	AL163284.2	NT	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
6540	19703	33075	2.22	5.0E-09	AA359454.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
							EST168746 Fetal lung II Homo sapiens cDNA 5' end
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV5S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV8S2A2P1, TCRBV7S2A1N4T, TCRBV13S913S>
6988	18507	31523	0.66	5.0E-09	U65059.1	NT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
8785	21864	35407	0.63	5.0E-09	P37071	SWISSPROT	PM2-JM0053-240300-005-c09 UM0053 Homo sapiens cDNA
10300	23355	36940	3.25	5.0E-09	AW798667.1	EST_HUMAN	2x60c09.s1 Soares_Ilella_NHT Homo sapiens cDNA clone IMAGE:795880 3'
11944	24930	38632	1.87	5.0E-09	AA450142.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
534	13727		1.64	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C085
987	14159		2.75	4.0E-09	AL163285.2	NT	Homo sapiens hypothetical protein (AF038169), mRNA
1497	14650	27732	1.86	4.0E-09	9558718	NT	EST55385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
2500	15627	28747	5.32	4.0E-09	AA350878.1	EST_HUMAN	2x04c06.t1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:768288 5'
8030	21113	34631	0.53	4.0E-09	AA495747.1	EST_HUMAN	yd11a07.s1 Soares_fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:66804 3'
8719	21799	35334	1.02	4.0E-09	T64942.1	EST_HUMAN	ym94f10.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443627 3'
11330	24393	38041	9.51	4.0E-09	A1886401.1	EST_HUMAN	2r34a12.t1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665278 5' similar to gb:L07807
11379	24440		1.44	4.0E-09	AA195142.1	EST_HUMAN	DYNAMIN-1 (HUMAN);
2427	15555	28582	4.51	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.t3
2619	15742	28856	1.06	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element;
2716	15834	28944	0.69	3.0E-09	P23249	SWISSPROT	hu09e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.t3
3408	16578	29593	0.9	3.0E-09	BE222239.1	EST_HUMAN	PROTEIN MOV-10 hu09e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.t3 MER18 repetitive element;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3454	16631		0.7	3.0E-09	AA442272.1	EST_HUMAN	z654d04.f1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4212	17361		0.62	3.0E-09	X16674.1	NT	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
4546	17684	30668	3.47	3.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
4634	17770	30751	1.19	3.0E-09	Q973R5	SWISSPROT	258.1 KDA PROTEIN C2TORF5 (KIAA0933)
8094	21166	34682	1.1	3.0E-09	BE465780.1	EST_HUMAN	h60a02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TRC055091
10453	23488	37096	1.87	3.0E-09	AL163247.2	NT	O55091 IMPACT PROTEIN ;
10792	23825	37448	0.46	3.0E-09	Q10940	SWISSPROT	Homo sapiens chromosome 21 segment HS21C047
11272	24340	37978	3.15	3.0E-09	BF108943.1	EST_HUMAN	HYPOTHETICAL 13.1 KD PROTEIN B0310.4 IN CHROMOSOME X
11272	24340	37979	3.15	3.0E-09	BF108943.1	EST_HUMAN	717208.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
835	14013		0.98	2.0E-09	X16674.1	NT	717208.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1287	14443	27511	4.7	2.0E-09	AL163284.2	NT	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
1691	14843		10.71	2.0E-09	AL118573.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
2403	15534	28661	2.24	2.0E-09	Q973R5	SWISSPROT	DKF2p761B1710.t1 761 (synonym: hemy2) Homo sapiens cDNA clone DKF2p761B1710 5'
4048	17204	30214	3.01	2.0E-09	Q60241	SWISSPROT	258.1 KDA PROTEIN C2TORF5 (KIAA0933)
4119	17273	30272	0.9	2.0E-09	A1263479.1	EST_HUMAN	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5284	18383	31348	0.62	2.0E-09	M23161.1	NT	q07609.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1855793 3'
5837	19027	32333	0.67	2.0E-09	A1004062.1	EST_HUMAN	Human transposon-like element mRNA
6278	19452		0.75	2.0E-09	AL163249.2	NT	o147b09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'
6919	20234		0.88	2.0E-09	AA357407.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
7609	20679	34155	8.81	2.0E-09	AA461430.1	EST_HUMAN	EST166142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7692	20757	34242	0.96	2.0E-09	W28834.1	EST_HUMAN	z63h06.t1 Soares_testis_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element;
7971	21021	34534	0.59	2.0E-09	A1243732.1	EST_HUMAN	52411 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8909	21888	35528	1.2	2.0E-09	AJ271735.1	NT	q188g10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854114 3'
10824	23857	37480	0.85	2.0E-09	AV688642.1	EST_HUMAN	Homo sapiens Xq pseudosubnormal region; segment 1/2
12745	14013		20.06	2.0E-09	X16674.1	NT	AV688642 GKG Homo sapiens cDNA clone GKCACA11 5'
12830	26188		1.86	2.0E-09	AA226070.1	EST_HUMAN	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
10419	14190		1.19	1.0E-09	W78152.1	EST_HUMAN	nc11c02.t1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;
1133	14258	27353	1.43	1.0E-09	5031624	NT	z179d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:348663 3' similar to gb.L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1133	14258	27354	1.43	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (GBF2) mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2571	15636		1.15	1.0E-09	AI356086.1	EST_HUMAN	qy64e11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER12.12 MER12 repetitive element ;
2954	16131	29148	2.02	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2992	16168	29184	6.17	1.0E-09	M28899.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2992	16168	29185	6.17	1.0E-09	M28899.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3103	16279	29283	0.99	1.0E-09	BE565440.1	EST_HUMAN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
4920	18050		6.15	1.0E-09	AA719297.1	EST_HUMAN	60108602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Zn35b03.s1 Scores_nfl_n3HPG Homo sapiens cDNA clone IMAGE:1543942 3'
5341	18454		0.6	1.0E-09	AA921998.1	EST_HUMAN	Alu repetitive element; contains element MER22 repetitive element ;
5620	18814	31882	0.85	1.0E-09	AL163283.2	NT	Grn44g12.s1 Scores_nfl_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1543942 3'
5952	19138	32454	1.29	1.0E-09	U07000.1	NT	Homo sapiens chromosome 21 segment HS21C083
6272	19446	32794	3.34	1.0E-09	P26694	SWISSPROT	Human breakpoint cluster region (BCR) gene, complete cds
8584	21665	35206	0.92	1.0E-09	AI688474.1	EST_HUMAN	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
10620	23555		2.72	1.0E-09	AL163283.2	NT	wd39b05.x1 Scores_nfl_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2830481 3' similar to contains MER25.11 MER25 repetitive element ;
12642	26120	31668	1.71	1.0E-09	11418127	NT	Homo sapiens chromosome 21 segment HS21C083
12767	25510		1.42	1.0E-09	T57366.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
13132	26020		1.66	1.0E-09	AF260225.1	NT	y651g12.s1 Strategene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74758 3'
1337	14494	27564	1.52	9.0E-10	AW867740.1	EST_HUMAN	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2895	16074	26092	3.74	9.0E-10	AI870071.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
6973	20201	33627	4.98	9.0E-10	AI452982.1	EST_HUMAN	we78h03.x1 Scores_Dieckgraele_colon_NHOD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW/RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 , contains element P1TR5 repetitive element ;
151	13376	26408	9.26	8.0E-10	U63630.2	NT	t44a09.x1 Scores_nsf_fw_0T_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to TR:000372 000372 PUTATIVE P150 ;
3423	16592	29607	0.65	8.0E-10	BE080748.1	EST_HUMAN	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
4318	17481	30446	5.45	8.0E-10	AA379832.1	EST_HUMAN	QV1-BT0631-150200-07401 BT0631 Homo sapiens cDNA
10170	23207		2.51	8.0E-10	U96308.2	NT	EST9564 Small intestine I Homo sapiens cDNA 5' end
719	13901	26941	21.38	7.0E-10	7706225	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
719	13901	26942	21.38	7.0E-10	Q13342	SWISSPROT	Homo sapiens TPA inducible protein (LOC51556), mRNA
1651	14804	27890	2.56	7.0E-10	P08547	SWISSPROT	Homo sapiens TPA inducible protein (LOC51556), mRNA
2626	15749		20.29	7.0E-10	P08547	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
3157	16332	29341	2.25	7.0E-10	X00865.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG H.sapiens DHFR gene, exon 3

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6314	19486	32841	4.06	7.0E-10	AA345220.1	EST_HUMAN	EST161247 Gall bladder II Homo sapiens cDNA 5' end
7574	20848	34124	1.37	7.0E-10	BF352883.1	EST_HUMAN	IL3-HT0619-110700-209-D12 HT0619 Homo sapiens cDNA
7834	20889		1.85	7.0E-10	P35094	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8163	21245	34764	1.54	7.0E-10	AF029701.2	NT	Homo sapiens presentin-1 gene, exons 1 and 2
8163	21245	34765	1.54	7.0E-10	AF029701.2	NT	Homo sapiens presentin-1 gene, exons 1 and 2
936	14111	27171	8.44	6.0E-10	AJ400877.1	NT	Homo sapiens ASC13 gene, C11orf14 gene, C11orf16 gene and C11orf17 gene
2742	15859	28971	1.83	6.0E-10	A1424405.1	EST_HUMAN	t02a07.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2095021 3'
4615	17762	30733	1.88	6.0E-10	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
4861	17694		3.15	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0254-031099-012-g12 CT0254 Homo sapiens cDNA
8983	22062	35602	0.96	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
8983	22062	35603	0.96	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 2) (LECAM2) (CD62E)
9834	22874	36458	0.48	6.0E-10	P98073	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (ELAM-1)
12223	25172		1.95	6.0E-10	AW971923.1	EST_HUMAN	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
780	13980		5.29	5.0E-10	AL046804.1	EST_HUMAN	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
3564	16729	29745	1.14	5.0E-10	Q07033	SWISSPROT	DKFZp434N219.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N219 5'
5105	18233	31202	1.4	5.0E-10	AF181897.1	NT	HYPOTHETICAL GENE 48 PROTEIN
7476	20550		1.85	5.0E-10	BF105159.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
9736	22801	36374	2.24	5.0E-10	P34678	SWISSPROT	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
9736	22801	36375	2.24	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
12040	25021	38725	1.31	5.0E-10	AF091415.1	NT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
114	13345		1.09	4.0E-10	A1221083.1	EST_HUMAN	Macaca tonkeana isolate 66910nkpnea NADH dehydrogenase subunit 4L gene, complete cds; and NADH dehydrogenase subunit 4 gene, mitochondrial genes encoding mitochondrial proteins, partial cds
2052	15193	28306	1.4	4.0E-10	AW594709.1	EST_HUMAN	cg09709.x1 Soares_placenta_8to6weeks_2Nblp4P869W Homo sapiens cDNA clone IMAGE:1759049 3'
2040	15763	28877	6.79	4.0E-10	AL163303.2	NT	similar to contains LTR8.b2 LTR8 repetitive element
7327	20409	33871	17.76	4.0E-10	AF224669.1	NT	hg55g03.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element
10398	23433	37039	0.71	4.0E-10	AW293243.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
10862	23696	37305	1.12	4.0E-10	A1287342.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
							UIH-B12-enl-a-07-0-UI st NCL CGAP_Sup4 Homo sapiens cDNA clone IMAGE:2727061 3'
							ae63h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10794	23827	37450	0.54	4.0E-10	BE169208.1	EST_HUMAN	PM1-HT0521-120200-001-108 HT0521 Homo sapiens cDNA
10794	23827	37451	0.54	4.0E-10	BE169208.1	EST_HUMAN	PM1-HT0521-120200-001-108 HT0521 Homo sapiens cDNA
838	14112	27173	2.24	3.0E-10	N36113.1	EST_HUMAN	y0206.s1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:272563 3' similar to contains L1.1 L1 repetitive element
1382	14537		5.3	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
4657	17793	30777	0.94	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4657	17793	30778	0.94	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5350	18463	31428	0.89	3.0E-10	L34079.1	NT	Human XRCC1 DNA repair gene, genomic
5571	18767	31808	0.78	3.0E-10	N50109.1	EST_HUMAN	y21g08.s1 Soares multiple sclerosis 2N6HMSP Homo sapiens cDNA clone IMAGE:282782 3'
6332	19503	32861	2.06	3.0E-10	P20350	SWISSPROT	RHOMBQID PROTEIN (VEINLET PROTEIN)
6481	19545	33010	3.62	3.0E-10	BE302970.1	EST_HUMAN	ba76608.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'
7937	20987	34495	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
7937	20987	34496	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
8928	22007	35546	1.57	3.0E-10	H87208.1	EST_HUMAN	y674b12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element
9249	22328	35872	1.52	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9249	22326	35873	1.52	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9541	22806		0.78	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10879	23713		1.95	3.0E-10	T65891.1	EST_HUMAN	yc11a12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:30398 5'
10820	23853		0.96	3.0E-10	AA769294.1	EST_HUMAN	rz36g03.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289908 3'
12941	25619	31977	1.87	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
36	13274	26278	2.08	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
36	13274	26279	2.08	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1948	15089		1.66	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
3051	16227		0.84	2.0E-10	BF675047.1	EST_HUMAN	602136840F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5924	19111		2.3	2.0E-10	Q28640	SWISSPROT	(HPRG)
6380	19549	32905	1.56	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7537	20810	34084	6.41	2.0E-10	BE791082.1	EST_HUMAN	601586208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
8203	21285	34807	0.58	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
8203	21285	34808	0.58	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9502	22558		1.06	2.0E-10	BF434595.1	EST_HUMAN	7c78d08.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1 repetitive element ;
11609	24632		1.33	2.0E-10	AI862153.1	EST_HUMAN	ta10f12.x1 Soares_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:2043695 3'
1538	14631		3.09	1.0E-10	AW867767.1	EST_HUMAN	MRO-SN0038-290300-001-701 SN0038 Homo sapiens cDNA
1637	14789	27874	3.37	1.0E-10	AW652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLOCXA11 3'
2649	15772		2.16	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-191199-058-e08 CT0225 Homo sapiens cDNA
3589	16793	29768	0.9	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-181199-013-g10 TT0003 Homo sapiens cDNA
3828	16793		0.57	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3947	16793		0.76	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
4123	17277		7.33	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4245	17391	30378	16.24	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4245	17391	30379	16.24	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4253	17399	30388	1.76	1.0E-10	AB031069.1	NT	Homo sapiens POCX1 mRNA for protein containing CXXC domain 1, complete cds
4285	17430		2.28	1.0E-10	M30829.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5277	18396		1.01	1.0E-10	A1797745.1	EST_HUMAN	we82704.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains repetitive element ;
7644	20713		0.58	1.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7860	20914	34419	0.89	1.0E-10	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8434	21515	35046	1.14	1.0E-10	AW408990.1	EST_HUMAN	fb_6A4 Fetal brain library Homo sapiens cDNA
8855	21934		1.62	1.0E-10	A1268340.1	EST_HUMAN	qm04e10.x1 NC1_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element ;
10406	23441		6.24	1.0E-10	AA081888.1	EST_HUMAN	zn23g06.r1 Stragene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548314 5'
11154	24225	37854	3.5	1.0E-10	A1038280.1	EST_HUMAN	cy55r03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
12165	18503		1.8	1.0E-10	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IFF2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
272	13490	26521	0.87	9.0E-11	BE145900.1	EST_HUMAN	IL2-HIT0203-291099-016-c08 HIT0203 Homo sapiens cDNA
2171	15306	28433	6.02	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
2171	15306	28434	6.02	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3470	16637	29657	2.98	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225.t1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5'
3470	16637	29658	2.98	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225.t1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5'
4622	17759	30741	0.8	9.0E-11	AA775985.1	EST_HUMAN	ae78f01.s1 Stratiotes schizobrain S11 Homo sapiens cDNA clone IMAGE:970297 3'
5692	18866		3.05	9.0E-11	BE079780.1	EST_HUMAN	RC6-81T0627-140200-011-E08 B10627 Homo sapiens cDNA
10357	23392	37002	1.17	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10357	23392	37003	1.17	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12556	25378	32072	2.45	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human aorta p4YA+ mRNA (#6572) Homo sapiens cDNA clone GEN-508608 5'
3195	16360		10.53	8.0E-11	H19971.1	EST_HUMAN	yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
4154	17306	30300	5.37	8.0E-11	N23712.1	EST_HUMAN	yw46e06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
5913	19101	32415	0.66	8.0E-11	AW674316.1	EST_HUMAN	ba60g04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900982 3'
6811	18955		0.92	8.0E-11	AW168158.1	EST_HUMAN	x445h11.x1 NCI_CGAP_Bm50 Homo sapiens cDNA clone IMAGE:2621061 3' similar to contains MER10.11
1479	14632	27717	2.09	7.0E-11	AA330642.1	EST_HUMAN	MER10 repetitive element;
8695	21775	35307	2.61	7.0E-11	AF163884.1	NT	EST134392 Embryo, 6 week I Homo sapiens cDNA 5' end
10434	23459		1.37	7.0E-11	P11369	SWISSPROT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
425	13620	26861	6.19	6.0E-11	M55270.1	NT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
425	13620	26862	6.19	6.0E-11	M55270.1	NT	ENDONUCLEASE]
6862	20014	33424	0.91	6.0E-11	L44140.1	NT	Human matrix Gla protein (MGP) gene, complete cds
7870	20924	34431	3.5	6.0E-11	P08547	SWISSPROT	Human matrix Gla protein (MGP) gene, complete cds
8559	21640	35179	6.99	6.0E-11	AV727859.1	EST_HUMAN	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
9514	22579	36145	0.5	6.0E-11	BE063509.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12	13250	26250	1	5.0E-11	AL163283.2	NT	AV727859 HTC Homo sapiens cDNA clone HTCS006 5'
3450	13250	26250	1.24	5.0E-11	AL163283.2	NT	CM0-BT0281-031195-087-e03 BT0281 Homo sapiens cDNA
6645	19804	33191	1.92	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C083
7699	20764	34248	11.57	5.0E-11	11416799	NT	Homo sapiens chromosome 21 segment HS21C083
1433	14586		1.38	4.0E-11	AA438042.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
2851	15955	29074	9.84	4.0E-11	BE885900.1	EST_HUMAN	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
3034	16203	29233	1.26	4.0E-11	AL163247.2	NT	z0101612.1 Soares testis NHT Homo sapiens cDNA clone IMAGE:730359 5'
4740	17875	30868	0.81	4.0E-11	D44686.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909285 5'
6605	15765	33154	3.29	4.0E-11	P20095	SWISSPROT	Homo sapiens chromosome 21 segment HS21C047
							HUMSUPY0089 Human brain cDNA Homo sapiens cDNA clone 069
							PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7141	20276	33716	0.82	4.0E-11	AA442630.1	EST_HUMAN	z56f10.r1 Soares_testis_NHT: Homo sapiens cDNA clone IMAGE:757963 5' similar to TR:G1056250 G1056250 PHEROMONE RECEPTOR VN4:
7532	20805		3.66	4.0E-11	AF224680.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9695	22650		1.56	4.0E-11	BE149425.1	EST_HUMAN	RC1-HT0256-210100-013-08 HT0256 Homo sapiens cDNA H82a12.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WP:ZK353.1 CE00385:
9862	22802	36487	0.79	4.0E-11	AI609753.1	EST_HUMAN	MR0-GN0024-180900-008-h09 GN0024 Homo sapiens cDNA
10859	23892	37513	0.94	4.0E-11	BF367283.1	EST_HUMAN	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12794	25530	32008	1.71	4.0E-11	11545732	NT	Mus musculus expressed in non-neuronal cells 2, protein (NM23B) (Nmes2), mRNA
1521	14674	27756	4	3.0E-11	6679077	NT	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
4391	17534		1.35	3.0E-11	AA309248.1	EST_HUMAN	q06c04.x1 Soares_testis_NHT: Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13 MER10 repetitive element:
982	14165	27215	1.43	2.0E-11	AI150502.1	EST_HUMAN	Y943e12.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:35144 5'
1212	14373	27434	20.98	2.0E-11	R24807.1	EST_HUMAN	Y943e12.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:35144 5'
1212	14373	27435	20.98	2.0E-11	R24807.1	EST_HUMAN	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3 beta (COR3 beta) genes, complete cds
1644	14796	27880	4.44	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3 beta (COR3 beta) genes, complete cds
1644	14796	27881	4.44	2.0E-11	L17432.1	NT	Human endogenous retrovirus HERV-P-T47D
2823	15937	29047	1.09	2.0E-11	AF087913.1	NT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3266	16440	29461	5.56	2.0E-11	P10263	SWISSPROT	tr54c09.x1 NCL_CGAP_Krt11 Homo sapiens cDNA clone IMAGE:2161936 3'
3403	16573	29586	0.92	2.0E-11	AI478617.1	EST_HUMAN	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
3448	16616	29634	0.67	2.0E-11	Q10473	SWISSPROT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3586	16750		1.01	2.0E-11	AF020503.1	NT	FRIEND VIRUS SUSCEPTIBILITY PROTEIN 1
3797	16958	29962	0.64	2.0E-11	P70213	SWISSPROT	RC3-BT0316-170200-014-a05 BT0316 Homo sapiens cDNA
4566	17704		1.07	2.0E-11	BE065537.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
4728	17863		0.8	2.0E-11	AL163227.2	NT	QV2-BT0258-261099-014-a01 BT0258 Homo sapiens cDNA
5051	18179		1.85	2.0E-11	BE062558.1	EST_HUMAN	EST178226 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to alpha-2- macroglobulin
5142	18265	31234	0.82	2.0E-11	AA307331.1	EST_HUMAN	QV2-PT0073-280300-109-h08 PT0073 Homo sapiens cDNA
6263	19437	32784	1.23	2.0E-11	AW877806.1	EST_HUMAN	

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6440	19607	32970	2	2.0E-11	AA581028.1	EST_HUMAN	m83h05.r1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW:PR16_YEAST
7346	20425	33888	0.85	2.0E-11	BF592845.1	EST_HUMAN	P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16.1
8066	21148		0.59	2.0E-11	P37072	SWISSPROT	797603.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3442665 3'
							OLFACTORY RECEPTOR-LIKE PROTEIN COR6
9424	22498		1.39	2.0E-11	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10491	23526	37135	5.13	2.0E-11	Q13606	SWISSPROT	OLFACTORY RECEPTOR 6II (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10734	23767	37376	1.09	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10734	23767	37377	1.09	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
11375	24436	38094	1.64	2.0E-11	AA035389.1	EST_HUMAN	Zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11375	24436	38095	1.64	2.0E-11	AA035389.1	EST_HUMAN	Zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11408	24469	38133	1.4	2.0E-11	AA261956.1	EST_HUMAN	zs18b04.r1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:685519 5'
12122	25102	38907	12.19	2.0E-11	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12297	26105		1.85	2.0E-11	AA704195.1	EST_HUMAN	Zf77e03.s1 Soares_fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:460924 3'
12328	25237		1.44	2.0E-11	AW842143.1	EST_HUMAN	RC4-OT0072-170100-011-c01 CN0027 Homo sapiens cDNA
12354	25256	32115	2.15	2.0E-11	BF377859.1	EST_HUMAN	GM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12641	25431		1.43	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12813	25542		3.62	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
13180	26767		2.5	2.0E-11	11417968	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
693	13878	28909	1.57	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
806	13986	27038	1.72	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1244	14403	27484	2.91	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1528	14881		1.82	1.0E-11	AF119914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2096	15235	28358	0.94	1.0E-11	P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2195	15330	28455	3.59	1.0E-11	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
2229	15363	28492	1.1	1.0E-11	AA309318.1	EST_HUMAN	EST-180188 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end similar to EST containing Alu repeat
3588	16752	29767	0.95	1.0E-11	BE004315.1	EST_HUMAN	CM0-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA
5447	18647	31925	14.68	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5953	19139	32455	0.78	1.0E-11	BF222846.1	EST_HUMAN	7p57d01.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3
8396	21477	35004	2.65	1.0E-11	4886546	NT	MER10 repetitive element
8781	21880	35403	4.61	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
9248	22325	35870	1.49	1.0E-11	BF365119.1	EST_HUMAN	yf73d08.r1 Soares_infant_brain_1NIB Homo sapiens cDNA clone IMAGE:28166 5'
							QV4-NN1149-250900-423-e03 NN1149 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9248	23235	35871	1.49	1.0E-11	BF365118.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
10626	23660		0.54	1.0E-11	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
11566	24621	38302	2.02	1.0E-11	BF680078.1	EST_HUMAN	602154607F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295977 5'
12903	26879		1.37	1.0E-11	Z20377.1	EST_HUMAN	HSAAACADH_P_Human fetal Brain Whole tissue Homo sapiens cDNA
3017	16193	28216	0.75	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
10002	23040	36632	1.17	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
10002	23040	36633	1.17	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9539	22604		0.88	8.0E-12	BE074720.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
12408	25287		4.98	8.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4783	17918	30905	1.57	7.0E-12	Q05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
11631	24711	38402	6.8	7.0E-12	AA704735.1	EST_HUMAN	223g01.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
13225	25803		1.18	7.0E-12	D16473.1	NT	Human mRNA, Xq terminal portion
3637	16801		0.96	6.0E-12	AV730594.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAW706 5'
4488	17608	30586	9.23	6.0E-12	AA732516.1	EST_HUMAN	nz8811.s1 NCI_OGAP_G0B1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
5336	18449	31418	5.12	6.0E-12	AI489161.1	EST_HUMAN	t65g12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2146438 3' similar to contains MER10.12 MER10 MER10 repetitive element;
9196	22274	35811	1.09	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9675	22637		1.81	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCI_OGAP_G0B1 Homo sapiens cDNA clone IMAGE:1387588 similar to contains MER28.12
13205	25786		1.25	6.0E-12	AW885946.1	EST_HUMAN	MER29 repetitive element;
1068	14234	27293	2.37	5.0E-12	T05573.1	EST_HUMAN	RC1-OT0072-080400-012-F11 OT0072 Homo sapiens cDNA
3477	16644	29663	1.28	5.0E-12	BE047778.1	EST_HUMAN	EST04462 Fetal brain, Stratagene (cds#936206) Homo sapiens cDNA clone HFBVDV33
3821	16981	29884	7.44	5.0E-12	AJ271736.1	NT	tz42b05.y1 NCI_OGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291217 5'
6145	19323	32866	6.13	5.0E-12	AL163278.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6145	19323	32867	6.13	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6620	19760	33168	9.96	5.0E-12	AW974760.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
7176	20052	33462	1.06	5.0E-12	AL040739.1	EST_HUMAN	EST36850 MAGe resequences, MAGN Homo sapiens cDNA
7187	20052	33462	0.93	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B1615 3'
8424	21605	35038	1.28	5.0E-12	AA033745.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B1615 3'
8867	21946		0.55	5.0E-12	AW887037.1	EST_HUMAN	Z01g12.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.13 L1 repetitive element;
9195	22273		0.77	5.0E-12	AL079581.1	EST_HUMAN	RC1-OT0086-220300-011-b07 OT0086 Homo sapiens cDNA
9308	22384	35936	2.52	5.0E-12	AJ271735.1	NT	DKFZp434J0426_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434J0426 5'
							Homo sapiens Xq pseudautosomal region; segment 1/2

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9823	22678	36247	1.22	5.0E-12	P34982	SWISSPROT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10482	23517		4.8	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10573	23608	37213	0.69	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10793	23826	37449	0.6	5.0E-12	6978754	NT	Rattus norvegicus Deleted in colorectal cancer (rat homolog) (Dcc), mRNA
254	13474	26505	3.29	4.0E-12	AA700326.1	EST_HUMAN	z74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
255	13474	26505	3.42	4.0E-12	AA700326.1	EST_HUMAN	z74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4742	17677	30860	0.88	4.0E-12	AI889884.1	EST_HUMAN	MARINER TRANSPOSASE. ;
7797	20853		0.71	4.0E-12	BF445140.1	EST_HUMAN	nad21b03.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7 b2
8437	21518		4.81	4.0E-12	AF108907.1	NT	MER7 repetitive element ;
11338	24401	38050	4.33	4.0E-12	AJ229043.1	NT	Homo sapiens S164 gene, partial cds; P51 and hypothetical protein genes, complete cds; and S171 gene, partial cds
12684	25458		2.11	4.0E-12	U78027.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
631	13816	26839	2.58	3.0E-12	AW341683.1	EST_HUMAN	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
631	13816	26840	2.58	3.0E-12	AW341683.1	EST_HUMAN	hd13a01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517
5276	18395	31363	0.78	3.0E-12	AL163268.2	NT	O14517 SMRP. ;
5568	18765	31806	1.44	3.0E-12	AF111168.2	NT	Homo sapiens chromosome 21 segment HS21C088
8570	21851	35183	0.5	3.0E-12	O35453	SWISSPROT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10891	23975	37606	2.32	3.0E-12	U37672.1	NT	SERINE PROTEASE HEPSIN
10891	23976	37607	2.32	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1685	14837	27921	1.24	2.0E-12	AW802131.1	EST_HUMAN	Human prostate specific antigen gene, 5' flanking region
3556	18721	29738	0.83	2.0E-12	J01884.1	NT	IL5-JM0071-120400-065-a05 UM0071 Homo sapiens cDNA
4230	17377	30365	1.29	2.0E-12	J01884.1	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4230	17377	30366	1.29	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4541	17679		2.03	2.0E-12	BE063509.1	EST_HUMAN	Rat U3A small nuclear RNA
5018	18147	31123	0.71	2.0E-12	O70306	SWISSPROT	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
5018	18147	31124	0.71	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
6006	19766		2.08	2.0E-12	AW971857.1	EST_HUMAN	TBX15 PROTEIN (T-BOX PROTEIN 15)
7328	20408	33670	3.85	2.0E-12	T08169.1	EST_HUMAN	EST383946 MAGC resequences, MAGL Homo sapiens cDNA
							EST06060 Infant Brain, Banto Soares Homo sapiens cDNA clone HIBBA13 5' end

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7499	20574	34047	1.33	2.0E-12	BE173035.1	EST_HUMAN	MRO-HT0559-200400-015-e08 HT0559 Homo sapiens cDNA
7838	20893	34395	2.19	2.0E-12	11422228	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
9508	22774		1.88	2.0E-12	AF196884.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
10101	23228		8.32	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-q01 HT0487 Homo sapiens cDNA
10733	23768	37375	0.76	2.0E-12	AI334130.1	EST_HUMAN	qq07R02.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR.Q13538
12129	25109	38813	1.53	2.0E-12	AW242934.1	EST_HUMAN	Q13538 ORF2: FUNCTION UNKNOWN;
12313	25228		1.34	2.0E-12	AL163283.2	NT	xn27R03.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2684865 3'
12516	25352		1.46	2.0E-12	11418248	NT	Homo sapiens chromosome 21 segment HS21C083
125	13354	26386	1.64	1.0E-12	AW627674.1	EST_HUMAN	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
2044	15185		1.78	1.0E-12	AI871720.1	EST_HUMAN	hH90a09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11
3138	16314	28328	1.04	1.0E-12	AF000991.1	NT	wm61f07.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1
3138	16314	28327	1.04	1.0E-12	AF000991.1	NT	repetitive element;
3978	17135	30138	40.43	1.0E-12	AU132248.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3978	17135	30139	40.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' -
6088	19289		1.6	1.0E-12	U82828.1	NT	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
6166	19342		1.82	1.0E-12	Q9Y2G7	SWISSPROT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
6282	19455	32804	0.59	1.0E-12	BF642800.1	EST_HUMAN	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961
6282	19455	32806	0.59	1.0E-12	BF642800.1	EST_HUMAN	EST000008 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
							EST000008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
6662	19821	33208	0.63	1.0E-12	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane
7265	20348	33800	2.53	1.0E-12	AF196884.1	NT	conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
							Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7300	20382	33840	10.78	1.0E-12	AI248533.1	EST_HUMAN	qh56a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to
							gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.11 MER10
							repetitive element;
7300	20382	33841	10.78	1.0E-12	AI248533.1	EST_HUMAN	qh66a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to
							gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.11 MER10
							repetitive element;

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8686	21768	35298	0.59	1.0E-12	U86059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
8902	21981	35521	1.25	1.0E-12	AA782323.1	EST_HUMAN	ac26d05.s1 Stralagene ovary (#937217) Homo sapiens cDNA clone IMAGE:857577 3'
12215	25166	38835	2.32	1.0E-12	AW962184.1	EST_HUMAN	EST374237 IMAGE reassessances, MAGG Homo sapiens cDNA
12437	25310		1.54	1.0E-12	A1738392.1	EST_HUMAN	w333h08.x1 NCI_CGAP_Cot6 Homo sapiens cDNA clone IMAGE:2392095 3'
12800	26068		1.93	1.0E-12	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
12788	26168		1.19	1.0E-12	P44836	SWISSPROT	PROBABLE TONB-DEPENDENT RECEPTOR HI0712 PRECURSOR
12951	25661		2.82	1.0E-12	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4056	17212	30223	1.21	9.0E-13	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
9801	22841		2.81	9.0E-13	N89653.1	EST_HUMAN	za26d06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:293651 3'
735	13917	26957	5.03	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
735	13917	26958	5.03	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1885	15029	28136	2.73	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
8303	21385	34906	0.63	8.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8303	21385	34907	0.63	8.0E-13	A1884398.1	EST_HUMAN	wm31h09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
10350	23385		2.82	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8429	21510		0.77	7.0E-13	Q95165	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12713	25474		32	7.0E-13	BE778223.1	EST_HUMAN	601483285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866813 5'
12976	25635		1.53	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAc-T1)
2188	15303	28430	5.65	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
5239	18361	31329	0.93	6.0E-13	A1267928.1	EST_HUMAN	qp44809.x1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1911352 3'
3399	16569		1.15	5.0E-13	R78338.1	EST_HUMAN	y82f04.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'
3484	16652		1.58	5.0E-13	AA435773.1	EST_HUMAN	zi77a12.s1 Soares testis NIH-Ht Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
7016	20152	33572	0.99	5.0E-13	P08983	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
11100	24173	37808	2.64	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1916	15059		4.88	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221089-001-e11 HT0224 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2531	159356		1.61	4.0E-13	AF003629.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
4869	18002		1.06	4.0E-13	AA454054.1	EST_HUMAN	z48407.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795469 5'
5704	18997	32189	4.47	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7355	20434	33998	1.09	4.0E-13	AB037760.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7788	20844	34337	1.08	4.0E-13	AA431529.1	EST_HUMAN	zw76g12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763
7898	20960		2.62	4.0E-13	N44291.1	EST_HUMAN	Y33g05.r1 Soares_melanocyte2NBHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32995
9042	22121	35663	1.38	4.0E-13	AL043810.1	EST_HUMAN	A32995 t complex sterility protein - mouse ;
9702	22751	36921	0.47	4.0E-13	AA076907.1	EST_HUMAN	DKFZp434A0128_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A0128 5'
10226	23262	36860	4.44	4.0E-13	AI289831.1	EST_HUMAN	7B04H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B04H11
11436	24500	38167	1.54	4.0E-13	AA435819.1	EST_HUMAN	q932406.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1899945 3' similar to contains Alu
11439	24500	38168	1.54	4.0E-13	AA435819.1	EST_HUMAN	repetitive element;
184	13408		4.35	3.0E-13	AF003528.1	NT	z176g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
888	14064		1.81	3.0E-13	AA430310.1	EST_HUMAN	z176g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
1502	14655	27737	0.98	3.0E-13	AG04151.1	EST_HUMAN	z176g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
2443	15571	28700	1.53	3.0E-13	AJ271736.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
2548	15673	28957	2.28	3.0E-13	AL163210.2	NT	regions
2729	15847	28957	3.69	3.0E-13	BF372982.1	EST_HUMAN	z176g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781406 6'
3256	16430	29771	2.44	3.0E-13	AA745844.1	EST_HUMAN	GM-BT043-090299-075 BT043 Homo sapiens cDNA
3592	16756	29772	9.73	3.0E-13	P18616	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 2/2
3592	16756	29772	9.73	3.0E-13	P18616	SWISSPROT	Homo sapiens chromosome 21 segment HS21C010
5657	18851	32133	0.88	3.0E-13	AA134017.1	EST_HUMAN	GM3-FT0100-140700-242-H08 FT0100 Homo sapiens cDNA
5657	18851	32134	0.88	3.0E-13	AA134017.1	EST_HUMAN	cb18402.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
6114	19294	32629	0.73	3.0E-13	AW005639.1	EST_HUMAN	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
8067	21149	34669	7.1	3.0E-13	U52111.2	NT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
							z188h10.r1 Stralagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to
							contains THR.L2 THR repetitive element ;
							z188h10.r1 Stralagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to
							contains THR.L2 THR repetitive element ;
							wz88c02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139
							O75139 KIAA0644 PROTEIN ;
							Homo sapiens x28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal
							protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR),
							CDM protein (CDM), adrenoleukodystrophy protein >

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8268	21350	34865	0.5	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra-reactive factor
8268	21350	34866	0.5	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra-reactive factor
10401	23436	37043	0.58	3.0E-13	AW835487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
10915	23698		3.1	3.0E-13	A064768.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
11301	24367	38008	3.41	3.0E-13	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-g03 BT0281 Homo sapiens cDNA
11898	24886	36585	1.62	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
154	13379	26411					Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cez2/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
249	13470	26502	2.06	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1289	14455	27521	8.93	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3070	16245	28266	0.61	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3070	16248	28267	0.61	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3598	16760	28776	1.88	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4224	17372		2.07	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6250	19424	32770	4.34	2.0E-13	Q06852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6335	19506		0.58	2.0E-13	X78417.1	NT	S. scrofa rps12 mRNA for ribosomal protein S12
6954	20267	33704	5.73	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
7189	20064	33474	0.6	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
7189	20064	33475	0.6	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
10675	23709	37317	2.41	2.0E-13	5031896	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
12388	25274		22.49	2.0E-13	AW892155.1	EST_HUMAN	CM0-HN0001-100390-274-e11 HN0001 Homo sapiens cDNA
302	13518	28551	1.34	1.0E-13	S74129.1	NT	FGF-1-fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
911	14086	27151	5.53	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1367	14521	27596	1.4	1.0E-13	X87944.1	NT	H. sapiens DMA, DME, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2078	15219	28339	2.61	1.0E-13	AA720574.1	EST_HUMAN	hw21g02.s1 NCL CGAP GCBO Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element:
4715	17850	30833	1.32	1.0E-13	BF34087.1	EST_HUMAN	602038009F1 NCL CGAP Bn84 Homo sapiens cDNA clone IMAGE:4185868 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8094	21176	34691	0.97	1.0E-13	AA577812.1	EST_HUMAN	nm24c01.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element/contains element MER24 repetitive element ;
8094	21176	34692	0.97	1.0E-13	AA577812.1	EST_HUMAN	nm24c01.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element/contains element MER24 repetitive element ;
10295	23330		1.04	1.0E-13	O15481	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
10508	23543	37154	0.6	1.0E-13	AF300701.1	NT	Mus musculus osteodectyl protein tyrosine phosphatase mRNA, complete cds
11691	24740	38431	9.74	1.0E-13	BF108755.1	EST_HUMAN	7146r10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element ;
12206	25160		1.38	1.0E-13	AV715377.1	EST_HUMAN	AV716377 DOB Homo sapiens cDNA clone DDBAIE03 5'
12920	26005		3.46	1.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
13077	25706		1.85	1.0E-13	X87579.1	NT	H.sapiens GD4 gene
343	13554	26583	3.76	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element ;
344	13555	26584	1.84	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element ;
2599	15994		4.13	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2811	15925	29036	7.9	9.0E-14	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3180	18355	29360	7.5	9.0E-14	AW513296.1	EST_HUMAN	xs54h05.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2707833 3'
3310	13554	26583	1	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element ;
3898	17057	30057	7.37	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4879	18010	30994	2.23	9.0E-14	AJ002153.1	NT	Sagittinus oedipus gene for seminal vesicle secreted protein semenogelin I
3587	16751		1.17	8.0E-14	BE488263.1	EST_HUMAN	hz71c09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
4068	17222		3.64	8.0E-14	R76269.1	EST_HUMAN	yf72e03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'
9647	21090	34605	38.93	8.0E-14	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
9760	22698	36266	3.22	8.0E-14	AA219316.1	EST_HUMAN	zq17c10.s1 Stratagene fetal telina 937202 Homo sapiens cDNA clone IMAGE:629970 3'
11717	24757		1.79	8.0E-14	BE062558.1	EST_HUMAN	QV2-BT0258-261099-014-a01 BT0258 Homo sapiens cDNA
12611	25410	32048	2.43	8.0E-14	AI688118.1	EST_HUMAN	wc82h08.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326143 3'
1658	16044		4.76	7.0E-14	AW151673.1	EST_HUMAN	x67r10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
9120	22199		0.73	7.0E-14	AL163285.2	NT	MER10 repetitive element ;
							Homo sapiens chromosome 21 segment HS21C085
378	13585	26620	12.43	6.0E-14	AF020603.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10027	23065	36882	2.19	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10027	23065	36883	2.19	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 6
633	13818	26842	4.17	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5166	18288	31254	1.32	5.0E-14	AW073791.1	EST_HUMAN	XP03805.x1 NCI_CGAP_GU11 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1 repetitive element;
5850	18844	32125	5.28	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1147	16030		1.61	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1928	15068	28174	10.15	4.0E-14	AJ007973.1	NT	Homo sapiens LGM2B28 gene
3847	17007		0.73	4.0E-14	A4046502.1	EST_HUMAN	Zf67a06.1 Scores_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:487858 5'
4407	17549	30533	1.04	4.0E-14	N46328.1	EST_HUMAN	Y773c12.s1 Scores_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.13 L1 repetitive element;
8145	21227		0.71	4.0E-14	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
12043	25024	38720	5.5	4.0E-14	BE242486.1	EST_HUMAN	TCAAP1D1470 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project-TCAA Homo sapiens cDNA clone TCAAP1470
12986	26203		5.69	4.0E-14	A1886224.1	EST_HUMAN	wrm08c03.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element;
972	14145	27204	1.58	3.0E-14	X95466.1	NT	R.norvegicus mRNA for CP-G2 protein
6873	20025	33434	0.93	3.0E-14	A420786.1	EST_HUMAN	ts91c12.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE ;
6873	20025	33435	0.93	3.0E-14	A420786.1	EST_HUMAN	FATTY ACID AMIDE HYDROLASE ;
7173	20306	33749	0.6	3.0E-14	A4386311.1	EST_HUMAN	EST185054 Brain IV Homo sapiens cDNA
8987	22066	35608	0.86	3.0E-14	N42166.1	EST_HUMAN	Y007610.r1 Scores_melanocyte_2NBHM Homo sapiens cDNA clone IMAGE:270523 5'
11512	18495	31533	5.87	3.0E-14	AV265354.1	EST_HUMAN	XP45612.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MERB repetitive element ;
12884	26041		1.88	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
13212	25994	31863	1.61	3.0E-14	BE891550.1	EST_HUMAN	601435233F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920169 5'
401	13598	26634	2.33	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
401	13598	26635	2.33	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
708	16019	26925	11.36	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

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Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2461	15588		1.04	2.0E-14	AW372868.1	EST_HUMAN	RC5-BT0377-091289-031-D12 3T0377 Homo sapiens cDNA
2535	15660		0.99	2.0E-14	7657529	NT	Homo sapiens ribosomal protein 1 (RTDR1), mRNA
2593	15718	28835	1.53	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5641	18835	31912	0.97	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5738	18931	32229	1.03	2.0E-14	A1312351.1	EST_HUMAN	ta78r01.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1 repetitive element;
5838	19028	32334	3	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
7023	20159	33987	1.04	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA
7437	20514	33987	1.06	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7676	20741	34221	24.46	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
7676	20741	34222	24.46	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
10121	23159	36758	0.59	2.0E-14	A1978795.1	EST_HUMAN	wr58g10.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element;
10630	23694	37273	0.51	2.0E-14	AV741648.1	EST_HUMAN	AV741648 CB Homo sapiens cDNA clone CBFBBF04 5'
11019	24098	37736	3.62	2.0E-14	AW139800.1	EST_HUMAN	UI-HB11-adv-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
12890	26045		2.5	2.0E-14	AF008181.1	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
13163	15660		1.25	2.0E-14	7657529	NT	Homo sapiens ribosomal protein 1 (RTDR1), mRNA
1092	14257	27313	2.32	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1438	14591	27694	7.01	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1438	14591	27695	7.01	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2057	15198	28312	8.9	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
2258	15391	28517	6.33	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2480	15607	28731	6.44	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
3010	16186	29210	1.41	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3236	16410	29424	3.14	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3236	16410	29425	3.14	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3992	17149	30155	1.89	1.0E-14	AA682994.1	EST_HUMAN	ae89c12.s1 Strabagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4596	17733	30713	2.01	1.0E-14	AW276852.1	EST_HUMAN	xq38h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
5930	19116	32428	1.98	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
8813	26834	33371	10.9	1.0E-14	11437150	NT	Homo sapiens prolamin (mouse)-like 1 (PROML1), mRNA
8813	26834	33372	10.9	1.0E-14	11437150	NT	Homo sapiens prolamin (mouse)-like 1 (PROML1), mRNA
1607	14780	27839	1.81	9.0E-16	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2242	16376		1.38	9.0E-15	AF198779.1	NT	Homo sapiens transcription factor IGEM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel ap
7865	20732	34207	4.24	9.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
8206	21268	34810	1.24	9.0E-15	BE5903559.1	EST_HUMAN	60167750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5'
13099	25718		2.87	9.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2872	13687		1.53	8.0E-15	BE261482.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7331	20412	33874	1.13	7.0E-15	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
10650	23884		2.34	7.0E-15	AW241958.1	EST_HUMAN	xn77402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element;
12270	25203		1.44	7.0E-15	AA284485.1	EST_HUMAN	zs57d08.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701583 5' similar to gb:L21934 STEROL O-ACYLTRANSFERASE (HUMAN); contains L1.t1 L1 repetitive element;
1018	14189	27250	7.51	6.0E-15	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5263	18382		0.98	6.0E-15	AW801258.1	EST_HUMAN	CM4-NN1011-100300-110-d10 NN1011 Homo sapiens cDNA
6041	19224	32546	1.02	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
6041	19224	32547	1.02	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
11583	26231		1.54	6.0E-15	AW83843.1	EST_HUMAN	QV1-LT0036-150200-070-c10 LT0036 Homo sapiens cDNA
423	13018	26658	3.57	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2819	15833	29044	1.76	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP13) gene, complete cds
5233	18355		0.91	5.0E-15	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE];
440	13240	26240	2.33	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6804	18959	33359	0.9	4.0E-15	AB007870.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
11316	21065	34577	2.11	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
11316	21065	34578	2.11	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4333	17476		7.67	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
5141	18264	31232	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5141	18264	31233	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6953	20266		1.11	3.0E-15	Q64625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7430	20307	33978	3.13	3.0E-15	M27885.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7430	20307	33979	3.13	3.0E-15	M27885.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10129	23167		2.38	3.0E-15	AA807128.1	EST_HUMAN	cc36a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11 MER19 repetitive element.
11033	24112	37748	8.11	3.0E-15	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complex cds)
12620	26081		65.8	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
260	13479	26511	3.71	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
379	13587	26621	3.28	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
379	13587	26622	3.28	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1559	14712		0.99	2.0E-15	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
3599	16763	29778	0.72	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3599	16763	29779	0.72	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4745	17880		2.76	2.0E-15	AB06335.1	EST_HUMAN	w07006.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TRQ61043 Q61043 NINEIN.
6311	19483	32838	1.11	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6311	19483	32839	1.11	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7263	20346		1.58	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7421	20499	33869	2.73	2.0E-15	AA704195.1	EST_HUMAN	z177603.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7554	20628	34102	5.05	2.0E-15	W05064.1	EST_HUMAN	za78410.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:298675 5' similar to WP-F44F4.8 CE02227 TRANSPOSASE ;
9107	22186	35730	2.86	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
9273	22349	35899	0.91	2.0E-15	AA397798.1	EST_HUMAN	z177608.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9273	22349	35900	0.91	2.0E-15	AA397798.1	EST_HUMAN	z177608.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9604	22659	36231	1.18	2.0E-15	AW379465.1	EST_HUMAN	GM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
9604	22659	36232	1.18	2.0E-15	AW379465.1	EST_HUMAN	GM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
11077	24152		3.69	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
13016	16763	29778	3.89	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13018	16763	29779	3.89	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2834	15948		3.09	1.0E-15	AI689984.1	EST_HUMAN	t22805.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE ;
3077	16253	29275	1.42	1.0E-15	BE043584.1	EST_HUMAN	hk40e02.y1 NCL CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2989162 5'
3211	16395	29396	1.18	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4479	17619	30601	0.61	1.0E-15	BE182696.1	EST_HUMAN	RC3-HT0649-100500-022-b05 HT0649 Homo sapiens cDNA
6502	18668	33032	1.72	1.0E-15	T95763.1	EST_HUMAN	ye40e10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains
7149	20294		1.96	1.0E-15	BE074217.1	EST_HUMAN	MER6 repetitive element ;
7184	20049	33460	0.79	1.0E-15	P39057	SWISSPROT	QV3-BT0599-270100-074-g06 BT0599 Homo sapiens cDNA
8427	21508	35040	0.99	1.0E-15	AL163280.2	NT	DYNEIN BETA CHAIN, CILIARY
8615	21695	35232	4.94	1.0E-16	AI200976.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
8615	21695	35233	4.94	1.0E-15	AI200976.1	EST_HUMAN	q68h06.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8239	22316	35898	0.78	1.0E-15	AL163207.2	NT	q68h06.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9242	22319	35862	0.96	1.0E-15	4507208	NT	Homo sapiens chromosome 21 segment HS21C007
9448	22594	36127	0.99	1.0E-15	Q39575	SWISSPROT	Homo sapiens spermidine synthase (SRM) mRNA
9832	22872	36455	0.94	1.0E-15	AA884653.1	EST_HUMAN	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
11057	24134	37770	3.04	1.0E-15	AF044083.1	NT	q437c03.s1 NCL CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459972 3' similar to contains L1.13 L1 repetitive element ;
13104	25932	31856	13.05	1.0E-15	AI763944.1	EST_HUMAN	Homo sapiens major histocompatibility locus class III region element ;
4625	17762	30744	0.93	9.0E-16	4503168	NT	t37c05.x1 NCL CGAP_OV23 Homo sapiens cDNA clone IMAGE:2218912 3' similar to contains Alu repetitive element ;
11241	24310	37947	1.41	9.0E-16	F08688.1	EST_HUMAN	Homo sapiens cut (Drosophila)-like 1 (CGAAT displacement protein) (CUTL1) mRNA
11895	24980	38685	1.48	9.0E-16	AI244341.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
11895	24980	38686	1.48	9.0E-16	AI244341.1	EST_HUMAN	q76a02.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
5819	19009	32315	0.85	7.0E-16	4885120	NT	MER10 repetitive element ;
7496	20571	34043	1.3	7.0E-16	Q88807	SWISSPROT	q76a02.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
7496	20571	34044	1.3	7.0E-16	Q88807	SWISSPROT	q76a02.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
13043	25995		38.08	7.0E-16	T94149.1	EST_HUMAN	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
							MER10 repetitive element ;
							Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
							PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
							(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
							PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
							(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
							ye28e12.11 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2208	18342		9.12	6.0E-16	AW972611.1	EST_HUMAN	EST384702 MAGE resequences, MAGL Homo sapiens cDNA
1522	14876	27757	0.96	5.0E-16	AJ251154.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
2745	15862	28973	2.21	5.0E-16	AA992176.1	EST_HUMAN	cd80-c04.s1 Soares_total_fetus_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to
11809	24796	38498	2.68	5.0E-16	BF217368.1	EST_HUMAN	contains element L1 repetitive element;
13152	25749		14.15	5.0E-16	11418127	NT	601885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
2312	15444		1.01	4.0E-16	AB001523.1	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2453	15581	28708	2.87	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens gene for TIME1 and PWP2, complete and partial cds
2453	15581	28708	2.87	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM00036-200300-115-g02 UM00036 Homo sapiens cDNA
3546	18711	29722	5.29	4.0E-16	Q16553	SWISSPROT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4260	17405	30361	8.68	4.0E-16	BE083875.1	EST_HUMAN	PM4-B10650-010400-002-g09 BT0650 Homo sapiens cDNA
4260	17405	30392	8.68	4.0E-16	BE083875.1	EST_HUMAN	PM4-B10650-010400-002-g09 BT0650 Homo sapiens cDNA
5257	18377	31343	0.91	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7890	20942	34448	42.68	4.0E-16	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9495	22552	35114	0.72	4.0E-16	11423191	NT	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
12293	25218		1.95	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12381	25270		8.68	4.0E-16	C05947.1	EST_HUMAN	C05947 Human pancreatic islet Homo sapiens cDNA clone hbc5355
12392	25277	32079	3.23	4.0E-16	6912459	NT	Homo sapiens Grib2-associated binder 2 (KIA0571), mRNA
12982	25454		1.33	4.0E-16	R18591.1	EST_HUMAN	y08611.11 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30489 5'
135	13361	26395	1.09	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486378 5'
135	13361	26398	1.09	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486378 5'
478	13673		1.56	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037.r1.434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'
488	13682		2.33	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1483	14636	27720	2.73	3.0E-16	Q28883	SWISSPROT	ZONADHESIN PRECURSOR
3041	16217	29237	4.71	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
4711	17846	30830	0.59	3.0E-16	AW160928.1	EST_HUMAN	au76b06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782163 5' similar to
5057	18185	31160	1.32	3.0E-16	AV661933.1	EST_HUMAN	SW:KID1 MOUSE Q61751 RENAL TRANSCRIPTION FACTOR KID-1;
5392	18594		0.89	3.0E-16	AA077225.1	EST_HUMAN	AV661393 GLC Homo sapiens cDNA clone GLOGSA01 3'
5734	18927	32223	1.67	3.0E-16	AF003529.1	NT	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
8858	21837	35473	4.26	3.0E-16	AI002836.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions am98h05.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THRB2 THR repetitive element;

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10094	23132		1.09	3.0E-16	BF690617.1	EST_HUMAN	602246538F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4332032 5'
10324	23359	36969	2.59	3.0E-16	L78910.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
13187	28171	31557	3.62	3.0E-16	AL043268.2	EST_HUMAN	DKFZp434L1623_11 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L1623 5'
984	14166		1.03	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment H521C079
2459	15588		0.96	2.0E-16	AA621761.1	EST_HUMAN	af02d04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2753	15870		1.14	2.0E-16	J03061.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4294	17437	30424	1.62	2.0E-16	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4603	17740	30718	1.27	2.0E-16	AI208733.1	EST_HUMAN	qp5603.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839197 3' similar to contains MER28.13
5299	18416	31385	0.64	2.0E-16	BE061178.1	EST_HUMAN	MER29 repetitive element;
6880	20032	33442	0.68	2.0E-16	Q31125	SWISSPROT	RC3-BT0046-131199-003-H12 BT0046 Homo sapiens cDNA
7893	20945	34451	0.98	2.0E-16	AI470723.1	EST_HUMAN	HISTIDINE-RICH PROTEIN KE4
							ff16e11.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element
							MER33 repetitive element;
8154	21236	34757	1.67	2.0E-16	AI732837.1	EST_HUMAN	nz4705.x5 NCI CGAP_P12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:O54849 O54849
8352	21433	34957	0.81	2.0E-16	BE858026.1	EST_HUMAN	HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905; contains MER7.11 MER7 repetitive element;
8352	21433	34958	0.81	2.0E-16	BE858026.1	EST_HUMAN	782H09.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8724	21804	35340	0.78	2.0E-16	AW877214.1	EST_HUMAN	782H09.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8724	21804	35341	0.78	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
189	13411	26438	2.28	1.0E-16	AF200719.1	NT	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
383	13630		22.93	1.0E-16	AA628592.1	EST_HUMAN	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
2028	15169	28276	3.42	1.0E-16	BF327842.1	EST_HUMAN	af39g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element;
5839	19029	32335	0.6	1.0E-16	AF169884.1	NT	QV0-BN0148-070700-293-e10 BN0148 Homo sapiens cDNA
5866	19727		18	1.0E-16	U45983.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6704	19882	33252	2.96	1.0E-16	Q02779	SWISSPROT	Homo sapiens COR8 chemokine receptor (CMKBR8) gene, complete cds
7726	19727		5.39	1.0E-16	U45983.1	NT	Homo sapiens COR8 chemokine receptor (CMKBR8) gene, complete cds
9483	22540	36103	0.81	1.0E-16	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-a05 PT0012 Homo sapiens cDNA
3832	16992	29994	2.08	9.0E-17	AW900046.1	EST_HUMAN	CM1-NN1003-200300-153-a01 NN1003 Homo sapiens cDNA
6864	20016		2.15	9.0E-17	AI392964.1	EST_HUMAN	tg22c11.x1 NCI CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.12
							MER28 repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8299	21381		3.66	6.0E-17	AW150257.1	EST_HUMAN	xg49g12.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.12 OFR repetitive element;
10428	23464		2.95	6.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1043	14209		2.43	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-001 OT0032 Homo sapiens cDNA
3398	17155		0.78	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5701	25809	32187	4.09	8.0E-17	BE172081.1	EST_HUMAN	MR0-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
7425	20502		1.73	8.0E-17	AV730769.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1487	14840		2.58	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBc2), mRNA
5438	18638		3.11	7.0E-17	AF218850.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
							Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
6826	19979	33387	7.91	7.0E-17	AF22843.1	NT	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
208	13431	26463	5.62	6.0E-17	AW963880.1	EST_HUMAN	H81d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878695 3' similar to contains L1.12 L1 repetitive element;
6443	19810	32973	2.06	6.0E-17	AW662772.1	EST_HUMAN	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP87)
10499	23534	37144	0.54	6.0E-17	P20138	SWISSPROT	yc05h08.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79839 5'
434	13234	28234	2.37	5.0E-17	T84110.1	EST_HUMAN	yc26b04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5'
7759	20818	34308	1.81	5.0E-17	T81043.1	EST_HUMAN	x20e04.x1 NCL_CGAP_KidB Homo sapiens cDNA clone IMAGE:2818822 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element;
8562	22704	36270	1.32	4.0E-17	AW129165.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
11783	24773	38469	2.51	4.0E-17	AL163247.2	NT	Cy45e04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR.Q16530
12308	25226		1.82	4.0E-17	AI073546.1	EST_HUMAN	Q16530 PMS3 MRNA; contains MER10.12 MER10 repetitive element;
2165	15300	28426	1.85	3.0E-17	AW119123.1	EST_HUMAN	xc189-c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3263	16437		1.17	3.0E-17	P35410	SWISSPROT	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3732	16833	29897	1.91	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
3732	16833	29898	1.91	3.0E-17	BE326522.1	EST_HUMAN	za14b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:3181999 3'
8463	21544	35074	1.12	3.0E-17	N68451.1	EST_HUMAN	PTR5.13 PTR5 repetitive element;
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9903	22943	36528	5.19	3.0E-17	AB028698.1	NT	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
10591	23626	37234	0.72	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
10591	23626	37235	0.72	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
12268	25201		4.2	3.0E-17	11417988	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13155	25751		1.23	3.0E-17	AV720204.1	EST_HUMAN	AV720204 GLC Homo sapiens cDNA clone GLCJF08 5'
363	13574	26605	2.65	2.0E-17	AL270080.1	EST_HUMAN	qf63a05.x1 NCI_OGAP_Eso2 Homo sapiens cDNA clone IMAGE:1859922 3' similar to contains Alu repetitive element
364	13574	26605	2.78	2.0E-17	AL270080.1	EST_HUMAN	qf63a05.x1 NCI_OGAP_Eso2 Homo sapiens cDNA clone IMAGE:1859922 3' similar to contains Alu repetitive element
1012	14184		1.43	2.0E-17	AA722932.1	EST_HUMAN	zq81d04.s1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:399751 3'
2518	15644	28765	2.59	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2518	15644	28766	2.59	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2896	16172	29191	6.96	2.0E-17	P12036	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN)(NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5482	18681	31696	1.75	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5482	18681	31697	1.75	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6394	19563		1.92	2.0E-17	AF035098.1	NT	Homo sapiens MHC class 1 region
6619	19779		1.39	2.0E-17	AL134881.1	EST_HUMAN	DKFZp762J0610 J1 762 (synonym: hmal2) Homo sapiens cDNA clone DKFZp762J0610 5'
8008	21056	34568	0.89	2.0E-17	AB037839.1	NT	Homo sapiens mRNA for KIAA1418 protein, partial cds
8275	21357	34875	1.24	2.0E-17	Q95158	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
8651	21731	35270	1.05	2.0E-17	AA300840.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin
10073	23111	36715	2.71	2.0E-17	BE298888.1	EST_HUMAN	600944690F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:296061 5'
10108	23146	36744	3.53	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10108	23146	36745	3.53	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10466	23501	37114	5.02	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10590	23625	37232	0.97	2.0E-17	P88063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10590	23625	37233	0.97	2.0E-17	P88063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10618	23652	37261	0.93	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10618	23652	37262	0.93	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
768	13950	26999	2.78	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1745	14894		2.01	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1807	14956	28050	4.83	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2184	15319	28445	2.05	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2412	15542	28669	3.16	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3657	16920		1.03	1.0E-17	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4256	17401		9.42	1.0E-17	R09942.1	EST_HUMAN	y630a07.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:128388 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6791	19946	33344	1.62	1.0E-17	A185042.1	EST_HUMAN	q655b05.x1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6791	19946	33346	1.62	1.0E-17	A185042.1	EST_HUMAN	q655b05.x1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7238	20322	33766	1.33	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8792	21871	35410	1.26	1.0E-17	BE082744.1	EST_HUMAN	QV0-BT0283-101-289-072-d07 BT0283 Homo sapiens cDNA
10210	23246	38836	1.04	1.0E-17	AW996538.1	EST_HUMAN	QV3-BN0046-220300-128-c10 BN0046 Homo sapiens cDNA
11703	24700	38393	1.52	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
9698	22747		3.05	9.0E-18	A1472167.1	EST_HUMAN	fb5d03.x1 Scores_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
3866	17045	30044	2.14	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
359	13570	26599	16.47	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
359	13570	26600	16.47	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
7601	20671	34145	1.09	7.0E-18	AW887642.1	EST_HUMAN	xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
12826	13570	26599	10.65	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
12826	13570	26600	10.65	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
3357	16539	29552	1.23	6.0E-18	X71791.2	NT	Rattus norvegicus partial Gdn/Pn-1 gene for glia-derived nectin/protease nexin I, enhancer region
4868	18001		3.99	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8444	21525		3.47	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8543	21624	35161	0.78	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21, segment HS21C010
9291	22367	35916	0.48	6.0E-18	A1908256.1	EST_HUMAN	RC-BT166-020499-014 BT166 Homo sapiens cDNA
9291	22367	35917	0.48	6.0E-18	A1908256.1	EST_HUMAN	RC-BT166-020499-014 BT166 Homo sapiens cDNA
11399	24460	38124	3.63	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21, segment HS21C046
11612	24664	38351	1.68	6.0E-18	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
12534	25364	32068	3.91	6.0E-18	U87929.1	NT	Human acornate hydratase (ACO2) gene, exon 4
1171	14334	27390	12.48	5.0E-18	A1280214.1	EST_HUMAN	qmr5g11.x1 Scores_placenta_8tc6weeks_2NbHP8tc6w Homo sapiens cDNA clone IMAGE:1893688 3'
4433	17573	30555	0.59	5.0E-18	10946965	NT	similar to contains: Alu repetitive element;
5387	18589	31561	1.29	5.0E-18	AF087913.1	NT	Mus musculus gasdermin (Gsdm), mRNA
8917	21996	35535	3.47	5.0E-18	BE143312.1	EST_HUMAN	Human endogenous retrovirus HERV-P-147D
							MR0-HT0161-221099-002-c08 HT0161 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11223	24292	37932	3.43	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
11223	24292	37933	3.43	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12675	25450		6.29	5.0E-18	AW867182.1	EST_HUMAN	MR1-SN0035-060400-007-g11 SN0035 Homo sapiens cDNA
13063	25698		28.95	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCGA02 3'
127	13355	26388	0.91	4.0E-18	BE044076.1	EST_HUMAN	h36h04.x1 NCL CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29 b3
127	13355	26387	0.91	4.0E-18	BE044076.1	EST_HUMAN	h36h04.x1 NCL CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29 b3
1754	14903	27898	52.82	4.0E-18	AA621814.1	EST_HUMAN	h36h04.x1 NCL CGAP_Ut1 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326
1938	15081		1.05	4.0E-18	AI738592.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
2274	15407	28536	1.26	4.0E-18	Q06430	SWISSPROT	wf33h08.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2382095 3'
2274	15407	28537	1.26	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
3892	17051	30050	0.61	4.0E-18	AI581586.1	EST_HUMAN	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
5479	18678	31691	2.47	4.0E-18	AI017565.1	EST_HUMAN	ar93h08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu repetitive element;
5479	18678	31692	2.47	4.0E-18	AI017565.1	EST_HUMAN	cu23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
8029	21112		0.62	4.0E-18	AA749811.1	EST_HUMAN	cu23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
11254	24323	37954	7.59	4.0E-18	AA371807.1	EST_HUMAN	mx84a08.s1 NCL CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1266998 similar to contains L1.12 L1 repetitive element;
872	14048	27114	3.81	3.0E-18	AA814196.1	EST_HUMAN	EST33633 Pituitary gland, subcloned (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
963	14128	27187	2.25	3.0E-18	BE088634.1	EST_HUMAN	db23h11.s1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN
4060	17216	30225	1.06	3.0E-18	AL163247.2	NT	P46782 40S RIBOSOMAL PROTEIN S5.
8968	20196	33622	4.72	3.0E-18	BE001671.1	EST_HUMAN	CNM0-BT0690-210300-288-g07 BT0690 Homo sapiens cDNA
11167	24238	37869	1.99	3.0E-18	BF218650.1	EST_HUMAN	CNM0-BT0690-210300-288-g07 BT0690 Homo sapiens cDNA
12832	25554		4.55	3.0E-18	AW022015.1	EST_HUMAN	PM0-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
261	13480	26512	4.2	2.0E-18	AW836820.1	EST_HUMAN	601884856F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103652 5'
1176	14339		74.12	2.0E-18	BE256097.1	EST_HUMAN	d31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485128 5'
3193	16388	29374	0.94	2.0E-18	Q39575	SWISSPROT	QV1-LT0036-150200-070-e07 LT0036 Homo sapiens cDNA
							601114362F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355044 5'
							DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5527	18724		4.2	2.0E-18	AA668610.1	EST_HUMAN	ak53a07 s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR:O14577
5623	18817	31856	3.51	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A08 FROM TQ31, COMPLETE SEQUENCE. ;
5623	18817	31887	3.51	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5699	19184		1.64	2.0E-18	BF347229.1	EST_HUMAN	Human DNA, SINE repetitive element
6294	19467	32820	0.91	2.0E-18	X60459.1	NT	602021164F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
6294	19467	32821	0.91	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6408	19577	32938	0.9	2.0E-18	BF352840.1	EST_HUMAN	Human IFNAR gene for interferon alpha/beta receptor
6448	19615	32979	2.93	2.0E-18	AW665853.1	EST_HUMAN	IL3-HT0619-220700-222-C12 HT0619 Homo sapiens cDNA
7594	20666	34141	0.59	2.0E-18	AA457619.1	EST_HUMAN	h94g01.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2979984 3' similar to contains
8341	21422	34947	0.5	2.0E-18	BE439524.1	EST_HUMAN	MER19.12 MER19 repetitive element ;
10253	23288	36884	0.95	2.0E-18	AW151673.1	EST_HUMAN	TR:G61634 G61634 POLYPEPTIDE PR77 ;
10253	23288	36885	0.95	2.0E-18	AW151673.1	EST_HUMAN	HTM1-160F1 HTM1 Homo sapiens cDNA
11217	24286	37925	2.91	2.0E-18	AW470791.1	EST_HUMAN	x67e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
12031	25014	38716	4.46	2.0E-18	AW151289.1	EST_HUMAN	MER10 repetitive element ;
12465	14339		12.57	2.0E-18	BE256097.1	EST_HUMAN	MER10 repetitive element ;
4537	17875		0.76	1.0E-18	T95406.1	EST_HUMAN	MER10 repetitive element ;
5471	18871	31651	2.64	1.0E-18	AV653405.1	EST_HUMAN	x67e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
5688	18882	32174	3.08	1.0E-18	D00099.1	NT	ha33d06.x1 NCL_CGAP_Kk12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3
5688	18882	32175	3.08	1.0E-18	D00099.1	NT	THR repetitive element ;
6584	19746	33128	1.31	1.0E-18	AL163280.2	NT	xg47e09.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2
8637	21717	35254	1.05	1.0E-18	AI148288.1	EST_HUMAN	MER8 repetitive element ;
							y643g05.1 Scores_fetal liver spceen INFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1
							L1 repetitive element ;
							AV653405 GLC Homo sapiens cDNA clone GLOK11 3'
							Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
							Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
							Homo sapiens chromosome 21 segment HS21C080
							cx69d09.x1 Scores_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680593 3' similar to contains L1
							L1 repetitive element ;
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10103	23141	36740	4.93	1.0E-18	U91328.1	NT	Homo sapiens glycine 3 (GPC3) gene, partial cds and flanking repeat regions
12416	25294	32084	4.65	1.0E-18	AF003529.1	NT	

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
559	13752	26780	5.1	9.0E-19	AA281961.1	EST_HUMAN	z11406.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
560	13762	26780	3.91	9.0E-19	AA281961.1	EST_HUMAN	z11406.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
8032	21115		3.69	9.0E-19	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8886	21965	35501	2.57	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8886	21965	35502	2.57	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11392	24453	38116	3.15	9.0E-19	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
12171	13762	26780	19.34	9.0E-19	AA281961.1	EST_HUMAN	z11406.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
1073	14239		1.58	8.0E-19	AW974902.1	EST_HUMAN	EST387007 IMAGE: ressequences, MAGN Homo sapiens cDNA
8342	21423	34948	1.12	8.0E-19	BE158938.1	EST_HUMAN	MFR0-HT0404-210200-001-g08 HT0404 Homo sapiens cDNA
2319	15451	28583	1.74	7.0E-19	4758139	NT	Homo sapiens DEAD(H) (Asp-Glu-Ala-AspHis) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
6885	19747	33129	2.11	7.0E-19	AF092090.1	NT	Rattus norvegicus opt151 mRNA, partial cds
7452	20529	34002	0.94	7.0E-19	P26444	SWISSPROT	BETA CRYSTALLIN A2
10216	23252	36841	0.54	7.0E-19	A1344951.1	EST_HUMAN	h01c08.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052302 3'
12316	28183		1.72	7.0E-19	AA705684.1	EST_HUMAN	z10b001.s1 Soares_fetal_liver_spleen_TNFSF_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3878	17038		1.16	6.0E-19	AW852930.1	EST_HUMAN	PMD-CT0248-131099-001-g01 C10248 Homo sapiens cDNA
4585	17722	30705	1.56	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4585	17722	30706	1.56	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4921	18051		1.2	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5078	19163	32483	5.17	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZF-X) (RC55)
6346	19516	32873	0.59	5.0E-19	AW663302.1	EST_HUMAN	h177606.y1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2968787 5'
10639	23673	37283	1.18	5.0E-19	AJ287699.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11829	24818	38509	8.14	5.0E-19	AW183725.1	EST_HUMAN	x87602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2684171 3' similar to contains element MSR1 repetitive element;
							Human germ-line T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S8A3N2T, TCRBV13S8A2T, TCRBV6S9P, TCRBV5S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S6A2T, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV6S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
13083	25895		1.34	5.0E-19	U66060.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIA0501
568	13760	26784	0.96	4.0E-19	AB007970.1	NT	60213091DF1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'
2747	15864	28975	1.15	4.0E-19	BF697362.1	EST_HUMAN	

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5512	18710	31725	1.2	4.0E-19	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3955	17113	30114	1.02	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3955	17113	30115	1.02	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4400	17543	30526	0.85	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4400	17543	30527	0.85	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4569	17707	30686	1.42	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
5394	18696		0.69	3.0E-19	AF223467.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
7543	20615		1.88	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
9658	21101	34614	1.09	3.0E-19	X89685.1	NT	M. musculus mRNA for TPCR33 protein
12563	25395		16.36	3.0E-19	AF165520.1	NT	Homo sapiens phospholipase I protein (PBI) mRNA, complete cds
2627	15750	28863	20.06	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4588	17708		1.34	2.0E-19	AJ311783.1	EST_HUMAN	Q93160.2 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386 POL/ENV GENE;
6179	19355	32703	0.81	2.0E-19	AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5'
7493	20588	34040	0.83	2.0E-19	Q67286	NT	Mus musculus keratin-associated protein 9-1 (Ktap9-1), mRNA
8525	21606	35145	10.24	2.0E-19	AA012854.1	EST_HUMAN	zn34c09.r1 Soares relina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
10113	23151	36783	0.84	2.0E-19	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
494	13699		1.86	1.0E-19	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3638310 5'
2233	15357	26496	1.64	1.0E-19	H30795.1	EST_HUMAN	yo79g07.r1 Soares adult brain N2b4HB5SY Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2782	15898		2.4	1.0E-19	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2909	16087		6.72	1.0E-19	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3488	16855	29669	1.18	1.0E-19	AA834967.1	EST_HUMAN	a49b12.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12 MER37 repetitive element;
5452	18852	31631	0.73	1.0E-19	A180886.1	EST_HUMAN	wm91b08.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2449287 3' similar to TR:Q16530 Q16530 PMS3 MRNA;
6199	19374	32725	2.6	1.0E-19	U12186.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
6337	26213		*0.63	1.0E-19	AA595527.1	EST_HUMAN	nh22d03.s1 NCI CGAP_P1 Homo sapiens cDNA clone IMAGE:953093 similar to contains L1.1 L1 repetitive element;
7806	20862	34355	1.05	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
7806	20862	34356	1.05	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
7977	25856		0.75	1.0E-19	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8644	21724	35261	1.94	1.0E-19	M64657.1	NT	Rabbit phosphatase kinase beta subunit mRNA, complete cds
8939	22018		2.72	1.0E-19	T99920.1	EST_HUMAN	ye72b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element;
9950	22989		0.69	1.0E-19	UG0822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
10390	23425	37032	25.12	1.0E-19	AW812259.1	EST_HUMAN	RCO-ST0174-191099-031-b05 ST0174 Homo sapiens cDNA
10400	23435	37042	1.59	1.0E-19	N44631.1	EST_HUMAN	W31e09.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:272872 5'
11184	24253	37888	1.87	1.0E-19	BE616026.1	EST_HUMAN	601279882F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611493 5'
6784	18939	33336	2.4	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6784	19039	33337	2.4	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7687	20752	34234	1.46	8.0E-20	A121371.1	EST_HUMAN	qg86f09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7687	20752	34235	1.46	8.0E-20	A121371.1	EST_HUMAN	qg86f09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3349	16521	29537	0.71	7.0E-20	BF326455.1	EST_HUMAN	PM4-AN0096-050900-003-a04 AN0096 Homo sapiens cDNA
7134	18560	31474	5.66	7.0E-20	AL138120.1	EST_HUMAN	DKFZp547D092_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D092 5'
8693	21773	35305	8.83	7.0E-20	AA557657.1	EST_HUMAN	nl46d04.s1 NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
8693	21773	35306	8.83	7.0E-20	AA557657.1	EST_HUMAN	nl46d04.s1 NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
12014	24958		2.89	7.0E-20	6912633	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
3645	18808	29822	3.64	6.0E-20	P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4387	17530	30511	4.58	6.0E-20	BE622434.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4718	17853		1.8	5.0E-20	AV725123.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTC8TA01 5'
7264	20347	33789	1.42	5.0E-20	AF075301.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
8131	21213	34733	6.86	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element;
8131	21213	34734	6.86	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element;
8285	21377	34998	0.78	5.0E-20	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9035	22114	35657	1.28	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9035	22114	35658	1.28	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9844	21087		1.13	5.0E-20	O60809	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.1
1649	14802	27889	0.94	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5765	18957		1.13	4.0E-20	Q98880	SWISSPROT	HISTONE H2B C (H2B/C)
8110	21192		5.61	4.0E-20	AI874952.1	EST_HUMAN	tb64g03.x1 NCI_CGAP_Ox35 Homo sapiens cDNA clone IMAGE:2293396 3'
10717	23750	37357	1.13	4.0E-20	AW937469.1	EST_HUMAN	QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2207	15341	28468	1.22	3.0E-20	U03898.1	NT	Human BXP21 gene
4325	17468	30455	1.29	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4747	17882	30864	1.08	3.0E-20	AA037618.1	EST_HUMAN	z339b12 st Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element;
9135	22214		2.69	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
10527	23562	37168	0.47	3.0E-20	BF185294.1	EST_HUMAN	6018435561 F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084343 5'
10900	23984		1.99	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
12331	25239	32109	6.09	3.0E-20	BE888422.1	EST_HUMAN	6015141801 F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
853	14030		5.65	2.0E-20	AW303868.1	EST_HUMAN	x24e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
1135	14300	27355	2.49	2.0E-20	AA516335.1	EST_HUMAN	P97461 40S RIBOSOMAL PROTEIN S5. ;
1135	14300	27355	2.49	2.0E-20	AA516335.1	EST_HUMAN	ng69h09.st NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:940087 similar to TR:G1224066
1135	14300	27355	2.49	2.0E-20	AA516335.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN. ;
2878	14030		5.32	2.0E-20	AW303868.1	EST_HUMAN	ng69h09.st NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:940087 similar to TR:G1224066
5061	18189	31163	5.15	2.0E-20	Q28983	SWISSPROT	G1224066 ORF2: FUNCTION UNKNOWN. ;
5061	18189	31164	5.15	2.0E-20	Q28983	SWISSPROT	x24e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
5258	18376		0.9	2.0E-20	5174538	NT	ZONADHESIN PRECURSOR
8309	21391	34915	0.97	2.0E-20	AA309457.1	EST_HUMAN	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
9391	22456	36030	2.65	2.0E-20	D10083.1	NT	EST180328 Liver: III Homo sapiens cDNA 5' end
9391	22456	36031	2.65	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12743	25878	31852	2.17	2.0E-20	H55371.1	EST_HUMAN	CHFR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
2070	15995	28327	6.61	1.0E-20	AA281961.1	EST_HUMAN	z11d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
4560	17698	30679	1.02	1.0E-20	BF115150.1	EST_HUMAN	MER19 repetitive element ;
7034	20170	33592	0.74	1.0E-20	AF049507.1	EST_HUMAN	h184b06.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1 repetitive element ;
9364	22439	35998	2.08	1.0E-20	11418491	NT	AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
11847	24836	38530	2.03	1.0E-20	AF223391.1	EST_HUMAN	Homo sapiens Autosomal Highly Conserved Protein (AHCOP), mRNA
12461	25323		2.91	1.0E-20	AA420453.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
						NT	nc60g08.r1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.13 L1 repetitive element ;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2979	16155		1.18	9.0E-21	AJ003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MP112-8J21
12174	25135		3.98	9.0E-21	AW698189.1	EST_HUMAN	RC3-NN0068-090500-021-503 NN0068 Homo sapiens cDNA
9011	22090		0.88	8.0E-21	AW674891.1	EST_HUMAN	b530a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2984714 5' similar to SW:NIAM_HUMAN
11830	24819	38510	3.91	8.0E-21	AA809411.1	EST_HUMAN	C95169 NADH-UBIQUINONE OXIDOREDUCTASE ASHI SUBUNIT PRECURSOR ;
12345	25250		3.8	8.0E-21	O21330	SWISSPROT	ob71f06.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
2130	15266	28385	3.85	7.0E-21	P15800	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2130	15266	28388	3.85	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
3792	16953	29958	1.36	7.0E-21	AL163300.2	NT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
4369	17512		6.28	7.0E-21	AA046502.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
6564	19726	33104	0.94	7.0E-21	AL163218.2	NT	ZK67a06.t1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487868 5'
8582	21653	35203	1.46	7.0E-21	AJ277557.1	NT	Homo sapiens chromosome 21 segment HS21C018
8875	21954	35490	4.94	7.0E-21	D14718.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
10319	23354	36963	1.07	7.0E-21	AW856922.1	EST_HUMAN	Human chromosomal protein HM1G1 related gene
10934	24016	37648	1.94	7.0E-21	AA723404.1	EST_HUMAN	RC0-CT0301-271199-031-F03 CT0301 Homo sapiens cDNA
4220	17369	30358	0.75	6.0E-21	BE408611.1	EST_HUMAN	Zg73d03.s1 Soares_fetal_heart_NbHH18W Homo sapiens cDNA clone IMAGE:398981 3' similar to
8336	22412		1.39	6.0E-21	BE162737.1	EST_HUMAN	gbM14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); contains THR.13 OFR
947	14120	27181	1.34	5.0E-21	5902031	NT	repetitive element ;
2354	15485	28617	1.23	5.0E-21	AA928194.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
4483	17623	30604	3.21	5.0E-21	BE968939.1	EST_HUMAN	PM1-HT0454-080100-002-H09 HT0454 Homo sapiens cDNA
4809	14120	27181	1.16	5.0E-21	5902031	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
4923	18053	31039	8.33	5.0E-21	4885474	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
6902	20217		0.77	5.0E-21	AW440864.1	EST_HUMAN	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
7157	20291	33734	1	5.0E-21	BE856505.1	EST_HUMAN	he05e10.x1 NCL CGAP_GML1 Homo sapiens cDNA clone IMAGE:2918154 3'
10801	23834	37457	0.54	5.0E-21	Q91690	SWISSPROT	783d11.x1 NCL CGAP_P728 Homo sapiens cDNA clone IMAGE:3303573 3' similar to contains OFR.t1
12559	25195	37458	1.28	5.0E-21	AA393574.1	EST_HUMAN	OFR repetitive element ;
1772	14921	28015	1.86	4.0E-21	AA970713.1	EST_HUMAN	ZINC FINGER PROTEIN GLI1 (GLI-1)
							ZINC FINGER PROTEIN GLI1 (GLI-1)
							ZK72c04.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'
							cd86e08.s1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530
							PMS3 MRNA ; contains OFR.t1 OFR repetitive element ;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7011	20147	33668	2.61	4.0E-21	AB019578.1	NT	Rattus norvegicus mRNA for r11M, complete cds
9983	23022	36614	0.82	4.0E-21	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10010	23048	36642	0.51	4.0E-21	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21G002
1884	15028	28135	1.1	3.0E-21	AA218891.1	EST_HUMAN	zq15c06.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629771 3'
2348	15479	28611	1.51	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3149	16324	29335	6.41	3.0E-21	AJ007873.1	NT	Homo sapiens LGMD2B gene
5616	18810	31878	0.92	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5616	18810	31879	0.92	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5855	19046		0.9	3.0E-21	AV681044.1	EST_HUMAN	AV681044 GLC Homo sapiens cDNA clone GLC GOA10 3'
6308	19480		2.74	3.0E-21	BF184739.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064945 5'
7215	20080	33493	7.52	3.0E-21	BF361093.1	EST_HUMAN	RC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA
8894	22934	36518	0.92	3.0E-21	AW897760.1	EST_HUMAN	CMT1-NN0053-280400-203-r08 NN0053 Homo sapiens cDNA
12879	26098	31685	3.58	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
150	13375		24.5	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
958	14131	27189	0.51	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
958	14131	27190	0.51	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1241	14400		3.03	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-r05 BT0311 Homo sapiens cDNA
2703	15921	28937	2.59	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2703	15921	28938	2.59	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5801	18798	31846	1.56	2.0E-21	A1624582.1	EST_HUMAN	ts30f03.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q98854
5894	18888	32178	0.8	2.0E-21	AA027211.1	EST_HUMAN	HYPOTHETICAL 51.1 KD PROTEIN;
5894	18888	32179	0.8	2.0E-21	AA027211.1	EST_HUMAN	z897a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
6157	19333	32679	0.74	2.0E-21	W44493.1	EST_HUMAN	z897a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8467	21548	35078	0.58	2.0E-21	AJ010770.1	NT	z897a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8558	21639	35176	8.13	2.0E-21	BE141785.1	EST_HUMAN	z897a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
9023	22102	35642	3.27	2.0E-21	AU136779.1	EST_HUMAN	QV04-HT0103-091199-060-g11 HT0103 Homo sapiens cDNA
11313	24377		2.04	2.0E-21	BE380127.1	EST_HUMAN	AU130779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
11599	24652	38335	2.83	2.0E-21	BE973829.1	EST_HUMAN	HT09d01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
						EST_HUMAN	MER29 repetitive element;
						EST_HUMAN	601880636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11599	24652	38338	2.88	2.0E-21	BE973829.1	EST_HUMAN	601680636F1 NIH_MGC_B3 Homo sapiens cDNA clone IMAGE:3951008 5'
12572	28359		6.44	2.0E-21	AF176815.1	NT	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds n46c04.s1 NCL_CGAP_P74 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
1284	14440	27509	1.89	1.0E-21	AA557657.1	EST_HUMAN	MER29 repetitive element;
1434	14637		4.93	1.0E-21	AI601264.1	EST_HUMAN	ar88d12.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
6616	19776		2.73	1.0E-21	AL079752.1	EST_HUMAN	DKFZ43410830_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I0830 5'
7342	20422	33885	4.7	1.0E-21	AI223104.1	EST_HUMAN	qg47e05.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:M64241 QIM PROTEIN (HUMAN);
10448	23483	37092	0.47	1.0E-21	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10448	23483	37093	0.47	1.0E-21	AL163203.2	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10812	23845		1.31	1.0E-21	5730038	NT	Homo sapiens chromosome Xp22 410-8
13014	25657		1.67	1.0E-21	AF046133.1	NT	bs44a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2286204 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT;
4530	17698	30854	2.38	9.0E-22	A702438.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
8803	21832	35420	2.02	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
8803	21832	35421	2.02	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
11031	24110	37746	3.1	9.0E-22	AV761874.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSGCCG05 5'
12007	24992	38696	1.39	9.0E-22	AU140358.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE2000394 5'
971	14144		7.93	8.0E-22	BE144748.1	EST_HUMAN	CWC-HT0179-281088-076-h05 HT0179 Homo sapiens cDNA
8080	21192		3.36	8.0E-22	AA046502.1	EST_HUMAN	2k07a06.r1 Scores_pregnant_uterus_NHPLU Homo sapiens cDNA clone IMAGE:487658 5'
682	13667	26898	3.78	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
4398	17541	30522	3.27	7.0E-22	Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
5150	18272	31241	0.91	7.0E-22	AB009681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8888	21957		1.24	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
9032	22111	35653	2.77	7.0E-22	M76590.1	EST_HUMAN	EST00738 Fetal brain, Striatum (cat#36208) Homo sapiens cDNA clone HFBCF07
9802	22842	36419	2.06	7.0E-22	AF009680.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TORBV12S2 region
8436	21517		1.25	6.0E-22	AW029123.1	EST_HUMAN	W005g07.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
6646	19805	33192	3.27	5.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10525	23560	37167	2.98	5.0E-22	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12833	25556		1.63	5.0E-22	BF476511.1	EST_HUMAN	naa27506.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3255898 3' similar to contains Alu repetitive element;
3726	16887		0.77	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
8608	26224		2.81	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10961	24042	37677	1.97	4.0E-22	BF218030.1	EST_HUMAN	601682813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13021	25672		3.85	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
981	14154		1.34	3.0E-22	AI469679.1	EST_HUMAN	hm14h10.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2158611 3' similar to gbL19593 HIGH AFFINITY INTERLEUKIN-3 RECEPTOR B (HUMAN); contains L11 L1 repetitive element;
2636	15759	28873	1.33	3.0E-22	AI859038.1	EST_HUMAN	w66b04.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2428839 3' similar to SW:RL21_HUMAN
3763	16924		1.65	3.0E-22	D14718.1	NT	P46778 B05 RIBOSOMAL PROTEIN L21;
4922	18052	31038	3.18	3.0E-22	AI090125.1	EST_HUMAN	Human chromosomal protein HMG1 related gene
8011	21061	34573	0.8	3.0E-22	P11369	SWISSPROT	qb28d07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element;
8425	21506		1.11	3.0E-22	BE156613.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8430	21511	35042	1.88	3.0E-22	BE089841.1	EST_HUMAN	QY0-HT0368-090200-099-112 HT0368 Homo sapiens cDNA
8555	21636	35172	1.14	3.0E-22	X60660.1	NT	RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
8555	21636	35173	1.14	3.0E-22	X60660.1	NT	R ratius RY2G5 mRNA for a potential ligand-binding protein
2008	15148		4.04	2.0E-22	N24942.1	EST_HUMAN	R ratius RY2G5 mRNA for a potential ligand-binding protein
2590	15715	28833	1.72	2.0E-22	P24916	SWISSPROT	yk73d05.s1 Soares_melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:267369 3'
3507	16674	29684	3.98	2.0E-22		SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
4341	17484	30466	1.41	2.0E-22	AW817794.1	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
5973	28814	32476	1.47	2.0E-22	W39456.1	EST_HUMAN	PM1-ST0262-261199-001-d12 ST0262 Homo sapiens cDNA
6306	19478	32833	3.58	2.0E-22	BF092116.1	EST_HUMAN	zz2001.l1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
6904	22944	36529	1.78	2.0E-22	AI276522.1	EST_HUMAN	RC0-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA
10001	23039	36630	0.85	2.0E-22	AA715315.1	EST_HUMAN	qf76h08.x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains MER29.13 MER29 repetitive element;
10001	23039	36631	0.85	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1219289 3'
12056	25037	38745	1.52	2.0E-22	AW418990.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1219289 3'
12139	25656	31854	2.33	2.0E-22	AL163280.2	NT	he24f04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
1927	15070	28175	2.05	1.0E-22	AW885517.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2651	15774	28887	2.36	1.0E-22	U50871.1	NT	PMA-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA
3497	16864	29676	1.53	1.0E-22	D14547.1	NT	Human familial Alzheimer's disease (STIM2) gene, complete cds
7920	20971	34478	1.09	1.0E-22	BE094667.1	EST_HUMAN	Human DNA, SINE repetitive element
10776	23809	37432	1.05	1.0E-22	AI365435.1	EST_HUMAN	MRO-BT0659-220200-002-h07 BT0659 Homo sapiens cDNA
							qz09b07.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2
							MER29 repetitive element;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10776	23809	37433	1.05	1.0E-22	A365435.1	EST_HUMAN	q209b07.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2 MER29 repetitive element;
13078	25707		12.31	9.0E-23	AW802801.1	EST_HUMAN	IL2-UM0076-070400-061-F11 UM0076 Homo sapiens cDNA
3661	16824	29833	0.74	8.0E-23	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3385	16555		2.21	7.0E-23	AV647246.1	EST_HUMAN	AV647246 GLC Homo sapiens cDNA clone GLCAW007 3'
11293	24359	38000	3.74	7.0E-23	5031982	NT	Homo sapiens Not66 (D. melanogaster)-like protein (NOT56L) mRNA
3520	16696		1.83	6.0E-23	AF199333.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
4383	17526	30507	1.15	6.0E-23	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
12283	25211	32097	4.93	6.0E-23	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12283	25211	32098	4.93	6.0E-23	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12483	25335	32058	3.18	6.0E-23	AI209130.1	EST_HUMAN	q358c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to SW.MV10_MOUSE P23249 PROTEIN MOV-10;
5560	18757	31798	4.01	5.0E-23	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), catractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
6369	25824	32898	3.69	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
7695	25824	32898	2.78	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6570	19732	33110	0.67	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6570	19732	33111	0.67	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8022	21105	34622	3.26	3.0E-23	AA130185.1	EST_HUMAN	z135g09.r1 Soares_pregnant_uterus_Nish-PU Homo sapiens cDNA clone IMAGE:503988 5' similar to contains MER29.12 MER29 repetitive element;
9450	22566	36130	3.72	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
9450	22566	36131	3.72	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
10523	23558		1.42	3.0E-23	AW897627.1	EST_HUMAN	RC3-NN0068-270400-011-h01 NN0068 Homo sapiens cDNA
11372	24433		1.35	3.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450
683	13668	26899	3.69	2.0E-23	AI289860.1	NT	polypeptide 5 (CYP3A5) gene, partial cds
1166	15988		3.46	2.0E-23	M55270.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
2856	15970	29079	1	2.0E-23	P22105	SWISSPROT	Human matrix Gla protein (MGP) gene, complete cds
2856	15970	29080	1	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2856	15970	29080	1	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripbr
3457	16624		1.11	2.0E-23	AI201488.1	EST_HUMAN	qs73f11.x1 NCL CGAP P128 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR-Q13537 Q13537
3810	16970		3.53	2.0E-23	BE165980.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
4086	17240	30246	4.43	2.0E-23	H59931.1	EST_HUMAN	MF3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
4085	17240	30247	4.43	2.0E-23	H59931.1	EST_HUMAN	Y16802.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:205418 5'
							Y16802.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:205418 5'
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
8057	21140		5.28	2.0E-23	AF280107.1	NT	Homo sapiens chromosome 21 segment HS21G103
9044	22123	35685	0.95	2.0E-23	AL163303.2	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
12265	25199		6.7	2.0E-23	M32698.1	NT	Homo sapiens T cell receptor beta locus. TCRBV733A2 to TCRBV12S2 region
12844	25561		3.68	2.0E-23	AF009660.1	NT	Homo sapiens OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
12863	26103		2.3	2.0E-23	AU133931.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21G052
4650	17786	30769	1.37	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21G010
4888	18018		5.42	1.0E-23	AL163210.2	NT	601236459F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
6861	20013		3.27	1.0E-23	BE378471.1	EST_HUMAN	zvr82c06.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.12
8551	21632	35168	4.61	1.0E-23	AA448097.1	EST_HUMAN	PTR5 repetitive element ;
10909	23992	37625	2.19	1.0E-23	BE409643.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
10909	23992	37628	2.19	1.0E-23	BE409643.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
13082	26074	31654	1.35	1.0E-23	AW901816.1	EST_HUMAN	QV0-NN1020-170400-185-at1 NN1020 Homo sapiens cDNA
							ab75a08.s1 Stragagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852768 3' similar to
566	13759		1.67	9.0E-24	AA663213.1	EST_HUMAN	TR-E19822 E19822 CA PROTEIN. ;
4771	17906	30888	1.12	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 13
4771	17906	30889	1.12	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 13
6578	19740	33121	0.95	8.0E-24	11422027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
3976	17133		0.94	7.0E-24	AW937654.1	EST_HUMAN	QV0-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA
5281	18400		16.79	7.0E-24	AL039493.1	EST_HUMAN	DKFZp434A2311.1_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A2311 5'
10876	23961		1.51	7.0E-24	AW303317.1	EST_HUMAN	Xv17f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element ;
724	13906		2.21	6.0E-24	AB001421.1	NT	Macaca fuscata mRNA for Testis-Specific Protein Y (TSPY), complete cds
861	14038	27100	12.8	6.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21G049
4078	17234	30241	9.39	5.0E-24	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
7635	20685	34493	1.27	5.0E-24	AFZ23391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4371	17514		0.9	4.0E-24	BF369469.1	EST_HUMAN	RCO-GN0090-250900-022-h09 GN0090 Homo sapiens cDNA nm31h05.s1 NCI CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW:POL_MLVK
6052	19234	32559	2.77	4.0E-24	AA594178.1	EST_HUMAN	P31795 POL POLYPROTEIN ;
8890	21959	35494	0.71	4.0E-24	AW813711.1	EST_HUMAN	RC3-ST0197-130100-014-f06 ST0197 Homo sapiens cDNA
11454	24514	38182	2.05	4.0E-24	BE544822.1	EST_HUMAN	601078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:346498 5'
12699	25446	32054	4.02	4.0E-24	AB028016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
7226	20134	33551	0.73	3.0E-24	U66061.1	NT	Human gamma T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV16S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>
7229	20134	33552	0.73	3.0E-24	U66061.1	NT	Human gamma T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV16S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY8, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>
8618	21698		2.94	3.0E-24	AW614871.1	EST_HUMAN	h86608.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867950 3' similar to contains MER29.b2 MER29 repetitive element ;
8673	21763		1.24	3.0E-24	AW602076.1	EST_HUMAN	EST374149 IMAGE resequencer, MAGG Homo sapiens cDNA
9666	22627	36198	3.79	3.0E-24	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
12766	25501	32034	1.34	3.0E-24	BF127782.1	EST_HUMAN	601810449F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053396 5'
2422	15551	28678	2.55	2.0E-24	AA167535.1	EST_HUMAN	zp11709.r1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:909161 5'
3899	17098		0.82	2.0E-24	AW898189.1	EST_HUMAN	RC3-NN0088-090500-021-b03 NN0088 Homo sapiens cDNA
7515	26219		0.63	2.0E-24	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7643	20712	34191	0.9	2.0E-24	AF088824.1	NT	Mus musculus fibroblast-interacting citron kinase (Cik) mRNA, complete cds
7648	20717	34194	0.58	2.0E-24	AJ003536.1	EST_HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MP12.5H13
8938	22017	35558	3.31	2.0E-24	AL118198.1	EST_HUMAN	DKFZp761L1712_1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
8977	22056		0.9	2.0E-24	H69214.1	EST_HUMAN	y62b09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains MER28 repetitive element ;
10058	23096	36698	1.06	2.0E-24	A1521759.1	EST_HUMAN	u77a09.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
10058	23096	36698	1.06	2.0E-24	A1521759.1	EST_HUMAN	u77a09.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
12580	26153	27972	21.43	2.0E-24	M28877.1	NT	Human O family dispersed repeat element
1731	14881		4.81	1.0E-24		NT	Homo sapiens CGI-127 protein (LOC51649), mRNA
2798	15855		1.65	1.0E-24	AW820194.1	EST_HUMAN	QV0-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA
3085	16261	29278	0.72	1.0E-24	D86423.1	NT	Mus musculus mRNA for HGT keratin, partial cds
4385	17528		1.93	1.0E-24	AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6531	19695	33068	1.13	1.0E-24	7106336	NT	Mus musculus keratin complex-1, gene C29 (Krt1-c29), mRNA
7720	20784	34272	4.85	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7907	20659	34465	5.07	1.0E-24	BE144526.1	EST_HUMAN	MRO-HT0166-271199-005-409 HT0166 Homo sapiens cDNA
8130	21212	34732	2.29	1.0E-24	AW901164.1	EST_HUMAN	QW0-NN1010-130300-281-407 NN1010 Homo sapiens cDNA
11989	24984	38689	1.37	9.0E-25	7706707	NT	Homo sapiens putative secreted protein (SIG11), mRNA
5111	18239	31206	2.7	7.0E-25	AA483944.1	EST_HUMAN	ne92e10.st NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2 MER1 repetitive element:
8413	21494	35025	3.7	7.0E-25	AA468646.1	EST_HUMAN	ne06a09.st NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element:
12003	24988	38693	3.64	7.0E-25	AA583540.1	EST_HUMAN	ni25h06.st NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST
7131	18557		5.04	6.0E-25	W87623.1	EST_HUMAN	P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA.
7889	20651	34458	11.72	6.0E-25	7305360	NT	2h5h07.r1 Sceres_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416989 5'
1683	14835	27920	1.61	5.0E-25	AW850271.1	EST_HUMAN	Mus musculus otogelin (Otog), mRNA
11596	24649	38333	3.12	5.0E-25	AW979107.1	EST_HUMAN	IL3-CT0219-161189-031-D04 CT0219 Homo sapiens cDNA
1478	14631	27716	2.66	4.0E-25	T98107.1	EST_HUMAN	EST391217 MAGE resequences, MAGEF Homo sapiens cDNA
3489	16656		2.81	4.0E-25	AW857671.1	EST_HUMAN	ye56h04.r1 Sceres_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:121783 5'
4436	17578		4.06	4.0E-25	BE170957.1	EST_HUMAN	PM3-O10093-280200-001-g07 OT0093 Homo sapiens cDNA
10144	23182	36779	0.83	4.0E-25	AA383873.1	EST_HUMAN	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
2256	16399	28516	1.02	3.0E-25	BE069922.1	EST_HUMAN	EST97317 Thymus J Homo sapiens cDNA 5' end similar to EST containing O family repeat
3396	16566	29582	3.12	3.0E-25	P29622	SWISSPROT	ROS-BT0377-131299-031-F02 BT0377 Homo sapiens cDNA
5015	18144	31119	0.7	3.0E-25	AL163210.2	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
8532	21613	35149	5.42	3.0E-25	AL163210.2	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
11287	24353	37993	2.7	3.0E-25	AA579013.1	EST_HUMAN	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
1378	14533	27607	4.9	2.0E-25	5032158	NT	Homo sapiens chromosome 21 segment HS21C010
2382	15513	28641	7.33	2.0E-25	BE888016.1	EST_HUMAN	ni30h10.st NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.11 L1 repetitive element:
2893	15731	28848	3.71	2.0E-25	P17008	SWISSPROT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
4307	17450	30436	1.61	2.0E-25	P17008	SWISSPROT	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
4307	17450	30437	1.61	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
9367	23006	36601	2.13	2.0E-25	AL449573	EST_HUMAN	40S RIBOSOMAL PROTEIN S16
375	13583	26817	0.81	1.0E-25	AL040229.1	EST_HUMAN	40S RIBOSOMAL PROTEIN S16
1277	14434		2.07	1.0E-25	9635487	NT	AL449573 Homo sapiens Testis (Slavides GS) Homo sapiens cDNA DKFZp434H0313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0313 5' Human endogenous retrovirus, complete genome

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4983	18112	31089	2.71	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-H09 HT0454 Homo sapiens cDNA
5288	18415	31383	1.16	1.0E-25	8923786	NT	Homo sapiens HSPC059 protein (HSPC059), mRNA
5298	18415	31384	1.16	1.0E-25	8923786	NT	Homo sapiens HSPC059 protein (HSPC059), mRNA
6697	19855		0.95	1.0E-25	AA18080.1	EST_HUMAN	Zq45b06.s1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element
6930	25838	33686	2.95	1.0E-25	AA582650.1	EST_HUMAN	nm54ht11.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087749 3'
8098	21180	34698	3.56	1.0E-25	AA709079.1	EST_HUMAN	z66g04.s1 Soares_fetal_heart_NbH-H19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR5.13 PTR5 repetitive element
9746	22810	36388	1.32	1.0E-25	X60660.1	NT	R_rattus RY2G5 mRNA for a potential ligand-binding protein
9746	22810	36389	1.32	1.0E-25	X60660.1	NT	R_rattus RY2G5 mRNA for a potential ligand-binding protein
11212	24281	37920	3.11	1.0E-25	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
12280	25209	38364	1.62	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
12280	25209	38365	1.62	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
2553	15678	28802	1.94	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11252	24321		2.35	9.0E-26	AI905368.1	EST_HUMAN	GV-BT087-301298-006 BT087 Homo sapiens cDNA
12140	25901		5.33	9.0E-26	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5811	16001		1.51	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1608	14761	27840	5.61	7.0E-26	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4089	17244	30251	1.68	7.0E-26	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
4275	17420	30407	1.92	7.0E-26	AW340153.1	EST_HUMAN	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908396 3'
5755	18947	32249	0.94	7.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11966	24951		6.85	7.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Stralagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:348943 5' similar to gb:U14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
12901	25596		5.49	7.0E-26	AW954559.1	EST_HUMAN	EST366629 IMAGE resequences, MAGC Homo sapiens cDNA
2300	15432	28565	3.83	6.0E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
3427	16596	29611	0.69	6.0E-26	AA206131.1	EST_HUMAN	z63h04.r1 Stralagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 5'
10753	23786	37400	0.82	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10753	23786	37401	0.82	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11979	24964	38666	2.15	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1204	14366	27426	0.89	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1204	14366	27427	0.89	5.0E-26	AI708235.1	EST_HUMAN	ss38h08.x1 Barstead aorta HP_LRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP-F49C12.11 CE03871;
9612	22697		3.29	4.0E-26	7657670	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
10897	23981	37613	2.84	4.0E-26	BE266187.1	EST_HUMAN	301191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3635210 5'
11604	24657	38342	1.38	4.0E-26	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1797	14946	28038	1.26	3.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
2059	15200	28314	1.14	3.0E-26	AL045856.2	EST_HUMAN	DKFZp434I066_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434I066 5'
2088	15228		3.34	3.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Striatogene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:MI4338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3878	17037	30035	1.41	3.0E-26	AA152464.1	EST_HUMAN	zo30f10.r1 Striatogene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 G695374 THYROID RECEPTOR INTERACTOR;
3878	17037	30036	1.41	3.0E-26	AA152464.1	EST_HUMAN	zo30f10.r1 Striatogene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 G695374 THYROID RECEPTOR INTERACTOR;
7051	20104	33521	6.09	3.0E-26	BF245458.1	EST_HUMAN	301864963F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
11867	24855	38550	1.97	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-c05 PT0012 Homo sapiens cDNA
11867	24855	38551	1.97	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-c05 PT0012 Homo sapiens cDNA
11902	24890	38591	7.79	3.0E-26	AA583173.1	EST_HUMAN	nn37d05.s1 NCI_CGAP_GCS Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.11
699	13882	26916	6.84	2.0E-26	AL163282.2	NT	OFR repetitive element;
1917	15060		3.07	2.0E-26	AL038093.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
3303	16477	29489	5.22	2.0E-26	X86994.1	NT	DKFZp566L171_s1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566L171 3'
10991	24070		1.93	2.0E-26	D87675.1	NT	M.musculus mRNA for astrocytic phosphoprotein, PEA-15
11493	24551	38226	2.96	2.0E-26	AI801412.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
11704	24701		2.06	2.0E-26	AF055086.1	NT	repetitive element; contains element MER20 MER20 repetitive element;
12989	25275		1.76	2.0E-26	AB037959.1	NT	Homo sapiens MHC class 1 region
12804	26098	31658	2.33	2.0E-26	BE170371.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
139	13365	26398	8.96	1.0E-26	BE170371.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2105	16244	28366	1.42	1.0E-26	AL038093.2	EST_HUMAN	QV4-HT0838-020300-123-e02 HT0838 Homo sapiens cDNA
2751	15668		6.28	1.0E-26	AF261085.1	NT	DKFZp434H1910_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H1910 5'
6980	20208		2.89	1.0E-26	BE165980.1	EST_HUMAN	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
11131	24203		1.95	1.0E-26	AL038487.1	EST_HUMAN	MIR3-HT0487-160200-113-g01 HT0487 Homo sapiens cDNA
12655	26178		2.77	1.0E-26	H55093.1	EST_HUMAN	DKFZp566C2148_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566C2148 5'
13175	25763		1.16	1.0E-26	AW408742.1	EST_HUMAN	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
							U1HF-BMO-adv-d-10-o-UJ.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063210 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7757	20816		0.87	9.0E-27	BF371227.1	EST_HUMAN	RC6-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
9503	22768		5.02	9.0E-27	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
12143	25118		6.5	9.0E-27	BF445556.1	EST_HUMAN	naa03c07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3253644 3' similar to contains OFR.t1 OFR repetitive element:
11	13249	26249	4.22	8.0E-27	A1831482.1	EST_HUMAN	wf9c04.x1 NCI_CGAP_Lut19 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2 THR repetitive element:
571	13763		4.57	8.0E-27	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1448	14601	27678	23.84	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN):
1448	14601	27679	23.84	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN):
2236	15369	28499	1.82	8.0E-27	AW864776.1	EST_HUMAN	PM2-SN0018-220300-002-007 SN0018 Homo sapiens cDNA
3254	16428	28446	1.8	8.0E-27	P12236	SWISSPROT	ADP ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3434	16602	28621	0.75	8.0E-27	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
5812	16002	32308	1.07	8.0E-27	AV732214.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBCB06 5'
7117	16543		2.65	8.0E-27	BE926560.1	EST_HUMAN	MR4-BT0398-250800-204-006 BT0398 Homo sapiens cDNA
7192	20057	33467	2.49	8.0E-27	N84970.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to REPETITIVE ELEMENT L1
9410	22494	36048	1.63	8.0E-27	AW857579.1	EST_HUMAN	CM1-CT0315-091269-063-007 CT0315 Homo sapiens cDNA
9410	22484	36049	1.53	8.0E-27	AW857579.1	EST_HUMAN	CM1-CT0315-091269-063-007 CT0315 Homo sapiens cDNA
701	13884		1.77	7.0E-27	Z70894.1	NT	Human endogenous retroviral element HC2
5201	18322		2.19	7.0E-27	AW626172.1	EST_HUMAN	h51h12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040
5058	22137		0.97	7.0E-27	D69884.1	NT	O76040 ORF2: FUNCTION UNKNOWN. ;
10988	24087		3.7	7.0E-27	AJ271795.1	NT	Human mRNA for KIAA0231 gene, partial cds
10984	24046	37679	3.21	8.0E-27	M26697.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12094	25074	38781	1.55	8.0E-27	U93163.1	NT	Human nuclear protein (B23) mRNA, complete cds
7654	27004		0.73	5.0E-27	AL163303.2	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
10442	23477	37081	3.21	5.0E-27	BF686614.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
10442	23477	37082	3.21	5.0E-27	BF686614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
6883	20035	33444	1.65	4.0E-27	9910569	NT	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
							Mus musculus sperm tail associated protein (Slap), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8125	21207		0.88	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8172	21254		1.31	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8945	22984	36577	0.61	4.0E-27	AW880859.1	EST_HUMAN	QV0-OT0033-070300-162-b70 OT0033 Homo sapiens cDNA
11903	24891	38592	2.62	4.0E-27	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
13213	26080	31655	1.17	4.0E-27	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2099	15239	28381	7.1	3.0E-27	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4388	17529	30510	1.55	3.0E-27	BE071924.1	EST_HUMAN	PNG-BT0527-080100-001-411 BT0527 Homo sapiens cDNA
5462	18662	31641	6.81	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
9505	22771	36342	3.49	3.0E-27	BF035327.1	EST_HUMAN	60145853 F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
42	13280	26286	9.28	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1044	15087		24.24	2.0E-27	AA555345.1	EST_HUMAN	nk01b10.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
3178	16353		13.34	2.0E-27	AW629172.1	EST_HUMAN	h151h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2976879 3' similar to TR:O78040
3295	16470	29489	1.45	2.0E-27	AF111167.2	NT	O76040 ORF2: FUNCTION UNKNOWN. ;
3296	16470	29490	1.45	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6814	19967	33373	0.79	2.0E-27	H02655.1	EST_HUMAN	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
8282	21364	34863	1.17	2.0E-27	AI866347.1	EST_HUMAN	SP:HMGC_MOUSE Q02591 HOMEBOX PROTEIN ;
9469	22526		2.6	2.0E-27	AA551527.1	EST_HUMAN	w28g07.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426268 3'
9995	23033	36625	0.83	2.0E-27	X60658.1	NT	repetitive element ;
10241	23276	36868	1.45	2.0E-27	M78590.1	EST_HUMAN	R. rattus RYA3 mRNA for a potential ligand-binding protein
10241	23276	36869	1.45	2.0E-27	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stralagene (cat#936206) Homo sapiens cDNA clone HFBCF07
11197	24285	37901	3.61	2.0E-27	AU121685.1	EST_HUMAN	EST00738 Fetal brain, Stralagene (cat#936206) Homo sapiens cDNA clone HFBCF07
11777	15087		6.43	2.0E-27	AA555345.1	EST_HUMAN	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 5'
12107	26087	39701	1.64	2.0E-27	AF216650.1	NT	nk01b10.s1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
449	13645		2.34	1.0E-27	AL163248.2	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
1021	14192	27251	4.97	1.0E-27	AB026988.1	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
6874	19833	33222	6.51	1.0E-27	6005855	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
							Homo sapiens chromosome 21 segment HS21C046
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
							Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7010	20146	33568	1.65	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
7010	20146	33567	1.55	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
8809	21898	35430	1.16	1.0E-27	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8186	22264		1.59	1.0E-27	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E08 BT0627 Homo sapiens cDNA
9923	22863	36551	2.85	1.0E-27	D87449.1	NT	Human mRNA for KIAA0260 gene, partial cds
12005	24990	38694	3.05	1.0E-27	AF111093.1	NT	Bos taurus latrophilin 3 splice variant b2b mRNA, complete cds
144	13368		2.26	9.0E-28	BE348399.1	EST_HUMAN	hw17c11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
321	13535	26567	2.17	9.0E-28	AU126260.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313;
10601	23636	37243	0.47	9.0E-28	AA174078.1	EST_HUMAN	AU126260 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
12224	25173		3.04	9.0E-28	BF377859.1	EST_HUMAN	zp18g12.s1 Strabagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609862 3'
12565	26003		13.39	8.0E-28	AW157571.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
1208	14370	27430	11.5	7.0E-28	AU142750.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to
11463	24522	38192	1.55	7.0E-28	11417866	NT	TR:O60302 O60302 KIAA0556 PROTEIN. ; contains element MER22 repetitive element ;
12181	25141		6.04	7.0E-28	AV735348.1	EST_HUMAN	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5'
9119	22188		1.28	6.0E-28	AF018052.1	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12866	25577		5.92	6.0E-28	AA504562.1	EST_HUMAN	AV735348 CB Homo sapiens cDNA clone CBFAKA12 5'
328	13542		2.75	5.0E-28	AI921003.1	EST_HUMAN	Homo sapiens zinc finger, protein ZNF191 (ZNF191) gene, complete cds
4116	17270	30269	38.94	5.0E-28	R70782.1	EST_HUMAN	aa06c03.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu
2689	15808	28928	1.48	4.0E-28	AW195066.1	EST_HUMAN	repetitive element; contains element PTR5 repetitive element ;
3177	16352	29358	1.34	4.0E-28	BE409100.1	EST_HUMAN	wo18c07.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1
7483	20558	34030	3.55	4.0E-28	AI198941.1	EST_HUMAN	y89f10.r1 Scores placenta N22HP Homo sapiens cDNA clone IMAGE:148443 5'
11105	24177		4.19	4.0E-28	AF028308.1	NT	xn33c09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2895604 3' similar to SW:GG95_HUMAN
11295	24324		14.89	4.0E-28	AB039241.1	NT	Q08379 GOLGIN-95 ;
11278	20558	34030	4.34	4.0E-28	AI198941.1	EST_HUMAN	601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
12622	25418		1.7	4.0E-28	AW854244.1	EST_HUMAN	qf66f10.x1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1
12773	26069		1.62	4.0E-28	AW862360.1	EST_HUMAN	RC3-CT0254-240400-210-112 CT0264 Homo sapiens cDNA
							RC8-CT0379-070100-031-H01 CT0379 Homo sapiens cDNA
							REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
							Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
							Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
							qf66f10.x1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1
							REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
							RC3-CT0254-240400-210-112 CT0264 Homo sapiens cDNA
							RC8-CT0379-070100-031-H01 CT0379 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1312	14458		2.29	3.0E-28	AF156382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
5227	18349		0.94	3.0E-28	AF09660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
9027	22108	35647	2.28	3.0E-28	BF354030.1	EST_HUMAN	MF3-HT0713-280500-013-f03 HT0713 Homo sapiens cDNA
11176	24245	37878	2.09	3.0E-28	U53688.1	NT	Homo sapiens MHC class 1 region
12653	25433		3.77	3.0E-28	AI831981.1	EST_HUMAN	W9807.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element ;
12803	25336		3.29	3.0E-28	BE082801.1	EST_HUMAN	RC2-BT0642-210200-013-f03 BT0642 Homo sapiens cDNA
12865	25576	31993	1.22	3.0E-28	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12865	25576	31994	1.22	3.0E-28	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
81	13326	26354	12.79	2.0E-28	BE062167.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1191	14353	27411	9.24	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2546	15671	28795	2.16	2.0E-28	AI348634.1	EST_HUMAN	gc35b06.x1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1 b2 L1 repetitive element ;
3446	16614	29632	0.81	2.0E-28	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
6437	19604	32968	1.48	2.0E-28	BF224402.1	EST_HUMAN	hr76c03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1 b1
6460	19627		3	2.0E-28	BF212905.1	EST_HUMAN	LOR1 repetitive element ;
8234	21316	34837	0.93	2.0E-28	AF005273.1	NT	601814106F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048761 5'
9783	22823		2.23	2.0E-28	AW972305.1	EST_HUMAN	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
11913	24900	36803	2.52	2.0E-28	AF224669.1	NT	EST384394 IMAGE resequences, MAGI Homo sapiens cDNA
12631	25424		1.74	2.0E-28	H06376.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
1508	14661	27744	2.85	1.0E-28	D38044.1	NT	y79c09.r1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:44300 5'
2294	15426	28560	3.91	1.0E-28	BF333236.1	EST_HUMAN	Human gene for Ahr-receptor, exon 7-9
4691	17826		0.95	1.0E-28	U09410.1	NT	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
8044	21127		1.95	1.0E-28	11429885	NT	Human zinc finger protein ZNF131 mRNA, partial cds
8208	21290		3.03	1.0E-28	8822763	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63091), mRNA
9478	22535	36099	4.75	1.0E-28	AA308744.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA
10080	23118	36720	5.91	1.0E-28	4758431	NT	EST179615 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR
10080	23118	36721	5.91	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12186	25145		7.66	1.0E-28	AA054182.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
13013	25681		4.56	1.0E-28	AL163247.2	NT	zif61c01.r1 Scores retina N2b4-HR Homo sapiens cDNA clone IMAGE:380448 5'
							Homo sapiens chromosome 21 segment HS21C047

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13135	26122	31643	1.8	9.0E-29	AW663987.1	EST_HUMAN	h176g08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878286 3'
12752	25498		2.57	8.0E-29	Q00130	SWISSPROT	HYPOTHETICAL GENE 60 PROTEIN
1632	14784	27870	1.98	7.0E-29	AW966447.1	EST_HUMAN	EST378521 IMAGE resequences, MAGI Homo sapiens cDNA
13197	25779		9.03	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
608	13797	26817	9.39	6.0E-29	AI936748.1	EST_HUMAN	w66b01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
12495	25342		5.19	6.0E-29	BE940436.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN; contains LTR7 b1 LTR7 repetitive element;
12587	25395		2.1	6.0E-29	BF688097.1	EST_HUMAN	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA
5113	18241		2.39	5.0E-29	AL163203.2	NT	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
8929	22008		8.35	5.0E-29	AW887641.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12795	25531		1.49	5.0E-29	BE812449.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
3304	18478		2.28	4.0E-29	AJ752387.1	EST_HUMAN	601451827F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855726 5'
8133	19312		7.06	4.0E-29	BE164930.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cnt15c02 random
8272	21354	34870	0.84	4.0E-29	AI678101.1	EST_HUMAN	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA
8272	21354	34871	0.84	4.0E-29	AI678101.1	EST_HUMAN	w635g08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
8944	22023	35563	3.59	4.0E-29	JO4988.1	NT	MER29.12 MER29 repetitive element;
4638	17674	30658	1.31	3.0E-29	AB042287.1	NT	w635g08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
4855	17888	30976	1.1	3.0E-29	BF333238.1	EST_HUMAN	Human 90 kD heat shock protein gene, complete cds
6053	19235	32560	0.83	3.0E-29	BE314018.1	EST_HUMAN	Homo sapiens PTS gene for 5-pyruvyltetrahydropterin synthase, complete cds
8931	22010	35548	3.23	3.0E-29	D38044.1	NT	QV1-B10821-120900-360-b03 B10821 Homo sapiens cDNA
9500	22556	36119	1.22	3.0E-29	AW303317.1	EST_HUMAN	601152657F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508527 5'
9731	22796		1.49	3.0E-29	AL163246.2	NT	Human gene for Ah-receptor, exon 7-9
10164	23201		0.81	3.0E-29	BE350127.1	EST_HUMAN	xv17f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu
11546	24602	35278	2.26	3.0E-29	AA403053.1	EST_HUMAN	repetitive element; contains MER19.12 MER19 repetitive element ;
12885	26272		1.36	3.0E-29	D63882.1	NT	Homo sapiens chromosome 21 segment HS21C046
13092	26132		1.62	3.0E-29	D63882.1	NT	fr099g01.x1 NCI_CGAP_K1d13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
505	13699	26727	0.98	2.0E-29	AF084869.1	NT	MER29 repetitive element;
505	13699	26728	0.98	2.0E-29	AF084869.1	NT	z62b01.r1 Soares_Jeffs_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769
							Q1335769 GAG-POL POLYPROTEIN. ;
							Human HsLIM15 mRNA for HsLIM15, complete cds
							Human HsLIM15 mRNA for HsLIM15, complete cds
							Homo sapiens envelope protein RIC-6 (env) gene, complete cds
							Homo sapiens envelope protein RIC-6 (env) gene, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1563	14716	27794	7.8	2.0E-29	AI963604.1	EST_HUMAN	wf65d10.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
1563	14716	27795	7.8	2.0E-29	AI963604.1	EST_HUMAN	wf65d10.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
1782	14931	28024	2.31	2.0E-29	X84900.1	NT	H.sapiens mRNA for laminin-5, alpha3b chain
1782	14931	28025	2.31	2.0E-29	X84900.1	NT	H.sapiens mRNA for laminin-5, alpha3b chain
4394	17537	30516	2.55	2.0E-29	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5946	19132	32446	0.79	2.0E-29	AI082459.1	EST_HUMAN	os71e04.x1 NCL_CGAP_GG2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1, L2 L1 repetitive element ;
6309	19481	32835	1.49	2.0E-29	AI806418.1	EST_HUMAN	wf27g07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356960 3' similar to contains element MER6 repetitive element ;
7732	19481	32835	1.28	2.0E-29	AI806418.1	EST_HUMAN	wf27g07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356960 3' similar to contains element MER6 repetitive element ;
8164	21246	34766	1.16	2.0E-29	BE667157.1	EST_HUMAN	601442206F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846648 5'
8777	21856	35398	0.81	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
8777	21856	35399	0.81	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
9708	22757	36327	2.76	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9708	22757	36328	2.76	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10444	23479	37084	3.65	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10444	23479	37085	3.65	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11767	24760		1.67	2.0E-29	11425108	NT	Homo sapiens splicing factor similar to dnaJ (SPF31), mRNA
8892	22071	35511	8.27	1.0E-29	AW963890.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
10850	23883	37503	2.81	1.0E-29	X60658.1	NT	Rattus RYA3 mRNA for a potential ligand-binding protein
6712	19870	33261	3.53	9.0E-30	AA791215.1	EST_HUMAN	nz20c07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 MER4 repetitive element ;
12268	28200		4.55	9.0E-30	11422745	NT	Homo sapiens zinc/ferritin regulated transporter-like (ZIRTL), mRNA
6449	19616		10.5	8.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
8465	21546	35076	2.26	8.0E-30	AA383873.1	EST_HUMAN	EST97317 Thymus I Homo sapiens cDNA 5' end similar to EST containing O family repeat
8882	21961	35495	2.79	8.0E-30	AI557072.1	EST_HUMAN	PT2.1, 13 B11.1, tumor2 Homo sapiens cDNA 3'
1646	14697		1.07	7.0E-30	BE091133.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA
1814	14963	28056	1.57	6.0E-30	D26303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3259	18433	29450	3.15	6.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
4881	16433	29450	1.02	6.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
10760	23793	37412	0.76	6.0E-30	AF177227.1	NT	Homo sapiens CTCL tumor antigen se20-10 mRNA, partial cde

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13161	18485		1.75	6.0E-30	X61755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4121	17275	30274	43.22	6.0E-30	A1399992.1	EST_HUMAN	ig92g03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element
5353	25928		5.79	5.0E-30	U87631.1	NT	Human acetylcholinesterase (AChE) gene, exon 7
11126	24198		2.12	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11423	24484	38148	2.76	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11423	24484	38149	2.76	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2210	15344	28470	2.38	4.0E-30	AW637471.1	EST_HUMAN	QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA
2210	15344	28471	2.38	4.0E-30	AW637471.1	EST_HUMAN	QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA
9108	22185	35729	1.55	4.0E-30	AW812488.1	EST_HUMAN	CM1-ST0181-091199-035-f08 ST0181 Homo sapiens cDNA
1175	14338		4.56	3.0E-30	A1338551.1	EST_HUMAN	qq83c05.x1 Sceres total fetus NB2HF8 gw Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER28 repetitive element
3853	17013	30013	1.15	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
8138	21220		0.53	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8683	21763		0.45	3.0E-30	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10649	23683	37294	0.74	3.0E-30	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER29.b3 MER29 repetitive element
11482	24541	38211	1.52	3.0E-30	P34058	SWISSPROT	TRANSCRIPTION FACTOR AP-2
692	13875	26908	1.42	2.0E-30	AW857315.1	EST_HUMAN	CM0-CT0307-310100-168-f03 CT0307 Homo sapiens cDNA
1108	14273		2.53	2.0E-30	F08888.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
1509	14662	27745	5.5	2.0E-30	BE175877.1	EST_HUMAN	RC5-HT0582-110400-073-H08 HT0582 Homo sapiens cDNA
2779	15895	29005	9.93	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
2986	16162	29179	6.83	2.0E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3889	17048	30048	1.95	2.0E-30	AW206581.1	EST_HUMAN	UJH-B11-af0-c-12-Q-U1 st NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4900	18030	31018	2.02	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
4900	18030	31019	2.02	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
8734	21814	35349	4.89	2.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFUJWara) Homo sapiens cDNA clone GEN-570C01 5'
8836	21915	35452	1.71	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8836	21915	35453	1.71	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
10201	23238	36828	3.78	2.0E-30	AW971568.1	EST_HUMAN	EST383657 IMAGE resequences, MAGL Homo sapiens cDNA

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10287	23322	36924	6.31	2.0E-30	AW470791.1	EST_HUMAN	ha33d06.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2876495 3' similar to contains THR.b3
297	13514	28548	10.87	1.0E-30	C18939.1	EST_HUMAN	THR repetitive element
551	13744	28769	1.62	1.0E-30	AW468897.1	EST_HUMAN	C18939 Human placenta cDNA (Tfujivara) Homo sapiens cDNA clone GEN:570C01 5'
734	13916	28956	5.15	1.0E-30	AL163203.2	NT	hd30b04.x1 Soares_NFL_T_C8C_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains
2288	15418	28550	11.56	1.0E-30	AA664377.1	EST_HUMAN	MER1.13 MER1 MER1 repetitive element
2533	15698	28782	2.15	1.0E-30	BF347728.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
3120	16296	28310	0.91	1.0E-30	AA315045.1	EST_HUMAN	ac77b08.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:368599 3'
7901	20963	34460	1.96	1.0E-30	BF183230.1	EST_HUMAN	602022560F1 NCL CGAP_Bri87 Homo sapiens cDNA clone IMAGE:4157991 5'
8176	21258	34780	0.49	1.0E-30	BE061588.1	EST_HUMAN	EST186888 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
12786	28117		1.57	1.0E-30	AA239211.1	EST_HUMAN	601809932F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040684 5'
12937	28025		5.31	1.0E-30	H55593.1	EST_HUMAN	MRO-BT0249-091289-101-g01 BT0249 Homo sapiens cDNA
3962	17022	30020	0.8	8.0E-31	T73025.1	EST_HUMAN	EST11698 Uterus Homo sapiens cDNA 5' end
3982	17022	30021	0.8	8.0E-31	T73025.1	EST_HUMAN	CHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
8519	21600	35135	0.88	9.0E-31	R18214.1	EST_HUMAN	yc65e06.r1 Stralagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
8519	21600	35136	0.88	9.0E-31	R18214.1	EST_HUMAN	yc65e06.r1 Stralagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
8825	21504		1.99	9.0E-31	Z38293.1	EST_HUMAN	yc65e06.r1 Stralagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
8827	21606	35445	0.65	9.0E-31	AF078779.1	NT	RELATED PROTEIN RAB-2 (HUMAN);
13193	25776	31934	1.29	8.0E-31		NT	RELATED PROTEIN RAB-2 (HUMAN);
1102	14287	27325	2.52	8.0E-31		NT	RELATED PROTEIN RAB-2 (HUMAN);
2484	15611		7.93	8.0E-31	AL163208.2	NT	RELATED PROTEIN RAB-2 (HUMAN);
729	13911		1.59	7.0E-31	AA372637.1	EST_HUMAN	HS005F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'
2733	15650	28982	2.1	7.0E-31	BE326517.1	EST_HUMAN	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
2733	15650	28983	2.1	7.0E-31	BE326517.1	EST_HUMAN	Mus musculus syndecan 4 (Sdc4), mRNA
8595	21676	35212	1.02	7.0E-31	AF208541.1	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
8595	21676	35213	1.02	7.0E-31	AF208541.1	NT	Homo sapiens chromosome 21 segment HS21C008
9468	22523		1.03	7.0E-31	BE408611.1	EST_HUMAN	EST84555 Odon adenocarcinoma IV Homo sapiens cDNA 5' end
3769	16930		3.42	6.0E-31	AF223391.1	NT	hw05a11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8347	21428		1.39	6.0E-31	AF055066.1	NT	hw05a11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
							Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
							Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
							601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							Homo sapiens MHC class 1 region

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8526	21607	35146	0.75	6.0E-31	BE350127.1	EST_HUMAN	h08g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3
10976	24055	37689	1.43	6.0E-31	AU119105.1	EST_HUMAN	MER29 repetitive element ;
12327	25236	32108	3.7	6.0E-31	AW372658.1	EST_HUMAN	ALU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'
12459	25947		2.54	6.0E-31	BE894488.1	EST_HUMAN	RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA
197	13420	28450	3.39	5.0E-31	M60894.1	NT	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
197	13420	28451	3.39	5.0E-31	M60894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8640	21720		1.29	5.0E-31	BF056540.1	EST_HUMAN	Homo sapiens type I DNA topoisomerase gene, exon 8
609	13798		3.02	4.0E-31	AJ271735.1	NT	7k06f04.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:3443478 3' similar to TR:Q13537 Q13537
							SIMILAR TO POGO ELEMENT . contains L1 L1 L1 repetitive element ;
							Homo sapiens Xq pseudautosomal region, segment 1/2
1642	14794	27878	1.14	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP
1881	15007		2.09	4.0E-31	AL163260.2	NT	ACETYL GALACTOSAMINYL TRANSFERASE (UDP-GALNAC:POLYPEPTIDE, N-
2849	15983		1.57	4.0E-31	5730038	NT	ACETYL GALACTOSAMINYL TRANSFERASE (GALNAC-T1)
10754	23787	37402	0.46	4.0E-31	AF084464.1	NT	Homo sapiens chromosome 21 segment HS21C080
12787	25526		1.55	4.0E-31	11430273	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
12924	26509		2	4.0E-31	AB008681.1	NT	Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds
2660	15782	28897	1.75	3.0E-31	6005871	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
7494	20569	34041	8.04	3.0E-31	4826853	NT	Homo sapiens gene for activin receptor type IIB, complete cds
7663	20730	34208	1.23	3.0E-31	11420329	NT	Homo sapiens SEC63, endoplasmic reticulum translocan component (S. cerevisiae) like (SEC63L), mRNA
8355	21436		1.51	3.0E-31	AL163206.2	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) (NDUF8B) mRNA
9778	22819	36397	2.59	3.0E-31	D14523.1	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
10822	23855	37477	0.65	3.0E-31	AA421242.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C006
10867	23952	37582	2.03	3.0E-31	P11174	SWISSPROT	Horse mRNA for ferritin L-chain, complete cds
11421	24482		3.47	3.0E-31	BF035327.1	EST_HUMAN	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
1697	15110	28211	1.58	2.0E-31	AW838171.1	EST_HUMAN	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
2288	15420	28552	1.05	2.0E-31	AI393383.1	EST_HUMAN	QV2.LT0051-260300-111-033 LT0051 Homo sapiens cDNA
2416	15545	28674	2.22	2.0E-31	AL119245.1	EST_HUMAN	tg44g05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2511	15637	28758	4.63	2.0E-31	AA458824.1	EST_HUMAN	DKFZp781G1513.1 781 (synonym: ham2) Homo sapiens cDNA clone IMAGE:2111672 3'
5389	18591	31563	0.76	2.0E-31	AW444466.1	EST_HUMAN	aa88f11.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains
							THR.12 THR repetitive element ;
							UI-H-B13-akb-T-09-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733633 3'

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5829	19020	32326	3.43	2.0E-31	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kic13 Homo sapiens cDNA clone IMAGE:3146286 3' similar to contains MER29.b3 MER29 repetitive element;
9277	22353		1.53	2.0E-31	AA877764.1	EST_HUMAN	h106f04.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
9408	22462	36046	3.46	2.0E-31	7661535	NT	Homo sapiens B9 protein (B9), mRNA
10110	23148	36748	1.1	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
10110	23148	36749	1.1	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
10280	23315	36914	2.75	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
10280	23315	36915	2.75	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12430	25305		3.49	2.0E-31	AF148512.1	NT	Homo sapiens hexokinase II gene, promoter region
12578	26202		2.59	2.0E-31	AI114527.1	EST_HUMAN	HA11110 Human fetal liver cDNA library Homo sapiens cDNA
17	13255	26256	9.91	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1698	14848	27932	2.66	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1698	14848	27933	2.66	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1698	14848	27934	2.66	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
6407	18609	31681	3.97	1.0E-31	AW391679.1	EST_HUMAN	MR3-ST0220-151239-028-a08_1 ST0220 Homo sapiens cDNA
6261	18435	32781	2.57	1.0E-31	AF048727.1	NT	Homo sapiens minichromosome 17 repeat region
7441	20518	33690	0.84	1.0E-31	AF128145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
8005	21055	34587	1.35	1.0E-31	BE972818.1	EST_HUMAN	601652052F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935293 5'
10441	23476	37080	0.5	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
11156	24227	37857	2.35	1.0E-31	AJ06434.1	EST_HUMAN	q21h03.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595 Q16595 FRATAXIN.;
8776	19931	33327	2.19	9.0E-32	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAA.G01 5'
7530	20603	34077	0.66	9.0E-32	L31770.1	NT	Bos taurus vacuolar H ⁺ -ATPase subunit mRNA, complete cds
7768	20825		0.91	9.0E-32	11430822	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
2139	15275	28397	5.1	8.0E-32	AJ056770.1	EST_HUMAN	ca15a09.x1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
5599	18794	31843	0.77	8.0E-32	AW997214.1	EST_HUMAN	RC2-BN0048-200300-015-e04 BN0048 Homo sapiens cDNA Human chromosome 22 immunoglobulin V(K) gene, part with 5' breakpoint between alpha and neighbouring non-amplified region
12406	25285		2.36	7.0E-32	X17283.1	NT	
7523	20598		1.32	6.0E-32	BE988016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12869	26181		2.5	6.0E-32	AA884653.1	EST_HUMAN	oh37c03.e1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459872 3' similar to contains L1.13 L1 repetitive element ;
1059	14225	27282	10.42	5.0E-32	AF116827.1	NT	Homo sapiens PRO1181 mRNA, complete cds
954	14127		1.64	4.0E-32	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7779	20835	34328	3.4	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7779	20835	34327	3.4	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8554	21635		0.93	4.0E-32	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
468	13663	26698	2.64	3.0E-32	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1484	14637	27721	15.82	3.0E-32	AV731500.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK07 5'
2973	16149	29168	0.75	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2973	16149	29169	0.75	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
9594	22649	36221	3.1	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
9594	22649	36222	3.1	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
11166	24237	37868	3.43	3.0E-32	AA777821.1	EST_HUMAN	z95a07.s1 Soares Fetal Liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:3139701 5'
12433	25307		7.95	3.0E-32	BE279086.1	EST_HUMAN	contains THR.13 THR repetitive element ;
12843	16149	29168	4.95	3.0E-32	5174574	NT	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
12843	16149	29169	4.95	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
13020	25671		6.47	3.0E-32	BE279086.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
6382	19551	32907	0.89	2.0E-32	M35418.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6608	19768	33156	6.55	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
6608	19768	33157	5.55	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
8473	21554	35085	3.34	2.0E-32	AA114294.1	EST_HUMAN	z166c08.r1 Stradagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
8473	21554	35086	3.34	2.0E-32	AA114294.1	EST_HUMAN	z166c08.r1 Stradagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
13154	25750	31923	1.28	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
13154	25750	31924	1.28	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
3163	16338		1.25	1.0E-32	BE743289.1	EST_HUMAN	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
7200	20055	33478	6.64	1.0E-32	11439789	NT	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
8795	21874	35413	4.56	1.0E-32	AA720574.1	EST_HUMAN	mw21g02.s1 NCI_CGAP GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element ;

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3570	16735		4.8	9.0E-33	BE327112.1	EST_HUMAN	hw07605.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:088539 O88539 WW DOMAIN BINDING PROTEIN 11.1
6550	19712		3.17	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8988	22067	35607	1.81	9.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4156870 5'
11038	24117		4.55	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
62	13300	26320	2.73	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
62	13300	26321	2.73	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2228	15362	28491	3.04	7.0E-33	AI560115.1	EST_HUMAN	6012609.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.H OFR
2714	15832		7.95	7.0E-33	AV730056.1	EST_HUMAN	repetitive element;
3314	16487		15	7.0E-33	AW971607.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE09 5'
9147	22226		0.87	7.0E-33	X64890.1	NT	EST383396 MAGI2 resequencing, MAGI2 Homo sapiens cDNA
11067	24142	37777	1.88	7.0E-33	BF347229.1	EST_HUMAN	Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphatase) (EC 3.1.3.48)
11526	24592	38258	1.59	7.0E-33	AW971608.1	EST_HUMAN	602021164F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4156870 5'
12413	25292	32082	9.74	7.0E-33	AA601416.1	EST_HUMAN	EST383657 MAGI2 resequencing, MAGI2 Homo sapiens cDNA
3830	16990		0.93	6.0E-33	AL163285.2	NT	not16h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.H L1
6192	19368	32717	0.91	6.0E-33	F30631.1	EST_HUMAN	repetitive element;
6192	19368	32718	0.91	6.0E-33	F30631.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
8778	21857	35400	1.96	6.0E-33	J04038.1	NT	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
8898	21978	35517	3.12	6.0E-33	11429198	NT	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
10214	23250	36839	2.03	6.0E-33	6755609	NT	Homo glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
10214	23250	36840	2.03	6.0E-33	6755609	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
1818	14657		1.9	5.0E-33	BF37315.1	EST_HUMAN	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1831	15074		1.32	5.0E-33	11141884	NT	Mus musculus SRY-box containing gene 8 (Sox8), mRNA
1947	18090	28180	1.63	5.0E-33	4507208	NT	QV1-FT0169-100700-271-402 FT0169 Homo sapiens cDNA
1947	18090	28181	1.63	5.0E-33	4507208	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
2346	15477		2.92	5.0E-33	AL163285.2	NT	Homo sapiens spermidine synthase (SRM) mRNA
4169	17319	30312	0.66	5.0E-33	AB014599.1	NT	Homo sapiens chromosome 21 segment HS21C085
10454	23489	37097	0.82	5.0E-33	AW264678.1	EST_HUMAN	Homo sapiens mRNA for KIAA0699 protein, partial cds
10454	23489	37098	0.82	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
						EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12212	25166		1.45	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1152	14316		2.25	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2194	15329	26454	3.37	4.0E-33	4758937	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2491	15518		1.16	4.0E-33	AA626621.1	EST_HUMAN	ab51b11.r1 Striatagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element;
2610	15734	26850	4.78	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4808	17743	30722	2.38	4.0E-33	AW283349.1	EST_HUMAN	UHH-B12-ah-c-03-Q.UJ.s1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5519	18717	31731	24.75	4.0E-33	AA050358.1	EST_HUMAN	271a08.r1 Striatagene colon (#937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12871.na1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6522	19687	33060	0.79	4.0E-33	8393894	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6522	19687	33061	0.79	4.0E-33	8393894	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1113	14278		5.62	3.0E-33	BE350127.1	EST_HUMAN	H09g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
1114	14278		5.83	3.0E-33	BE350127.1	EST_HUMAN	MER29 repetitive element;
2522	16064		1.16	3.0E-33	AV647851.1	EST_HUMAN	AY647851 GLC Homo sapiens cDNA clone GLCBFC09 3'
10655	23689	37298	0.87	3.0E-33	AA861510.1	EST_HUMAN	ak32b12.s1 Soares_basif_NHT Homo sapiens cDNA clone IMAGE:1407647 3' similar to TR:Q13579 Q13579 MARINER TRANSPOSASE;
18	13256		1.67	2.0E-33	A1160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element;
107	13256		5.53	2.0E-33	A1160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element;
4539	17677		4.53	2.0E-33	BE159039.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element;
5100	18228	31199	8.64	2.0E-33	AA626683.1	EST_HUMAN	MRO-H10405-160300-202-c08 HT0405 Homo sapiens cDNA
5204	18325	31294	1.6	2.0E-33	11421332	NT	ab51g11.r1 Striatagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734.cd51 TUBULIN BETA-5 CHAIN (HUMAN);
5204	18325	31295	1.6	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
6553	19715	33091	1.39	2.0E-33	A1277482.1	EST_HUMAN	qb66d01.x1 Soares_NbHMPu.S1 Homo sapiens cDNA clone IMAGE:1880167 3'
9301	22377		2.15	2.0E-33	A1052256.1	EST_HUMAN	oz21d03.x1 Soares_fetal_liver_spleen_1NFLS_31 Homo sapiens cDNA clone IMAGE:1679873 3' similar to gb:M29535 TRANSLOCATION INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
9	13247		1.61	1.0E-33	AF003628.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7585	20637	34113	0.86	1.0E-33	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10227	28229		1.4	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11602	24665	38340	1.56	1.0E-33	AW996818.1	EST_HUMAN	QV3-BN0047-230200-102-503 BN0047 Homo sapiens cDNA
11962	24647	38652	2.44	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12768	25511		1.25	1.0E-33	AW904491.1	EST_HUMAN	RC5-NN1055-260400-021-G03 NN1055 Homo sapiens cDNA
12829	13247		5.7	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12860	28626	31979	2.19	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCCNC12 5'
13179	25766		4.77	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
2240	15373	28501	0.96	8.0E-34	8922751	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
4620	17757	30739	1.93	8.0E-34	BE052570.1	EST_HUMAN	QV2-BT0259-071298-019-g07 BT0258 Homo sapiens cDNA
7974	21024	34537	0.67	8.0E-34	BE069882.1	EST_HUMAN	MR4-BT0399-200100-001-003 BT0399 Homo sapiens cDNA
1476	14629	27714	2.5	7.0E-34	T70845.1	EST_HUMAN	yd15e05.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA
10204	14629	27714	0.54	7.0E-34	T70845.1	EST_HUMAN	yd15e05.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:108320 5'
12482	25334		3.85	7.0E-34	H12866.1	EST_HUMAN	Y14c70.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148722 5'
483	13677	28711	1.74	6.0E-34	U10891.1	NT	Human G2 protein mRNA, partial cds
483	13677	28712	1.74	6.0E-34	U10891.1	NT	Human G2 protein mRNA, partial cds
5247	18368	31336	1.68	6.0E-34	AW998811.1	EST_HUMAN	PMO-BN0065-100300-001-c08 BN0065 Homo sapiens cDNA
12290	25215	32089	2.22	6.0E-34	U03886.1	NT	Mus musculus DAB/2J hair-specific (hacl-1) gene
1929	15072		3.15	5.0E-34	7708500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
5173	18295	31257	5.24	5.0E-34	U30883.1	NT	Human splicing factor SRP55-1 (SRP-55) mRNA, complete cds
9067	22146	35693	1.17	5.0E-34	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10890	23974	37605	2.02	5.0E-34	AB037856.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
11532	24588		1.93	5.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2054	15195	28309	2.09	4.0E-34	AB046657.1	EST_HUMAN	HS4506.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2249194 3'
3241	18415	29430	0.9	4.0E-34		NT	Homo sapiens splicing factor 3a, subunit 3, 60kD (SF3A3), mRNA
5981	19166	32486	0.82	4.0E-34	AA861773.1	EST_HUMAN	ak35c01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1407636 3'
9238	22315	35957	0.83	4.0E-34	BF209778.1	EST_HUMAN	601874950F1 NIH_MGC_34 Homo sapiens cDNA clone IMAGE:4102213 5'
6361	19531	32880	0.86	3.0E-34	M37277.1	NT	Human Ig gamma H-chain D-region genes, partial cds
11420	24481		2.96	3.0E-34	BF055327.1	EST_HUMAN	60145831F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3862088 5'
9152	22230	35774	0.75	2.0E-34	AB78101.1	EST_HUMAN	w435g06.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER28.12 MER28 repetitive element
9152	22230	35775	0.75	2.0E-34	AB78101.1	EST_HUMAN	w435g06.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER28.12 MER28 repetitive element
11431	24492	38156	8.54	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11431	24492	38157	8.54	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
1534	14687	27767	10.13	1.0E-34	P12236	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
1738	14887		7.18	1.0E-34	AU136024.1	EST_HUMAN	ALU136024 PLACE1 Homo sapiens cDNA clone PLACE1003383 5'
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3764	16925	29927	2.51	1.0E-34	AF003528.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4181	17331	30323	0.79	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4602	17331	30324	0.79	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4602	17739		8.28	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240400-016-h08 BT0506 Homo sapiens cDNA
6266	18440	32787	2.26	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
6266	19440	32788	2.26	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
9527	22892	36163	0.64	1.0E-34	P23286	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
9808	22638	36523	8.07	1.0E-34	AL036635.1	EST_HUMAN	DKFZ4564A1563_r1 564 (synonym: hfb2) Homo sapiens cDNA clone DKFZp564A1563 5'
11459	24518	38186	1.51	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11459	24518	38187	1.51	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11473	24532	38202	2.92	1.0E-34	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12680	26125		2.44	1.0E-34	AA807097.1	EST_HUMAN	cc31c11.s1 NCI_CGAP_GC31 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb:X68203
12950	26660		5.84	1.0E-34	AL163210.2	NT	TYROSINE-PROTEIN KINASE RECEPTOR FL T4 PRECURSOR (HUMAN);
3735	16896	29900	1.3	9.0E-35	AW663302.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
232	13453		7.21	8.0E-35	6031190	NT	ht77b06.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868787 5'
							Homo sapiens prohibitin (PHB) mRNA
1776	14925	28019	3.63	8.0E-35	BF59937.1	EST_HUMAN	nea33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
							O75912 DIACYLGLYCEROL KINASE IOTA ;
1776	14925	28020	3.63	8.0E-35	BF59937.1	EST_HUMAN	nea33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
4989	18118	31087	2.61	8.0E-35	BF183195.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA ;
10929	24011	37645	1.53	8.0E-35	BE378480.1	EST_HUMAN	601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
12404	25283		5.89	8.0E-35	BF599282.1	EST_HUMAN	601236468F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
6813	19773	33164	1.61	7.0E-35	11425417	NT	60218462411 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300660 3'
1415	14598	27675	1.06	6.0E-35	AA757115.1	EST_HUMAN	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
2025	15166	28271	4.83	6.0E-35	6005975	NT	af153h03.s1 Scores_testes_NHT Homo sapiens cDNA clone 1308937 3'
4164	17314	30309	0.8	6.0E-35	AW297181.1	EST_HUMAN	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
8081	21163	34680	4.03	6.0E-35	6005921	NT	U1-H-BW0-adj-d-09-o-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'
8081	21985	34524	0.57	6.0E-35	X94232.1	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
8081	21985	34524	0.57	6.0E-35	X94232.1	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8806	21983	36525	0.57	6.0E-35	X94232.1	NT	H.sapiens mRNA for novel T-cell activation protein
9867	22907	36492	0.61	6.0E-35	AB002364.1	NT	Human mRNA for KIAA0368 gene, partial cds
10107	23145	36743	2.97	6.0E-35	AB037786.1	NT	Homo sapiens mRNA for KIAA1385 protein, partial cds
148	13373	26406	0.61	5.0E-35	AF154630.1	NT	Homo sapiens carboxyl phosphate synthetase I mRNA, complete cds
1746	14895	27999	2.25	5.0E-35	X63392.1	NT	H.sapiens immunoglobulin kappa light chain variable region L14
2844	15958	29067	0.99	5.0E-35	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
3074	16250	29271	2.87	5.0E-35	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
4529	17667	30653	1.72	5.0E-35	AF023368.1	NT	Homo sapiens cdk2 kinase (CLK2), propin1, cote1, glucocorticoidase (GBA), and melanin genes, complete cds; metaxin pseudogene and glucocorticoidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
8378	21459		4.25	5.0E-35	BE890992.1	EST_HUMAN	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
8405	21495	35015	2.17	5.0E-35	AI208785.1	EST_HUMAN	qg35c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249 HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
8405	21495	35016	2.17	5.0E-35	AI208785.1	EST_HUMAN	qg35c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249 HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
11451	24511		2.54	5.0E-35	AA001786.1	EST_HUMAN	zh84f12.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1465	14619	27703	20.46	4.0E-35	BE257807.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1862	15008	28114	11.21	4.0E-35	H91193.1	EST_HUMAN	y48a07.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:241235 5' similar to contains PTR5 repetitive element ;
7358	20437		1.67	4.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
8715	21795	35332	8.05	4.0E-35	AL046896.1	EST_HUMAN	DKFZp434L148_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5'
12098	25078	38786	2.5	4.0E-35	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
1610	14763	27843	33.92	3.0E-35	BE268182.1	EST_HUMAN	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
2408	15539		2.64	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5456	18656	31634	23.43	3.0E-35	BF433100.1	EST_HUMAN	7c25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2. ;
5456	18656	31635	23.43	3.0E-35	BF433100.1	EST_HUMAN	7c25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2. ;
9689	22738		1.45	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10378	23413	37022	1.5	3.0E-35	AW003063.1	EST_HUMAN	wr03a05.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480492 3' similar to SW:POL1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE. ;

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
111	16005	26372	1.25	2.0E-35	N88995.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
1215	14376	27436	1.89	2.0E-35	T11909.1	EST_HUMAN	REPETITIVE ELEMENT
2292	15424	28558	4.56	2.0E-35	AB018413.1	NT	A971F Heart Homo sapiens cDNA clone A971
2748	15955	28976	1.13	2.0E-35	AW665005.1	EST_HUMAN	Homo sapiens mRNA for Gab2, complete cds
3386	16556	29570	1.08	2.0E-35	6912459	NT	h186a12.x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979166 3' similar to
3396	16556	29571	1.08	2.0E-35	6912459	NT	SW:TR12_HUMAN Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12 ;
3847	16810		0.77	2.0E-35	AB020702.1	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
4019	17176	30184	0.85	2.0E-35	BE247575.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
4019	17178	30185	0.85	2.0E-35	BE247575.1	EST_HUMAN	Homo sapiens mRNA for KIAA0895 protein, partial cds
4792	17927		3.01	2.0E-35	H49239.1	EST_HUMAN	TCBAP2E-4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor HGSC project:TCBA Homo sapiens cDNA clone TCBAP4328
5700	18894	32186	1.93	2.0E-35	BF332417.1	EST_HUMAN	TCBAP2E-4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor HGSC project:TCBA Homo sapiens cDNA clone TCBAP4328
7263	20336	33785	0.6	2.0E-35	BE832636.1	EST_HUMAN	Yt19a12.r1 Scores fetal liver spleen INFLS: Homo sapiens cDNA clone IMAGE:274079 5'
7253	20338	33786	0.8	2.0E-35	BE832636.1	EST_HUMAN	QV0-BT0701-210400-193-b04 BT0701 Homo sapiens cDNA
11036	24115	37749	2.93	2.0E-35	X59417.1	NT	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
12157	16556	29571	1.22	2.0E-35	6912459	NT	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
12342	25247	32111	1.33	2.0E-35	BE904978.1	EST_HUMAN	H. sapiens PROS-27 mRNA
12342	25247	32112	1.33	2.0E-35	BE904978.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12931	25614		7.22	2.0E-35	AL163210.2	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
13056	16005	26372	1.74	2.0E-35	N88995.1	EST_HUMAN	601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
47	13286	26295	5.76	1.0E-35	AA631949.1	EST_HUMAN	601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
47	13286	26296	5.76	1.0E-35	AA631949.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
771	13952	27000	35.82	1.0E-35	AW369473.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
771	13952	27001	35.82	1.0E-35	AW369473.1	EST_HUMAN	REPETITIVE ELEMENT
932	14107		1.28	1.0E-35	T87847.1	EST_HUMAN	frfrc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
2507	15730	28847	1.89	1.0E-35	7705994	NT	frfrc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
2826	15940	28050	1.34	1.0E-35	BE350127.1	EST_HUMAN	IL2-ST0162-131099-006-412 ST0162 Homo sapiens cDNA
							IL2-ST0162-131099-006-412 ST0162 Homo sapiens cDNA
							ydb3a01.r1 Scores fetal liver spleen INFLS: Homo sapiens cDNA clone IMAGE:115762 5' similar to
							SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
							Homo sapiens hypodermal protein (LOC517233), mRNA
							h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
							MER29 repetitive element ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2826	15940	29051	1.34	1.0E-35	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
3212	16398	29397	1.87	1.0E-35	6006030	NT	MER29 repetitive element;
3232	16406	29418	1.57	1.0E-35	AV650422.1	EST_HUMAN	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
3232	16406	29419	1.57	1.0E-35	AV650422.1	EST_HUMAN	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
4542	17680	30661	4.82	1.0E-35	7659905	NT	AV650422 GLC Homo sapiens cDNA clone GLCCE06 3'
4542	17680	30662	4.82	1.0E-35	7659905	NT	AV650422 GLC Homo sapiens cDNA clone GLCCE06 3'
5627	18821	31896	1.49	1.0E-35	11526238	NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
7135	18561	31475	0.74	1.0E-35	AW808665.1	EST_HUMAN	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
7135	18561	31476	0.74	1.0E-35	AW808665.1	EST_HUMAN	Homo sapiens chromatin assembly factor 1, subunit B (p80) (CHAF1B), mRNA
7652	20720	34196	0.89	1.0E-35	AB033105.1	NT	MIR1-ST0111-111199-011-d07 ST01111 Homo sapiens cDNA
7819	20874	34373	0.91	1.0E-35	11418002	NT	MIR1-ST0111-111199-011-d07 ST01111 Homo sapiens cDNA
9742	26661	36383	2.46	1.0E-35	AU158595.1	EST_HUMAN	Homo sapiens mRNA for KIAA1067 protein, partial cds
9742	26661	36384	2.46	1.0E-35	AU158595.1	EST_HUMAN	Homo sapiens KIAA0645 gene product (KIAA0645), mRNA
10805	23838	37462	0.72	1.0E-35	BF589594.1	EST_HUMAN	AUT55595 PLACE3 Homo sapiens cDNA clone PLAGE3000382 3'
10805	23838	37463	0.72	1.0E-35	BF589594.1	EST_HUMAN	AUT55595 PLACE3 Homo sapiens cDNA clone PLAGE3000382 3'
12055	25036	38743	1.49	1.0E-35	AB028980.1	NT	naa06d06.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3264051 3' similar to TR:O31341
12055	25036	38744	1.49	1.0E-35	AB028980.1	NT	O31341 BETA-GALACTOSIDASE ;
12062	29043		2.04	1.0E-35	A1525119.1	EST_HUMAN	O31341 BETA-GALACTOSIDASE ;
12188	26077		6.35	1.0E-35	11418274	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
12405	26284		1.26	1.0E-35	11418110	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
12806	25539		2.49	1.0E-35	BE792832.1	EST_HUMAN	promna-7.D01.r butumor Homo sapiens cDNA 5'
6131	18310	32650	0.67	8.0E-36	X78479.1	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
9430	22504	36070	0.76	8.0E-36	AA348480.1	EST_HUMAN	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
2997	16173	29192	1.53	7.0E-36	AW857576.1	EST_HUMAN	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
3188	16363		5.25	7.0E-36	4557468	NT	B. bovis BB50 mRNA for scinderin
6273	18392	31360	1.09	7.0E-36	Q27409	SWISSPROT	EST54938 Hippocampus II Homo sapiens cDNA 5' end similar to endogenous retrovirus 9, 5' LTR
5273	18392	31361	1.09	7.0E-36	Q27409	SWISSPROT	CMT-CT0315-091299-083-d07 CT0315 Homo sapiens cDNA
7832	20887	34389	6.31	7.0E-36	U06672.1	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
7832	20887	34390	6.31	7.0E-36	U06672.1	NT	ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MGFP1) (MGFP-1)
12570	25388	32040	27.38	7.0E-36	AF052051.1	NT	ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MGFP1) (MGFP-1)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database No.	Top Hit Database Source	Top Hit Descriptor
2060	15201	28315	1.92	6.0E-36	7706622	NT	Homo sapiens hnjn2 (NINJ2), mRNA
2490	15617		5.59	6.0E-36	AB035346.1	NT	Homo sapiens TCL6 gene, exon 12
3729	16830	29894	0.59	6.0E-36	BF515101.1	EST_HUMAN	U1-H-BW1-ant-c-12-0-UJ.st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5446	18646	31624	7.17	6.0E-36	AI435159.1	EST_HUMAN	tr93b06.x1 Soares NSF_F9_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126195 3' similar to gp.M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
7258	20341	33792	3.03	6.0E-36	AW780143.1	EST_HUMAN	tr06h02.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3036827 3' similar to SW:IMA2_HUMAN
8853	21932	35471	4.62	6.0E-36	AF208161.1	NT	P52292 IMPORTIN ALPHA-2 SUBUNIT;
10430	23465		0.63	6.0E-36	C16927.1	EST_HUMAN	Homo sapiens syncytin precursor, mRNA, complete cds
11841	24830	38521	3.49	6.0E-36	AI380499.1	EST_HUMAN	C16927 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-535C11 5'
140	13366	26399	15.16	5.0E-36	AJ271735.1	NT	tr95c09.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2
2809	15923	28033	21.08	5.0E-36	BE388436.1	EST_HUMAN	MER9 repetitive element;
3700	16861	29863	3.24	5.0E-36	AL163209.2	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4909	18039	31028	1.31	5.0E-36	5729729	NT	601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
4909	18039	31029	1.31	5.0E-36	5729728	NT	Homo sapiens chromosome 21 segment HS21C009
7966	21016	34528	0.59	5.0E-36	11079227	NT	Homo sapiens API5-like 1 (API5L1), mRNA
12155	13366	26399	6.11	5.0E-36	AJ271735.1	NT	Homo sapiens API5-like 1 (API5L1), mRNA
12458	25322	32095	2.36	5.0E-36	11417662	NT	Homo sapiens N-ethylmaleimide-sensitive factor (NSF), mRNA
1252	14411	27473	1.57	4.0E-36	BE010038.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
1677	14829	27913	1.36	4.0E-36	BE382574.1	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2297	15428		4.14	4.0E-36	AW247772.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
3435	16603	29622	1.1	4.0E-36	BE388289.1	EST_HUMAN	2820020 Sprieme NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3628386 5'
3435	16603	29623	1.1	4.0E-36	BE389299.1	EST_HUMAN	601298574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:2820020 5'
4877	18008	30992	0.69	4.0E-36	AL163204.2	NT	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
5833	18024		0.96	4.0E-36	R84023.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
6180	19366	32704	2.49	4.0E-36	11497041	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
7831	20896	34388	1.78	4.0E-36	M33320.1	NT	y19105.1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:139713 5'
8752	21831	35369	1.45	4.0E-36	D87675.1	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
8752	21831	35370	1.45	4.0E-36	D87675.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
11235	24304	37941	3.13	4.0E-36	AA400370.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
12475	25328		1.91	4.0E-36	11420516	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
12520	25851		4.27	4.0E-36	AV753629.1	EST_HUMAN	z69c10.11 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743250 5'
714	13896	26934	2.93	3.0E-36	AF069810.1	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
							AV753629 TP Homo sapiens cDNA clone IPGABH01 5'
							Homo sapiens neurexin III-alpha gene, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2373	1504	28630	1.19	3.0E-36	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
4624	17761	30743	7.5	3.0E-36	10181139	NT	Mus musculus Junctophilin 1 (Jp1-pending), mRNA
11368	24429	38086	1.84	3.0E-36	BF035327.1	EST_HUMAN	60145853.F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3238	16412	29427	2.5	2.0E-36	BE259267.1	EST_HUMAN	601106343.F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
5074	18202	31174	10.78	2.0E-36	AW880376.1	EST_HUMAN	QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
5803	18798	31848	2.68	2.0E-36	AF267747.1	NT	Mus musculus p47-phox gene, complete cds
5970	19156	32471	3.75	2.0E-36	T08756.1	EST_HUMAN	EST06848 Infant Brain, Bonto Scores Homo sapiens cDNA clone HIBBJ28 5' end
6706	18664	33254	13.94	2.0E-36	T69629.1	EST_HUMAN	yc44a07.r1 Stragene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5'
9588	22643	36212	0.94	2.0E-36	BF512794.1	EST_HUMAN	UI-H-BW1-amu-a-11-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
9749	22687	36258	0.74	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9749	22687	36259	0.74	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
908	14083	27148	1.74	1.0E-36	BE409310.1	EST_HUMAN	601300836.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2212	15346	28474	1.71	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2212	15346	28475	1.71	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2275	15406	28538	1.83	1.0E-36	BF673761.1	EST_HUMAN	602136493.F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'
3425	16594	32344	3.33	1.0E-36	AF156962.1	NT	Homo sapiens human endogenous retrovirus W prov6-19 protease (pro) gene, partial cds
5847	19037	32344	0.64	1.0E-36	AL044446.1	EST_HUMAN	DKFZp434G022_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G022 5'
6020	19203	32523	1.23	1.0E-36	4827064	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6312	19484		4.27	1.0E-36	AI867714.1	EST_HUMAN	wb37c12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element;
6519	19884	33055	1.9	1.0E-36	R25012.1	EST_HUMAN	y336g10.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP-CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6519	19884	33056	1.9	1.0E-36	R25012.1	EST_HUMAN	y336g10.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP-CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6820	19973	33381	0.72	1.0E-36	AL120542.1	EST_HUMAN	DKFZp761A229_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A229 5'
8147	21229	34747	4.06	1.0E-36	AA148034.1	EST_HUMAN	z651a12.r1 Stragene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8147	21229	34748	4.06	1.0E-36	AA148034.1	EST_HUMAN	z651a12.r1 Stragene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8243	21325	34841	0.76	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8243	21325	34842	0.76	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8373	21454	34977	0.68	1.0E-36	AI141688.1	EST_HUMAN	AU141688 THYR01 Homo sapiens cDNA clone THYR01001033 5'
8373	21454	34978	0.68	1.0E-36	AI141688.1	EST_HUMAN	AU141688 THYR01 Homo sapiens cDNA clone THYR01001033 5'
9228	22307	35850	3.33	1.0E-36	AW103668.1	EST_HUMAN	x682b07.r1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614357 3'
10320	23355	36064	3.83	1.0E-36	BF364169.1	EST_HUMAN	QV3-NN1023-010600-199-h01 NN1023 Homo sapiens cDNA
10534	23569	37176	0.64	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10534	23569	37177	0.64	1.0E-36	AW855883.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA
11190	24259	37895	2.55	1.0E-36	AW897638.1	EST_HUMAN	CM3-NN0081-140400-147-h12 NN0061 Homo sapiens cDNA
11682	24741	38432	3.55	1.0E-36	AW504143.1	EST_HUMAN	UHF-BN0-ale-c-03-Q-UJ.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
12048	25028		10.8	1.0E-36	11646901	NT	Homo sapiens PP3227 protein (PP3227), mRNA
12340	25245		2.93	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12835	25556		5.76	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
13131	25737		2.78	1.0E-36	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7539	20612	34087	2.27	9.0E-37	AW009277.1	EST_HUMAN	ws80507.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
7539	20612	34088	2.27	9.0E-37	AW009277.1	EST_HUMAN	ws80507.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
12619	25417		3.57	9.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp5081-cleaved sublibrary Homo sapiens cDNA not directional
3436	16604	29624	1.4	8.0E-37	4757979	NT	Homo sapiens chimerin (chimerin) 2 (CHN2) mRNA
5363	18566		1.7	8.0E-37	BE598077.1	EST_HUMAN	CM0-JT0003-050800-503-d09 UT0003 Homo sapiens cDNA
5949	19135	32448	3.48	8.0E-37	BE350127.1	EST_HUMAN	h08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3
5949	19135	32449	3.48	8.0E-37	BE350127.1	EST_HUMAN	h08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3
5998	19183	32505	7.08	8.0E-37	AW840840.1	EST_HUMAN	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA
8068	21150	34670	6.2	8.0E-37	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, DOB, DOB2 and RING8, 9, 13 and 14 genes
1313	14469		4.92	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422.t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434E0422 5'
5228	18350	31320	3.04	7.0E-37	AW968823.1	EST_HUMAN	EST380809 IMAGE resequences, MAGJ Homo sapiens cDNA
10894	24073	37706	8.66	7.0E-37	A1817700.1	EST_HUMAN	wk25b11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12
11134	24206	37831	1.89	7.0E-37	A1536702.1	EST_HUMAN	PTR5 repetitive element;
8634	21714	35251	0.59	6.0E-37	AF169689.1	EST_HUMAN	tm87g03.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1 repetitive element;
12864	25575		2.3	6.0E-37	U78308.1	NT	Homo sapiens protocadherin alpha 10 alternate isoform (PCDH-alpha10) mRNA, complete cds
12884	25641		4.5	6.0E-37	AF207273.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo olfr17-01 (OR17-01) pseudogene, complete cds
6218	19393	32741	4.3	5.0E-37	AA307123.1	EST_HUMAN	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
6218	19393	32742	4.3	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8956	22035	35576	1.03	5.0E-37	AV750211.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
11160	24231		4.02	5.0E-37	7657117	NT	AV750211 NPC Homo sapiens cDNA clone NPCBGH08 5'
12335	25242		3.63	5.0E-37	AF149773.1	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2485	15622	28741	2.97	4.0E-37	AA702784.1	EST_HUMAN	280b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
6416	19585	32947	0.88	4.0E-37	AW794502.1	EST_HUMAN	RO6-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA
9558	28321	36192	0.56	4.0E-37	AA843806.1	EST_HUMAN	ak09cd2.s1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1405442 3'
2074	15214	28332	3.42	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
2074	15214	28333	3.42	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
2581	15708		1.54	3.0E-37	AW961150.1	EST_HUMAN	EST373222 IMAGE resequences, MAGF Homo sapiens cDNA
3030	16206		4.02	3.0E-37	AW961150.1	EST_HUMAN	EST373222 IMAGE resequences, MAGF Homo sapiens cDNA
5885	19170	32492	0.7	3.0E-37	AL138274.1	EST_HUMAN	DKFZp547G067_r1 547 (synonym: hibr1) Homo sapiens cDNA clone IMAGE:2373896 3' similar to TR:Q13537
7728	20780	34279	0.72	3.0E-37	AJ749952.1	EST_HUMAN	ai34c05.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2373896 3' similar to TR:Q13537
392	13629	26686	0.89	2.0E-37	D89780.1	NT	Q13537 SIMILAR TO POGO ELEMENT ;
392	13629	26687	0.89	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
1105	14270	27328	2.53	2.0E-37	AU131202.1	EST_HUMAN	Homo sapiens mRNA for AML1, complete cds
1105	14270	27328	2.53	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
2021	15162	28297	1.32	2.0E-37	AL163247.2	NT	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
3899	17156	30162	6.71	2.0E-37	4503210.1	NT	Homo sapiens chromosome 21 segment HS21C047
4360	17503	30486	0.6	2.0E-37	4826685	NT	Homo sapiens cytochrome P450, subfamily XXV1A (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
5504	18703	33224	0.9	2.0E-37	BF036327.1	EST_HUMAN	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp) box polypeptide 1 (DDX1) mRNA
6076	18835	33224	0.9	2.0E-37	11690617	NT	60145853 IF1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
6798	19953	33353	3.72	2.0E-37	AA346720.1	EST_HUMAN	Homo sapiens mouse thiamin pyrophosphokinase homolog (TPK1), mRNA
8185	21267	34780	0.47	2.0E-37	BE537764.1	EST_HUMAN	EST 62931 Fetal heart II Homo sapiens cDNA 5' end
8185	21267	34791	0.47	2.0E-37	BE537764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
8227	21309	34829	2.32	2.0E-37	BF204032.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
11856	24844	38541	10.07	2.0E-37	AF176013.1	NT	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111406 5'
12797	26770		1.44	2.0E-37	11417972	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
13184	25770		4.19	2.0E-37	11417972	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
2154	15290	28417	6.95	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
3267	18441		1.03	1.0E-37	AW862082.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
5055	18183	31158	2.34	1.0E-37	BF371719.1	EST_HUMAN	RC3-CT0347-210400-016-H03 CT0347 Homo sapiens cDNA
6127	19306		0.89	1.0E-37	7305360	NT	QV6-FN0780-280700-318-c10 FN0780 Homo sapiens cDNA
8409	21460	35019	1.12	1.0E-37	BE546032.1	EST_HUMAN	Mus musculus obogelin (Otog), mRNA
8933	22012	35551	3.59	1.0E-37	AA171406.1	EST_HUMAN	601072419F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
							zp21b02.r1 Stragene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to contains L1.12 L1 repetitive element ;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10937	24019	37652	2.19	1.0E-37	M22878.1	NT	Human somatic cytochrome c (Hc1) processed pseudogene, complete cds
12671	25447		1.94	1.0E-37	BE771814.1	EST_HUMAN	CM3-FT0098-140700-243-407 FT0098 Homo sapiens cDNA
5998	19095	32308	1.72	8.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Plocdo (LOC56768), mRNA
1249	14408	27470	1.96	8.0E-38	11436995	NT	Homo sapiens Grib2-associated binder 2 (KIAA0871), mRNA
2567	15592	28817	1.21	8.0E-38	BF946221.1	EST_HUMAN	602018401F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4153992.5
12735	14408	27470	1.37	8.0E-38	11436995	NT	Homo sapiens Grib2-associated binder 2 (KIAA0871), mRNA
13210	26049		1.44	8.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
2254	16387	28616	1.7	7.0E-38	AW972825.1	EST_HUMAN	EST384920 MAGE resequences, MAGL Homo sapiens cDNA
3107	16283	29299	1.98	6.0E-38	BF033033.1	EST_HUMAN	601450722F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3859348.5
5706	18999	32192	0.98	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5708	18999	32193	0.98	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7482	20557	34029	0.59	6.0E-38	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
12189	25147		4.27	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12704	25468	32025	6.66	6.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
13160	25913	31881	1.79	6.0E-38	11418184	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
745	13926	29967	0.9	5.0E-38	AW971819.1	EST_HUMAN	EST383908 MAGE resequences, MAGL Homo sapiens cDNA
2525	15650	28774	4.57	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIR gene (partial), exon 8
3793	16957	29961	0.94	5.0E-38	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
3971	16957	29961	0.77	5.0E-38	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
5288	15650	28774	0.98	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIR gene (partial), exon 8
7172	20305	33748	1.63	5.0E-38	BE871810.1	EST_HUMAN	601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854074.5
121	13351	26380	4.28	4.0E-38	Z25466.1	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
121	13351	26381	4.28	4.0E-38	Z25466.1	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1183	14346	27403	1.15	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2167	15302		4.42	3.0E-38	AF003630.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3787	16948		1.49	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (hira-like) (HIRAP4), mRNA
3958	17116	30119	2.46	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3958	17116	30120	2.46	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4736	17871		0.61	3.0E-38	BE278301.1	EST_HUMAN	601157639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272.5
6893	25836	33468	5.89	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7393	20471	33937	0.58	3.0E-38	AW302481.1	EST_HUMAN	xv04801.x1 NCL_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2827009.3
7763	20822	34313	6.53	3.0E-38	BF373664.1	EST_HUMAN	CM3-FT0181-140700-241-407 FT0181 Homo sapiens cDNA
8851	21930	36469	2.11	3.0E-38	H85494.1	EST_HUMAN	y88504.1 Soares melanocyte 2Nbl-IM Homo sapiens cDNA clone IMAGE:249775.5
8851	21930	36470	2.11	3.0E-38	H85494.1	EST_HUMAN	y88504.1 Soares melanocyte 2Nbl-IM Homo sapiens cDNA clone IMAGE:249775.5

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10177	23214		1.84	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11598	24651		1.88	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12990	14346	27403	1.23	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
61	13280	26303	1.96	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1411	14565	27639	3.56	2.0E-38	5602097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1678	14830	27914	13.95	2.0E-38	AA437353.1	EST_HUMAN	z30d01.1 Scores ovary tumor Nbl-HOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ; z30d01.1 Scores ovary tumor Nbl-HOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1678	14830	27915	13.95	2.0E-38	AA437353.1	EST_HUMAN	z30d01.1 Scores ovary tumor Nbl-HOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
3822	16786		0.92	2.0E-38	AF07087C.1	NT	Homo sapiens protein phosphatase 2C alpha 2 mRNA, complete cds
4704	17839	30824	18.99	2.0E-38	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
5252	18339	31312	0.68	2.0E-38	AA437181.1	EST_HUMAN	z30d01.1 Scores testis NHT Homo sapiens cDNA clone IMAGE:768129 5' similar to TR:G817957
5836	19026	32331	0.75	2.0E-38	Z26634.2	NT	G817957 GLYCINE RECEPTOR SUBUNIT ALPHA 4 ;
5838	19026	32332	0.75	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7897	20949	34457	1.47	2.0E-38	AV721103	EST_HUMAN	Homo sapiens mRNA for ankyrin B (440 kDa)
8680	21760		4.47	2.0E-38	BE165990.1	EST_HUMAN	MR3-H10487-150200-113-g01 HT0487 Homo sapiens cDNA
9096	22175	35719	0.49	2.0E-38	F06450.1	EST_HUMAN	HSC:18F031 normalized infant brain cDNA Homo sapiens cDNA clone c-18f03
9165	22243	35786	1.26	2.0E-38	AF069755.1	NT	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
9422	22496		1.36	2.0E-38	BE22256.1	EST_HUMAN	hu08g02.x1 NCI_QGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:O02710 O02710
10665	23699	37309	1.67	2.0E-38	D63479.2	NT	GAG POLYPROTEIN. ;
11781	24771	38467	4.86	2.0E-38	BE712790.1	EST_HUMAN	Homo sapiens mRNA for KIAA0145 protein, partial cds
11939	24925	38628	2.86	2.0E-38	AF190501.1	NT	QV2-HT0668-080800-293-a05 HT0668 Homo sapiens cDNA
11939	24925	38627	2.86	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12244	25186		6.21	2.0E-38	AV726988.1	EST_HUMAN	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12246	25187		1.26	2.0E-38	AB012723.1	NT	AV726988 HTC Homo sapiens cDNA clone HTCAH-107 5'
12546	25370		3.36	2.0E-38	M55630.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12569	25381	32073	4.81	2.0E-38	H55941.1	EST_HUMAN	Human topoisomerase I pseudogene 2
12632	25425		2.87	2.0E-38	S74906.1	NT	CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
13174	25762		1.35	2.0E-38	11418248	NT	E1 beta-pyruvate dehydrogenase beta [promoter] [human, placenta, Genomic, 1280 nt]
							Homo sapiens sulfotransferase-related protein (SULTX3), mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1117	14282		1.96	1.0E-38	AA401570.1	EST_HUMAN	zu62602.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742639 5' similar to contains element MER19 repetitive element;
2055	15195	28310	2.82	1.0E-38	4885288	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
2077	15217	28336	1.33	1.0E-38	7661989	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2564	15689	28815	1.89	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4271	17416	30405	0.93	1.0E-38	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4439	17579	30568	0.6	1.0E-38	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6), mRNA, and translated products
4444	17584	30563	2.15	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4444	17584	30564	2.15	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4719	17854	30837	1.08	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
5268	18387	31355	1.89	1.0E-38	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
6151	19327	32872	4.59	1.0E-38	7305360	NT	Mus musculus atogelin (Otog), mRNA
6151	19327	32873	4.59	1.0E-38	7305360	NT	Mus musculus atogelin (Otog), mRNA
7563	20635	34110	2.55	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
9354	22429	35987	0.68	1.0E-38	11422250	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
9610	22665	36236	6.31	1.0E-38	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
12403	25877		4.79	1.0E-38	AL163284.2	NT	MER29 repetitive element;
12116	25896	38801	1.64	9.0E-39	AA112438.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
55	13294	26309	4.93	8.0E-39	4502312	NT	zm2707.r1 Stragene pancreas (#937208) Homo sapiens cDNA clone IMAGE:526885 5'
1425	14579	27652	1.3	8.0E-39	4758229	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1876	15020		1.8	8.0E-39	AB23404.1	EST_HUMAN	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9), mRNA
2160	15296	28421	7.08	7.0E-39	AL163227.2	NT	h053f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890
11047	24124	37768	2.4	6.0E-39	BF331829.1	EST_HUMAN	POL PROTEIN;
13064	25697		2.24	6.0E-39	BE670394.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
1032	14201	27259	1.64	5.0E-39	AF003528.1	NT	QV1-BT0631-040900-367-602 BT0631 Homo sapiens cDNA
3050	18226	29247	9.33	5.0E-39	AI750154.1	EST_HUMAN	7e34c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6
12720	25479		1.53	5.0E-39	11420289	NT	CE00828;
							Homo sapiens X-linked arthritic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
							a36604.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
							Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;contains LTR7.1 LTR7 repetitive element;
							Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
564	13756	28782	4.39	4.0E-39	AB015810.1	NT	Chlorocephus aethiops mRNA for ribosomal protein S4X, complete cds
3683	16826	28835	0.9	4.0E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5950	19136	32450	0.6	4.0E-39	11422113	NT	Homo sapiens EBNA-2 α -activator (100kD) (p100), mRNA
5950	19136	32451	0.6	4.0E-39	11422113	NT	Homo sapiens EBNA-2 α -activator (100kD) (p100), mRNA
8287	21349	34864	1.02	4.0E-39	AA682949.1	EST_HUMAN	ae92g04.s1 Stragene echizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains ORF.b1 OFR repetitive element ;
9530	22595	36165	0.46	4.0E-39	DB4116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
9530	22595	36166	0.46	4.0E-39	DB4116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12744	25494	-	6.36	4.0E-39	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12884	25586	-	2.56	4.0E-39	BE836452.1	EST_HUMAN	QV6-FN0063-260600-278-008 FN0063 Homo sapiens cDNA
48	13287	28297	11.96	3.0E-39	AA631949.1	EST_HUMAN	frnc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	13287	28298	11.96	3.0E-39	AA631949.1	EST_HUMAN	frnc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	13287	28299	11.96	3.0E-39	AA631949.1	EST_HUMAN	frnc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
12236	25180	38348	6.59	3.0E-39	AI084557.1	EST_HUMAN	α 63a10.s1 Soares_NHMPu.S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
12236	25180	38349	6.59	3.0E-39	AI084557.1	EST_HUMAN	α 63a10.s1 Soares_NHMPu.S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
12284	25212	-	5.72	3.0E-39	H37903.1	EST_HUMAN	yp51c06.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190954 3'
920	14095	-	7.78	2.0E-39	BE409203.1	EST_HUMAN	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3836289 5'
935	14110	-	11.55	2.0E-39	AI525119.1	EST_HUMAN	promtra-7 D01.r b7tumor Homo sapiens cDNA 5'
1057	14223	-	3.9	2.0E-39	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
1560	14713	-	33.59	2.0E-39	AW372318.1	EST_HUMAN	PMO-BT0340-211298-003-002 BT0340 Homo sapiens cDNA
2030	15171	28279	4.48	2.0E-39	AA720574.1	EST_HUMAN	rw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.B3 THR repetitive element ;
2692	15812	28928	1.89	2.0E-39	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4523	17682	30649	1.74	2.0E-39	BF370207.1	EST_HUMAN	RC4-FN0037-290700-011-a10 FN0037 Homo sapiens cDNA
5608	18803	31868	4.45	2.0E-39	AA508980.1	EST_HUMAN	ng89g03.s1 NCI_CGAP_P18 Homo sapiens cDNA clone IMAGE:941693
7528	20599	34073	2.08	2.0E-39	AA080867.1	EST_HUMAN	zn05g02.r1 Stragene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:546651 5'
7702	20767	34251	0.68	2.0E-39	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
7702	20767	34252	0.68	2.0E-39	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
8506	21586	35120	0.63	2.0E-39	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9828	22866	-	0.79	2.0E-39	AI886660.1	EST_HUMAN	tu35e03.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2253052 3'
11716	24756	38452	2.13	2.0E-39	DB6964.1	NT	Human mRNA for KIAA0205 gene, partial cds
1543	14895	27774	2.83	1.0E-39	AI008345.1	NT	Homo sapiens KVLQ1 gene

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1543	14695	27775	2.83	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1581	14714	27791	5.98	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
1763	14912	28007	1.14	1.0E-39	H55224.1	EST_HUMAN	CHR220163 Chromosome 22 exon Homo sapiens cDNA clone C22_205 5'
4782	17917	30903	9.32	1.0E-39	AW651985.1	EST_HUMAN	EST364065 MAGE resequences, MAGB Homo sapiens cDNA
4782	17917	30904	9.32	1.0E-39	AW651985.1	EST_HUMAN	EST364065 MAGE resequences, MAGB Homo sapiens cDNA
4824	17957	30943	9.13	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5474	18673	31886	0.82	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5474	18673	31887	0.82	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5747	18939	32239	1.2	1.0E-39	T80876.1	EST_HUMAN	Alu repetitive element contains L1R1 repetitive element
5781	18973	32278	4.65	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
5781	18973	32279	4.65	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
6965	20193		1.95	1.0E-39	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7521	20594	34069	2.15	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8762	21841	35382	1.04	1.0E-39	O46530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNAse K6)
11165	24236	37867	1.4	1.0E-39	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA
569	13761	26785	2	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1263	14420	27484	16.02	9.0E-40	4756145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1263	14420	27485	16.02	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1480	14833	27718	15.75	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3895	17044	30043	1.18	9.0E-40	4503764	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
4081	18467	30242	3.99	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4466	17606	30594	5.63	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3108	16282	29298	1.04	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 H1.5 cDNA Library Homo sapiens cDNA clone 7H15A04
4033	17189		3.43	8.0E-40	BE396541.1	EST_HUMAN	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619168 5'
7894	20946	34462	2.21	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7894	20946	34453	2.21	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
11136	24208	37834	2.63	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

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2788	15904	29011	9.91	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2788	15904	29012	9.91	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
6060	19242		1.85	6.0E-40	BE504766.1	EST_HUMAN	h249g01.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:3210480 3'
6275	19449		1.38	6.0E-40	7661998	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
7075	20128	33544	3.04	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7075	20128	33545	3.04	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
10182	23219	36811	6.09	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
10182	23219	36812	6.09	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
2670	15791	28907	2.75	5.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1925	15068	28173	3.81	4.0E-40	AI686005.1	EST_HUMAN	h91b01.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN. ;
2175	15310		6.81	4.0E-40	AF003526.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4508	17647	30635	7.2	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8070	21152	34672	0.84	4.0E-40	AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
8181	21263	34785	6.98	4.0E-40	AA742809.1	EST_HUMAN	rv34e10.r1 NCL CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
9255	22332	35681	5.84	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
9255	22332	35682	5.84	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
10955	24036	37671	1.95	4.0E-40	AW847585.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4250	17396	30385	0.9	3.0E-40	AI925949.1	EST_HUMAN	wh12807.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
4993	18122		0.83	3.0E-40	AA055118.1	EST_HUMAN	zr10h09.s1 Soares 'fetal heart' NBHH19W Homo sapiens cDNA clone IMAGE:377153 3'
6392	19752	33137	0.68	3.0E-40	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
6777	19932	33328	7.06	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8575	21656	35197	3.86	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
9169	22247	35790	1.27	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9412	22486	36050	1.6	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10899	23983	37615	1.49	3.0E-40	D86864.1	NT	Human mRNA for KIAA0209 gene, partial cds
11544	24900	38276	9.12	3.0E-40	6005813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
335	13548		3.91	2.0E-40	AI230306.1	EST_HUMAN	q952h08.x1 Soares 'testis' NHT Homo sapiens cDNA clone IMAGE:1838847 3'
817	13996		5.58	2.0E-40	AW303868.1	EST_HUMAN	xx24e10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S6 ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1872	15016		2.33	2.0E-40	AV731601.1	EST_HUMAN	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1988	15130	28233	2.8	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1988	15130	28234	2.8	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2133	15269	28389	1.39	2.0E-40	AI968562.1	EST_HUMAN	ZINC FINGER PROTEIN.1
2238	15371	28500	2.21	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
2764	15871		1.66	2.0E-40	BE275932.1	EST_HUMAN	501121597F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3345784 5'
3196	16371	28378	5.27	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
5021	18150	31128	1.43	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5021	18150	31129	1.43	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
908	14081		1.2	1.0E-40	AA225989.1	EST_HUMAN	nc09a09.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608
2686	15806	28922	1.82	1.0E-40	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3863903 5'
2750	15897		3.98	1.0E-40	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
3370	16542		2.14	1.0E-40	4507142	NT	SYNTAXIN 17.;
4733	17868	30851	3.69	1.0E-40	4508012	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
6385	19554	32912	0.68	1.0E-40	W92708.1	EST_HUMAN	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
6385	19554	32913	0.68	1.0E-40	W92708.1	EST_HUMAN	zh78f11.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7236	20320	33763	1.83	1.0E-40	AA573201.1	EST_HUMAN	zh78f11.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7236	20320	33764	1.83	1.0E-40	AA573201.1	EST_HUMAN	zh78f11.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:995167 3'
7381	20456	33922	0.82	1.0E-40	P26808	SWISSPROT	h42804.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
11157	24228	37858	6.41	1.0E-40	AU148345.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H I]
11993	24978	38683	1.49	1.0E-40	AA614255.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
11993	24978	38684	1.49	1.0E-40	AA614255.1	EST_HUMAN	np09h03.s1 NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:1115881 similar to TR:G1136406
12079	25069		1.86	1.0E-40	AL163246.2	NT	G1136406 KIAA0173 PROTEIN.;
12687	29032		6.94	1.0E-40	BF334712.1	EST_HUMAN	G1136408 KIAA0173 PROTEIN.;
3906	17065	30084	0.59	9.0E-41	W01596.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
8106	21188	34708	1.6	8.0E-41	AL163203.2	NT	MR2-CT0222-21099-002-e10 G10222 Homo sapiens cDNA
851	18024	27089	2.52	7.0E-41	AI934394.1	EST_HUMAN	za36a02.i1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284802 5'
851	16024	27090	2.52	7.0E-41	AI934394.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
851	16024	27090	2.52	7.0E-41	AI934394.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
851	16024	27090	2.52	7.0E-41	AI934394.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5379	18581	31450	0.9	7.0E-41	11545770	NT	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA
6132	15311	32651	2.71	7.0E-41	11419208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6483	19650	33012	1.04	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7133	18559	31473	0.96	7.0E-41	U72335.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4
11718	24758	39453	2.06	7.0E-41	4758445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA
11931	24917	39620	1.41	7.0E-41	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
13182	26028		8.58	7.0E-41	11417972	NT	Homo sapiens pascicillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
291	13508	26543	1.13	6.0E-41	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
2179	15314	28443	3.09	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
8158	21240	34760	1.31	6.0E-41	BF513783.1	EST_HUMAN	U1H-BW1-amp-b-03-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
13156	25952		1.25	6.0E-41	AW873637.1	EST_HUMAN	h6408.x1 Soares_NF1_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3042183 3' similar to contains MER32.b3 MER32 repetitive element
1845	14891	28092	1.37	5.0E-41	T82628.1	EST_HUMAN	yc03e10.s1 Strategene lung (#637210) Homo sapiens cDNA clone IMAGE:79626 3'
4223	17371		1.17	5.0E-41	4885636	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
6678	19637		2.34	5.0E-41	BE067042.1	EST_HUMAN	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA
402	13599		1.69	4.0E-41	BE156318.1	EST_HUMAN	QV0-PT0367-150200-114-g09 HT0367 Homo sapiens cDNA
1122	14287	27342	2.37	4.0E-41	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA100583 5'
1442	14595	27670	14.6	4.0E-41	A1027117.1	EST_HUMAN	aw45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE; contains LTR5.b1 LTR5 repetitive element;
1442	14595	27671	14.6	4.0E-41	A1027117.1	EST_HUMAN	aw45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE; contains LTR5.b1 LTR5 repetitive element;
1454	14607	27687	3.34	4.0E-41	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
1655	14817	27900	7.72	4.0E-41	AI500406.1	EST_HUMAN	trn8604.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element;
2953	16130	29144	5.02	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2953	16130	29145	5.02	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4262	17407	30393	2.13	4.0E-41	X92885.1	NT	H.sapiens DNase I hypersensitive site (HSS-3) enhancer element
6638	19797		1.8	4.0E-41	AV759295.1	EST_HUMAN	AV759295 BM Homo sapiens cDNA clone BMFBHC06 5'
9955	22935	36519	5.06	4.0E-41	BF304683.1	EST_HUMAN	60188808F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
11969	24854		7.38	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CuAACCC07 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12900	25917		1.3	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
13110	25725	31942	1.61	4.0E-41	BE887118.1	EST_HUMAN	601508315F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910059 5'
970	14143	27203	1.8	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4455	17595	30575	4.03	3.0E-41	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5809	18804	31689	11.76	3.0E-41	X87689.1	NT	H. sapiens mRNA for putative p64 CLCP protein
6511	19676	33046	1.23	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7987	21017	34529	0.71	3.0E-41	R54765.1	EST_HUMAN	X75608.1 Soares breast 2NbhBst Homo sapiens cDNA clone IMAGE:154575 5'
12119	25099	38804	1.36	3.0E-41	AW984941.1	EST_HUMAN	QV0-BN0040-170300-160-H08 BN0040 Homo sapiens cDNA
12119	25099	38805	1.36	3.0E-41	AW984941.1	EST_HUMAN	QV0-BN0040-170300-160-H08 BN0040 Homo sapiens cDNA
12196	25153		1.98	3.0E-41	AA030768.1	EST_HUMAN	af7710.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1031947 3'
12783	25525		1.43	3.0E-41	BF125922.1	EST_HUMAN	601762940F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026031 5'
1871	14744	27827	31.25	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
2013	15153	28258	2.17	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2293	15425	28559	1.26	2.0E-41	D98992.1	NT	Human mRNA for KIAA0207 gene, complete cds
2341	15472	28806	5.52	2.0E-41	X89693.1	NT	G.gorilla DNA for ZNF80 gene homolog
2889	14744	27827	11.69	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3406	16576	28591	0.89	2.0E-41	AA449549.1	EST_HUMAN	z08b04.1 Soares fetal Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785839 5'
3941	17100	30097	0.89	2.0E-41	5032108	NT	Homo sapiens son of sevenless (Drosophila) homolog 1 (SOS1) mRNA
4744	17879	30862	1.23	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4744	17879	30863	1.23	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
5656	18850	32132	0.6	2.0E-41	AA584575.1	EST_HUMAN	nc12a07.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100460 3' similar to gb:X52851_rna1
6763	19919	33314	0.88	2.0E-41	4504778	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN)
7850	20905	34409	9.27	2.0E-41	AF038404.1	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
8259	21341	34858	1.36	2.0E-41	M98944.1	NT	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds
8259	21341	34859	1.36	2.0E-41	M98944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8288	21370	34891	1.42	2.0E-41	AA328265.1	EST_HUMAN	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8175	22253	35786	1.65	2.0E-41	P52742	SWISSPROT	EST31723 Embryo, 12 week 1 Homo sapiens cDNA 5' end
9617	22672	36241	0.66	2.0E-41	11417118	NT	ZINC FINGER PROTEIN 135
9617	22672	36242	0.56	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11775	24767	39463	2.87	2.0E-41	AA372637.1	EST_HUMAN	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
13148	25747		1.2	2.0E-41	11420516	NT	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3276	18450	29470	1.05	1.0E-41	BE869735.1	EST_HUMAN	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3278	19450	29471	1.05	1.0E-41	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4689	17824	30811	9.46	1.0E-41	6678468	NT	Mus musculus tubulin alpha 6 (Tubae6), mRNA
9618	22673	36243	1.57	1.0E-41	AI217888.1	EST_HUMAN	q175c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755858 3'
12334	23241		1.87	1.0E-41	11528291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8717	21797		1.19	9.0E-42	BE179191.1	EST_HUMAN	RCO-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA
9375	22450	36011	2.81	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9375	22450	36012	2.81	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
475	13670	26702	5.34	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2176	15311	28439	8.63	8.0E-42	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12375	26035		30.09	8.0E-42	AA493896.1	EST_HUMAN	nt07c02.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304 367BP EXPRESSED SEQUENCE TAG MRNA:
12396	25904		2.91	8.0E-42	AW068062.1	EST_HUMAN	xc97a04.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2592174 3' similar to contains OFR.12 OFR repetitive element:
955	14128		2.23	7.0E-42	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
8666	21746		0.5	7.0E-42	R10963.1	EST_HUMAN	Y83g04.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:129174 5'
9445	22561	36124	1.32	7.0E-42	AI204359.1	EST_HUMAN	q66g12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
1903	15046	28155	3.24	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1903	15046	28156	3.24	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2363	15494		3.6	6.0E-42	AW236656.1	EST_HUMAN	xp23f08.x1 NCI_CGAP_JN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L.1 L1 repetitive element:
5584	18779	31824	1.65	6.0E-42	AB028890.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
5834	18779	31824	1.5	6.0E-42	AB028890.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
138	13364		8.34	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
451	13647	26683	1.56	5.0E-42	BE217913.1	EST_HUMAN	h031e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
499	13694		3.05	5.0E-42	5730039	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
500	13695		1.14	5.0E-42	5730039	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6825	19978	33385	0.94	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6825	19978	33386	0.94	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6941	20264	33691	2.57	5.0E-42	11417957	NT	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
7351	20430	33892	1.55	5.0E-42	AF071569.1	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta isoform mRNA, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8978	22057	35599	2.88	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1284 protein, partial cds
10832	23865	37487	0.55	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10832	23865	37488	0.55	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
11248	24815	37855	1.77	5.0E-42	8023162	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
772	13953	27002	5.6	4.0E-42	AF050506.1	NT	Homo sapiens MHC class 1 region
772	13953	27003	5.6	4.0E-42	AF050506.1	NT	Homo sapiens MHC class 1 region
1091	14256	27312	1.82	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4311	17454	30442	1.39	4.0E-42	X59417.1	NT	H. sapiens PROS-27 mRNA
4343	17486	30469	1.1	4.0E-42	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4384	17507	30488	4.67	4.0E-42	4506496	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4708	17841	30825	17.64	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
5285	18404	31372	0.93	4.0E-42	7661035	NT	Homo sapiens DKFZP564O2082 protein (DKFZP564O2082), mRNA
10701	23734	37339	0.57	4.0E-42	AW371201.1	EST_HUMAN	Clontech BT0282-171289-127-403 BT0282 Homo sapiens cDNA
10884	23968	37597	2.32	4.0E-42	AW818530.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
10884	23968	37598	2.32	4.0E-42	AW818530.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
11240	24309	37846	1.43	4.0E-42	AF435225.1	EST_HUMAN	h11d02.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
11698	24695	38387	1.69	4.0E-42	BF035327.1	EST_HUMAN	601456531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
1512	14685	27750	3.79	2.0E-42	BF376834.1	EST_HUMAN	RCO-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2486	15593	28718	1.6	2.0E-42	AF590218.1	EST_HUMAN	AV690218 GKO Homo sapiens cDNA clone GKCCBB08 5'
2483	15610		4.24	2.0E-42	AW898344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2496	15623	28742	3.6	2.0E-42	AW250059.1	EST_HUMAN	2819283 3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2619283 3'
5875	19065	32372	11.82	2.0E-42	AW955368.1	EST_HUMAN	EST367438 IMAGE resequences, MAGC Homo sapiens cDNA
5875	19065	32373	11.82	2.0E-42	AW955368.1	EST_HUMAN	EST367438 IMAGE resequences, MAGC Homo sapiens cDNA
6892	20044	33452	0.9	2.0E-42	A052586.1	EST_HUMAN	aw63d05.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1653417 3'
10046	23084	36885	1.28	2.0E-42	BE538919.1	EST_HUMAN	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
10280	23295	36892	0.64	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNAse K3)
10260	23295	36893	0.64	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNAse K3)
12037	25018	38723	1.53	2.0E-42	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
752	13932	26977	1.75	1.0E-42	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
1067	14233	27292	2.2	1.0E-42	AW295809.1	EST_HUMAN	UHH-B11-afh-e-04-0-J1.s1 NCL_CGAP_Sub03 Homo sapiens cDNA clone IMAGE:2721871 3'
1125	14290	27345	1.74	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1125	14290	27346	1.74	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1271	16033	27498	11.99	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1271	16033	27499	11.99	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1735	14884	27977	1.15	1.0E-42	11423219	NT	Homo sapiens rec (LOC51201), mRNA
2087	15227	28349	1.18	1.0E-42	AF110296.1	NT	Homo sapiens PDNP1 gene, exon 17
2609	13733	28849	1.42	1.0E-42	5174458	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
3029	18205	29228	9.15	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3799	19960	29964	3.31	1.0E-42	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3895	17054	30054	1.11	1.0E-42	5031610	NT	Homo sapiens Golgi vesicular membrane trafficking protein p18 (BET1) mRNA
4036	17192	30202	0.99	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C067
4361	17504	30486	3.47	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4716	17851	30834	0.61	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST0197-161069-012-a03 ST0197 Homo sapiens cDNA
4867	18000	30984	2.37	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (Pi31), mRNA
4867	18000	30985	2.37	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (Pi31), mRNA
4901	18031	31020	6.13	1.0E-42	4506759	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
11440	24501	38169	1.39	1.0E-42	BE408811.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
10291	23326	36929	8.16	9.0E-43	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
669	13855	26883	20.77	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
669	13855	26884	20.77	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
718	13900	26936	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
718	13900	26939	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
718	13900	26940	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
5816	19006	32312	0.72	8.0E-43	H13952.1	EST_HUMAN	y08e11.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148172 5'
3731	16892	29896	7.48	7.0E-43	AW246442.1	EST_HUMAN	2822251.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
8968	22047		3.98	7.0E-43	A1936748.1	EST_HUMAN	wp69b01.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2466965 3' similar to TR:015475 O15475 UNANIMATED HERV-H PROTEIN, contains LTR7.b1 LTR7 repetitive element ;
1374	14529		11.62	6.0E-43	AA491890.1	EST_HUMAN	nc72408.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:309803 similar to gb105095 60S
2657	15780		4.03	6.0E-43	AV708201.1	EST_HUMAN	RIBOSOMAL PROTEIN L30 (HUMAN);
4863	18092	31068	252.27	6.0E-43	AI421540.1	EST_HUMAN	AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'
6441	19608	32871	2.53	6.0E-43	9956973	NT	126-c04.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2097318 3' similar to SW:BRR2_YEAST P32039 PRE-MRNA SPLICING HELICASE BRR2 ;
							Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7048	20101	33518	1.8	6.0E-43	AW488897.1	EST_HUMAN	h30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810881 3' similar to contains MER1.3 MER1 MER1 repetitive element;
10096	23094	36686	1.77	6.0E-43	AA195154.1	EST_HUMAN	z35608.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665410 5' similar to TR:G529641
11363	24424		2.45	6.0E-43	AL119158.1	EST_HUMAN	G529641 DBT, COMPLETE: CDS, contains element PTR7 repetitive element;
145	13370		1.82	5.0E-43	AL163213.2	NT	DKFZp761L1712_r1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761L1712 5'
515	13709	28736	3.4	5.0E-43	AA382780.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
2908	16066	28100	1.59	5.0E-43	AV732578.1	EST_HUMAN	EST196033 Testis I Homo sapiens cDNA 5' end
6435	20086	33512	0.9	5.0E-43	A1613509.1	EST_HUMAN	AV732378 HTF Homo sapiens cDNA clone HTFANC08 5'
7043	20096	33512	0.89	5.0E-43	A1613509.1	EST_HUMAN	tw22607.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260452 3'
8381	21462	34885	0.84	5.0E-43	AA442271.1	EST_HUMAN	tw22607.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260452 3'
8381	21462	34886	0.84	5.0E-43	AA442271.1	EST_HUMAN	z654603.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
9080	22169		0.73	5.0E-43	H74277.1	EST_HUMAN	z654603.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
9584	22706	38272	4.09	5.0E-43	AA465288.1	EST_HUMAN	y449512.1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:229610 6'
10609	23643	37251	2.6	5.0E-43	A1733244.1	EST_HUMAN	aa33308.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
10651	23685	37285	1.02	5.0E-43	AL049110.1	EST_HUMAN	aa33308.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
11001	24080	37715	4.53	5.0E-43	AW863007.1	EST_HUMAN	pv14 GENE;
11213	24282	37921	2.24	5.0E-43	W29011.1	EST_HUMAN	DKFZp434D0119_r1 434 (synonym: hias3) Homo sapiens cDNA clone DKFZp434D0119
986	15987	27227	4.4	4.0E-43	AF003528.1	NT	MR2-SN0007-290400-004-c02 SN0007 Homo sapiens cDNA
5373	18576	31444	1.09	4.0E-43	A1036338.1	EST_HUMAN	5524 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
6489	19885	33028	0.68	4.0E-43	6996009	NT	Homo sapiens X-linked arylidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7280	20363		1.6	4.0E-43	11416793	NT	cy47h03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1668013 3'
8371	21462	34875	5.18	4.0E-43	A1244341.1	EST_HUMAN	Homo sapiens glycyt-RNA synthetase (GARS), mRNA
8371	21462	34978	5.18	4.0E-43	A1244341.1	EST_HUMAN	Homo sapiens protocadherin beta 8 (PCDH8), mRNA
10521	23556	37164	1.02	4.0E-43	6008987	NT	qj76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element;
12311	25227		2.7	4.0E-43	R20950.1	EST_HUMAN	qj76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element;
13030	25898		1.33	4.0E-43	A1436083.1	EST_HUMAN	qj76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element;
							Homo sapiens zinc finger protein 161 (ZNF161), mRNA
							y06503.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element;
							th52b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:002710 002710 GAG POLYPROTEIN.;

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1240	14399		3.46	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1730	14880	27971	2.52	3.0E-43	X97869.1	NT	H. sapiens gene encoding La autanigen
2120	16055	28377	1.1	3.0E-43	R83422.1	EST_HUMAN	yp82f01.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:1939-5 5' similar to contains M5R1 repetitive element;
3682	16825	29834	1.22	3.0E-43	S60002.1	NT	AML1-EVI-1-AML1-EVI-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
4405	17548	30532	0.9	3.0E-43	AA548154.1	EST_HUMAN	nk55d06.s1 NCI CGAP_P77 Homo sapiens cDNA clone IMAGE:1017419
6014	19198	32515	0.94	3.0E-43	D34613.1	NT	Human TBXAS1 gene for thromboxane synthase, promoter region and exon 1
6487	19654	33016	1.56	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6487	19654	33017	1.56	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6867	20019	33428	5.09	3.0E-43	U65487.1	NT	[Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
8357	21438		4.39	3.0E-43	AA458824.1	EST_HUMAN	aa8811.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.12 THR repetitive element;
9020	22099	35639	1	3.0E-43	7661721	NT	Homo sapiens hypothetical protein (HSA011816), mRNA
10068	23106	36709	0.68	3.0E-43	11420217	NT	Homo sapiens similar to ornithine carbamoyltransferase (H. sapiens) (LOC883648), mRNA
12026	25010	38712	1.42	3.0E-43	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
188	13410		7.24	2.0E-43	A1900764.1	EST_HUMAN	gd61c09.x1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7.13 PTR7 PTR7 repetitive element;
6604	19764	33152	1.2	2.0E-43	BE222776.1	EST_HUMAN	hu53a08.x1 NCI CGAP_Bm41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element;
6604	19764	33153	1.2	2.0E-43	BE222776.1	EST_HUMAN	hu53a08.x1 NCI CGAP_Bm41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element;
7426	20503	33973	1.29	2.0E-43	AW207390.1	EST_HUMAN	U1H-B11-af1-a-08-0-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
8003	21584		3.16	2.0E-43	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
11476	24535		4.75	2.0E-43	T03007.1	EST_HUMAN	Human ribosomal protein L23a mRNA, complete cds
1681	14833	27917	2.95	1.0E-43	AF154836.1	NT	FB1G5 Fetal brain, Stratagene Homo sapiens cDNA clone FB1G5 3'end similar to LINE-1
1681	14833	27918	2.95	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1742	14891	27965	4.12	1.0E-43	AL163284.2	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
2766	15902	29009	4.73	1.0E-43	BF348283.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
5526	18723	31740	0.88	1.0E-43	4885544	NT	802022313F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157666 5'
6744	19900	33291	6.84	1.0E-43	4507168	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
6744	19900	33291	6.84	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
6744	19900	33292	6.84	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7106	18533	31488	1.19	1.0E-43	R19791.1	EST_HUMAN	W40601.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to SP:BD38_MOUSE P28856 BRAIN PROTEIN DN38 ;
8117	21189	34720	0.6	1.0E-43	AF175265.1	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
8256	21338		2.17	1.0E-43	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
9037	22116	35659	28.54	1.0E-43	AW963576.1	EST_HUMAN	EST375749 IMAGE resequences, MAGH Homo sapiens cDNA
10498	23633	37143	0.66	1.0E-43	AW953229.1	EST_HUMAN	EST365299 IMAGE resequences, MAGB Homo sapiens cDNA
11206	24275	37912	5.81	1.0E-43	AI884961.1	EST_HUMAN	w87h01.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494705 3'
11647	24726	38418	3.05	1.0E-43	AI1424378	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
12248	25189		2.28	1.0E-43	AL137984.1	EST_HUMAN	DKFZp761D1015_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761D1015 5'
12550	25373	32071	3.16	1.0E-43	AI675418.1	EST_HUMAN	w89b04.x1 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:2313775 3'
12805	25338	32013	3.21	9.0E-44	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
913	14088	27154	5.32	8.0E-44	AI222985.1	EST_HUMAN	q723g01.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
8736	21815	35350	2.89	8.0E-44	X94354.1	NT	q723g01.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
10545	23580	37189	0.5	8.0E-44	11423497	NT	H. sapiens DNA for Cone cGMP-PDE gene
10545	23580	37190	0.5	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
11436	24497	38164	2.87	8.0E-44	Y10498.2	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
11987	24972	38877	1.76	8.0E-44	L29139.1	NT	Homo sapiens mRNA for thymidine kinase, partial
12501	25345	32065	2.89	8.0E-44	11527389	NT	Homo sapiens myosin mRNA, partial cds
12544	25735	31946	2.17	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (HRHFB2122), mRNA
12045	25938	31760	1.85	8.0E-44	11418089	NT	Homo sapiens putative nuclear protein (PRKCAP), mRNA
13126	25735	31946	2.29	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (HRHFB2122), mRNA
676	13862		1.13	7.0E-44	R06035.1	EST_HUMAN	ye89e01.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124920 5'
2307	15439	28573	1.19	7.0E-44	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3031	16207	29229	4.44	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3031	16207	29230	4.44	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3965	17123	30126	2.71	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4366	17499	30478	0.85	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4358	17499	30480	0.85	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
8379	21480	34983	2.39	7.0E-44	AU169839.1	EST_HUMAN	AU159839 Y79AA1 Homo sapiens cDNA clone Y79AA1000490 3'
6229	19404	32754	0.67	8.0E-44	Z20946.1	EST_HUMAN	HSAAA0EYU P, Human foetal Brain Whole tissue Homo sapiens cDNA
314	13530		4.25	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
342	13553		2.42	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8072	21154	34673	4.12	5.0E-44	A1568523.1	EST_HUMAN	ht40d02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11
9884	22726		1.39	5.0E-44	AU124571.1	EST_HUMAN	OFR OFR repetitive element
3501	10668	29678	4.27	4.0E-44	AL163303.2	NT	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
5128	18253		0.89	4.0E-44	A1435225.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
7639	20708	34187	0.87	4.0E-44	BE883178.1	EST_HUMAN	ht11402.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
8466	21547	35077	0.86	4.0E-44	L21948.1	EST_HUMAN	601508601F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910152 5'
8079	22158		0.71	4.0E-44	BE178618.1	EST_HUMAN	Human fibrillin (FBN1) locus polymorphism
11513	24570	38247	5.64	4.0E-44	U60878.1	NT	RC3-HT0585-01040-023-J08 HT0585 Homo sapiens cDNA
1827	14976		1.5	3.0E-44	6912477	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
3167	16342	29350	5.11	3.0E-44	AA168851.1	EST_HUMAN	Homo sapiens keratin alpha 6 (keratin alpha 7) (KPNAG) mRNA
7970	21020	34533	0.65	3.0E-44	BE884820.1	EST_HUMAN	7p18b05.t1 Stratiene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609777 5'
9719	22784	36355	0.63	3.0E-44	AF005273.1	NT	601510547F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912010 5'
1074	14240	27298	1.43	2.0E-44	4826685	NT	Sus scrofa domestica subnuclear apomucin mRNA, complete cds
1074	14240	27297	1.43	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1234	14393	27455	3.61	2.0E-44	5803200	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1234	14393	27456	3.61	2.0E-44	5803200	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1340	14496	27568	0.82	2.0E-44	AF133588.1	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1400	14554	27628	1.5	2.0E-44	BE465325.1	EST_HUMAN	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
2219	15553	28484	3.07	2.0E-44	AF070651.1	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
2605	15728		1.26	2.0E-44	4507592	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
2642	15765	28879	0.94	2.0E-44	D25303.1	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
2678	15798		2.3	2.0E-44	5901933	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
3558	16724	29740	1.34	2.0E-44	D87675.1	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
4692	17827	30813	1.75	2.0E-44	AW864376.1	EST_HUMAN	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
6220	19385	32744	1.75	2.0E-44	11449901	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
6966	18515	31507	2.18	2.0E-44	AF038968.1	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
7572	20644	34121	3.8	2.0E-44	11419226	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
7572	20644	34122	3.8	2.0E-44	11419226	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
8623	21703	35238	0.7	2.0E-44	7706370	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
8623	21703	35239	0.7	2.0E-44	7706370	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
8819	21868	35437	1.8	2.0E-44	BE388058.1	EST_HUMAN	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12152	25122		4.59	2.0E-44	BE244902.1	EST_HUMAN	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2795
12730	26094		1.56	2.0E-44	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
53	13292	26308	5.24	1.0E-44	7657334	NT	Homo sapiens Misschaper/NIK-related kinase (MINK) mRNA
53	13292	26307	6.24	1.0E-44	7657334	NT	Homo sapiens Misschaper/NIK-related kinase (MINK) mRNA
594	13784	26804	1.63	1.0E-44	AW853132.1	EST_HUMAN	RC1-CT0249-030300-026-112 CT0249 Homo sapiens cDNA
1224	14384		1.96	1.0E-44	AW894803.1	EST_HUMAN	RC1-BN0039-110300-012-501 BN0039 Homo sapiens cDNA
1605	14758		8.06	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2289	15431	28563	6.17	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Soares total fetus N52HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.13 THR repetitive element ;
2299	19431	28584	6.17	1.0E-44	AA434554.1	EST_HUMAN	contains THR.13 THR repetitive element ;
							Homo sapiens transcription factor IGDM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaplophysin genes, complete cds; and L-type calcium channel a2
2818	15932	29043	1.74	1.0E-44	AF196779.1	NT	aa01c09.s1 Soares_NHMP2u_S1 Homo sapiens cDNA clone IMAGE:811984 3'
3819	18978		3	1.0E-44	AA455969.1	EST_HUMAN	Homo sapiens alpha satellite DNA, M1 monomer type
5221	18343	31314	0.68	1.0E-44	AL130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5221	18343	31315	0.69	1.0E-44	AL130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
8460	21541	35070	0.91	1.0E-44	AW967073.1	EST_HUMAN	EST178147 MAGE resequences, MAGJ Homo sapiens cDNA
8460	21541	35071	0.91	1.0E-44	AW967073.1	EST_HUMAN	EST178147 MAGE resequences, MAGJ Homo sapiens cDNA
8848	21927	35466	0.96	1.0E-44	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9227	22305	35848	0.59	1.0E-44	AI337183.1	EST_HUMAN	q88g07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2009628 3'
11284	24333		4.13	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DGB Homo sapiens cDNA clone DCBBYEC3 5'
11820	24809	38505	3.47	1.0E-44	10092664	NT	Homo sapiens Sushi domain (SCR repeat) containing (B65A6.2), mRNA
11890	24878	38574	3.21	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
11890	24878	38575	3.21	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
4701	17836	30821	0.98	9.0E-45	8922391	NT	Homo sapiens hypodermal protein FLJ10379 (FLJ10379), mRNA
4701	17836	30822	0.98	9.0E-45	8922391	NT	Homo sapiens hypodermal protein FLJ10379 (FLJ10379), mRNA
6787	19942	33340	1.41	9.0E-45	AB023212.1	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
2591	15716	28834	3.9	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5193	18315	31283	9.63	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
8298	21380	34902	1.03	8.0E-45	AA377985.1	EST_HUMAN	EST180893 Synovial sarcoma Homo sapiens cDNA 5' end
1583	14735		2.36	6.0E-45	AI675425.1	EST_HUMAN	w489c06.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2313802 3' similar to contains L1.11 L1 repetitive element ;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4087	17242		3.77	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
12911	26154		1.89	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
915	14080		1.71	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2058	15199	28313	4.42	5.0E-45	BF333627.1	EST_HUMAN	CM4-CN0044-180200-515-f01 CN0044 Homo sapiens cDNA
3281	19455	29477	2.87	5.0E-45	AL523766.1	EST_HUMAN	tg94f07.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1 ;
5629	18923	31897	8.95	5.0E-45	AA397781.1	EST_HUMAN	z72d03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element ;
6143	19321	32664	1.09	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6143	19321	32665	1.09	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6190	19366	32714	0.92	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6190	19366	32715	0.92	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6318	19490	32847	0.87	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6318	19490	32848	0.87	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8471	21552	35082	1.12	5.0E-45	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9241	22318	35661	1.45	5.0E-45	4759223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA
11987	24382	36888	2.5	5.0E-45	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
1167	14330	27385	6.3	4.0E-45	X95826.1	NT	H.sapiens ART4 gene
2365	15496	28622	2.15	4.0E-45	BE285622.1	EST_HUMAN	601184440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
9157	22235		0.81	4.0E-45	AA226220.1	EST_HUMAN	nc26507.s1 NCL_CGAP_Prl1 Homo sapiens cDNA clone IMAGE:1008284 similar to contains element L1 repetitive element ;
12166	26089	31659	1.36	4.0E-45	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
3411	16580		0.93	3.0E-45	T71480.1	EST_HUMAN	y435f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
4199	16580		1.03	3.0E-45	T71480.1	EST_HUMAN	y435f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
6968	19336	32895	1.34	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnaic11), mRNA
6366	18536	32896	1.34	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnaic11), mRNA
8645	21725		1.76	3.0E-45	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
8991	22070	35610	4.31	3.0E-45	4758451	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
10515	23550	37159	7.52	3.0E-45	AL183227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10515	23550	37160	7.52	3.0E-45	AL183227.2	NT	Homo sapiens chromosome 21 segment HS21C027
13040	26078		3.45	3.0E-45	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2572	16597		3.12	2.0E-45	AL183218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3097	16273	29287	0.92	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit: BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6651	19810	33198	5.45	2.0E-45	L01665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7786	20842	34334	1.1	2.0E-45	BE782184.1	EST_HUMAN	601467793F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3870838 5'
8610	21690	35228	0.91	2.0E-45	AW604834.1	EST_HUMAN	RCO-LT0001-150200-032-311 L T0001 Homo sapiens cDNA
8784	22624	36402	0.51	2.0E-45	AI030786.1	EST_HUMAN	ts6a01.x1 NCI CGAP KIA8 Homo sapiens cDNA clone IMAGE:2232552 3'
11042	25867	37754	12.66	2.0E-45	BE934350.1	EST_HUMAN	MRO-HT0923-190800-201-e02 HT0923 Homo sapiens cDNA
11450	24510	38177	2.71	2.0E-45	AA458770.1	EST_HUMAN	aa87f12.r1 Stratiene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to
11794	24784	38481	3.35	2.0E-45	AW270280.1	EST_HUMAN	TR-G1144569 G1144569 R-SLY1.1
11794	24784	38482	3.35	2.0E-45	AW270280.1	EST_HUMAN	XP72803.x1 NCI CGAP OV40 Homo sapiens cDNA clone IMAGE:2745888 3'
13087	25710		2.73	2.0E-45	11418157	NT	XP72803.x1 NCI CGAP OV40 Homo sapiens cDNA clone IMAGE:2745888 3'
126	13617		1.22	1.0E-45	BE389855.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
422	13617		1.99	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3606183 5'
485	13679	26714	1.02	1.0E-45	4508412	NT	601284360F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3606183 5'
1201	14363	27423	1.66	1.0E-45	7657290	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
3172	16347	29354	10.41	1.0E-45	U32169.1	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3581	16746	29764	0.85	1.0E-45	8659558	NT	Human pro- $\alpha 2$ chain of collagen type XI (COL11A2) gene, complete cds
3664	16927	29836	0.69	1.0E-45	AB046811.1	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf1), mRNA
4599	17736	30716	6.4	1.0E-45	BE396633.1	EST_HUMAN	Homo sapiens mRNA for KIAA1591 protein, partial cds
4848	17991		1.06	1.0E-45	H57443.1	EST_HUMAN	601289116F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3618803 5'
5081	18209	31181	1.56	1.0E-45	11545798	NT	Y05502.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:204363 5'
8220	21302	34822	0.7	1.0E-45	11422236	NT	Homo sapiens niban protein (NIBAN), mRNA
8220	21302	34823	0.7	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8806	21895	35425	0.9	1.0E-45	D87875.1	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
9321	22397	35950	3.92	1.0E-45	BE687843.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
9722	22787	36358	0.99	1.0E-45	AB002297.1	NT	601511226F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3912535 5'
12369	25263	32117	3.5	1.0E-45	11418099	NT	Human mRNA for KIAA0289 gene, partial cds
12562	25384		19.43	1.0E-45	11526291	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
12568	25387		6.42	1.0E-45	11418177	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
13047	25666	31963	4.02	1.0E-45	11418157	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
8423	21504	35037	2.71	9.0E-46	9910293	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
8835	21914		6.82	9.0E-46	AL163208.2	NT	Mus musculus varatin complex 2, gene 6g (K12-6g), mRNA
10697	23730	37335	6.89	9.0E-46	AW246964.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
							2822449 Spriime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2513	15639	28760	7.67	8.0E-46	AI43261.1	EST_HUMAN	h32708.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_rna2
2513	15639	28761	7.67	8.0E-46	AI43261.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
8244	21326		2.72	8.0E-46	BE167244.1	EST_HUMAN	h32708.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_rna2
4703	17838		4.79	7.0E-46	BE366165.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
4928	18058		1.33	7.0E-46	BE064386.1	EST_HUMAN	RCS-HT0506-280200-012-C12 HT0506 Homo sapiens cDNA
6167	19343	32689		7.0E-46	8922708	NT	60127292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
6623	19783	33171	1.8	7.0E-46	BF105845.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
12706	28469		2.6	7.0E-46	AL163246.2	NT	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
2812	15926	29037	6.87	6.0E-46	AI884381.1	EST_HUMAN	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042736 5'
2812	15926	29038	6.87	6.0E-46	AI884381.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
6257	19431	32778	11.57	6.0E-46	AI635446.1	EST_HUMAN	wn31f08.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
7366	20445	33807	0.99	6.0E-46	AW513244.1	EST_HUMAN	wn31f08.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
7541	20614	34091	0.67	6.0E-46	BF509740.1	EST_HUMAN	ts58h10.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363
11673	23901		2.14	6.0E-46	BE784971.1	EST_HUMAN	sa GENE ;
209	13432		5.31	6.0E-46	AL163210.2	NT	xx42e04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2708654 3' similar to gb:L08069 DNAJ
3617	16781	29786	1.17	5.0E-46	BE677194.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
3617	16781	29797	1.17	5.0E-46	BE677194.1	EST_HUMAN	U11-B14-epg-5-06-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087288 3'
6874	20026	33436	1.52	5.0E-46	BF590442.1	EST_HUMAN	601478409F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3880395 5'
7080	20174	33598	3.69	5.0E-46	BF347228.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
7244	20327	33772	0.75	5.0E-46	AW682253.1	EST_HUMAN	7481g01.x1 Lupsig_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279403 3'
7544	20616	34093	0.59	5.0E-46	BE549744.1	EST_HUMAN	7481g01.x1 Lupsig_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279403 3'
658	13844		3.85	4.0E-46	AA601143.1	EST_HUMAN	naa3807.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258757 3' similar to TR:O75202
1740	14889	27981	2.89	4.0E-46	AW170544.1	EST_HUMAN	O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC ;
							80202164F1 NCI_CGAP_Bin67 Homo sapiens cDNA clone IMAGE:4156670 5'
							QV4-S10212-120100-075-09 ST0212 Homo sapiens cDNA
							7638005.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230481 3'
							nc64e08.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_rna1
							FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
							h188e03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1
							LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1740	14889	27982	2.99	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1
2798	15913	29021	7.4	4.0E-46	M18048.1	NT	LYSOZYME C PRECURSOR (HUMAN) contains element VIER37 repetitive element ;
5553	18750	31786	2.1	4.0E-46	M38852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
5553	18750	31787	2.1	4.0E-46	M38852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
12851	25565	31989	1.36	4.0E-46	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
2359	15490	28620	0.94	3.0E-46	7657203	NT	Homo sapiens acidic B2 kDa protein mRNA (HSU15552), mRNA
4513	17652	30640	1.21	3.0E-46	4506376	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4898	18028	31015	1.11	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline, Ig-Light-Lambda, VLambda
4898	18028	31016	1.11	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline, Ig-Light-Lambda, VLambda
8949	22028	35569	12.45	3.0E-46	A1831482.1	EST_HUMAN	wj49c04.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2
9206	22284	35824	0.61	3.0E-46	L08850.1	NT	THR repetitive element ;
9206	22284	35825	0.61	3.0E-46	L08850.1	NT	Human AD amyloid mRNA, complete cds
11873	24861	38556	1.78	3.0E-46	D31765.1	NT	Human AD amyloid mRNA, complete cds
860	14037	27099	12.65	2.0E-46	AA468646.1	EST_HUMAN	ne08a09.s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR
1593	14746		3.78	2.0E-46	AA678246.1	EST_HUMAN	repetitive element ;
1671	14823	27906	5.63	2.0E-46	U78027.1	NT	z127a11.s1 Soares_fetal_liver_spleen_1NFLS S1 Homo sapiens cDNA clone IMAGE:431996 3'
5089	18217	31188	1.26	2.0E-46	AA399286.1	EST_HUMAN	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
7653	20721	34197	7.1	2.0E-46	9910569	NT	(L44) and FTP3 (FTP3) genes, complete cds
8260	21342		1.29	2.0E-46	BE869151.1	EST_HUMAN	z159e02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE
11524	24580		1.82	2.0E-46	7657233	NT	Q01730 RSP-1 PROTEIN ;
12264	26040		1.4	2.0E-46	BF028854.1	EST_HUMAN	Mus musculus sperm tail associated protein (Stap), mRNA
12555	25631		1.57	2.0E-46	H48391.1	EST_HUMAN	801445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849297 5'
12596	25401		3.31	2.0E-46	AA001786.1	EST_HUMAN	Homo sapiens small acidic protein (IMAGE145052), mRNA
12834	25523	31864	4.26	2.0E-46	AW277214.1	EST_HUMAN	801785228F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3987326 5'
1261	14418	27483	4.31	1.0E-46	4502894	NT	y02d01.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:206977 5'
2356	15487	28619	4.88	1.0E-46	AW978516.1	EST_HUMAN	z184f12.r1 Soares_fetal_liver_spleen_1NFLS S1 Homo sapiens cDNA clone IMAGE:428015 5'
							xq78h03.x1 NCL CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
							Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
							EST380625 IMAGE resequences, MAGP Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2473	15500	28725	3.53	1.0E-46	H97330.1	EST_HUMAN	EST48b096 WATM1 Homo sapiens cDNA clone 48b095
3321	16494	29511	2.12	1.0E-46	AA631012.1	EST_HUMAN	np78b02.s1 NCL CGAP_P2 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H.sapiens MT-11 mRNA. (HUMAN);
4995	18124		3.13	1.0E-46	AB023197.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
5817	19007	32313	5.89	1.0E-46	BF194707.1	EST_HUMAN	7c62b01.x1 NCL CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
6098	25818	32809	5.34	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272165), mRNA
6098	25818	32810	5.34	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6746	19602	33295	0.64	1.0E-46	BF196247.1	EST_HUMAN	7n48a07.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567852 3' similar to contains element MER22 repetitive element;
11102	19007	32313	3.72	1.0E-46	BF194707.1	EST_HUMAN	7c62b01.x1 NCL CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
11410	24471	38136	1.61	1.0E-46	AJ245621.1	NT	Homo sapiens CT12 gene
12323	25233	32105	1.39	1.0E-46	BF531102.1	EST_HUMAN	502072284F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'
12323	25233	32106	1.39	1.0E-46	BF531102.1	EST_HUMAN	502072284F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'
13176	25764		1.99	1.0E-46	AV715377	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
787	13666		3.7	9.0E-47	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5047	18175	31152	3.05	9.0E-47	AW770928.1	EST_HUMAN	h93a04.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3006534 3' similar to TR:O75703 O75703 HYPOTHETICAL 12.4 KD PROTEIN. ;
6506	19672	33038	0.86	9.0E-47	11425439	NT	Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
11388	24449	38110	1.4	9.0E-47	11492209	NT	Homo sapiens similar to aldo-keto reductase family 1, member B1 (aldose reductase) (H. sapiens)
12874	26027	31675	1.64	9.0E-47	11417966	NT	(LOC33093), mRNA
1851	14697	28100	32.2	8.0E-47	Y18536.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1851	14697	28101	32.2	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2781	15897	29007	1.5	8.0E-47	5453955	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
3089	16265	29283	2.04	8.0E-47	AJ229043.1	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
3715	16876	29881	0.77	8.0E-47	AB041926.1	NT	Homo sapiens 959 kb contig between AM1.1 and CBR1 on chromosome 21q22, segment 3/3
3715	16876	29882	0.77	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
12962	25922		1.98	7.0E-47	AV683284.1	EST_HUMAN	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
2613	15737	29851	3.04	6.0E-47	AL163246.2	NT	AV683284 GSK Homo sapiens cDNA clone GKCA5H11 5'
8890	21969	35505	0.52	6.0E-47	U77054.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
9476	22533	36097	6.83	6.0E-47	AI695189.1	EST_HUMAN	HSU77054 Human Homo sapiens cDNA clone N7
9913	22953	36538	0.69	6.0E-47	AB042824.1	NT	h98h02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2266659 3'
9913	22953	36539	0.69	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
9913	22953	36539	0.69	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6707	10865	33255	5.73	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
11035	24114		5.58	5.0E-47	M78590.1	EST_HUMAN	EST00738 Fetal brain, Strategene (cat#336206) Homo sapiens cDNA clone HFBCF07
1432	14585	27650	7.03	4.0E-47	4557556	NT	Homo sapiens E1A binding protein p300 (EP300), mRNA
6971	20199	33625	0.82	4.0E-47	BE938696.1	EST_HUMAN	MRA-TN0108-280800-201-cl4 TN0108 Homo sapiens cDNA
8877	21757	35292	2.22	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8877	21757	35293	2.22	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8818	21897	35436	0.83	4.0E-47	AW983777.1	EST_HUMAN	RC3-BN0034-220300-015-105 BN0034 Homo sapiens cDNA
11938	24922		1.98	4.0E-47	AW515509.1	EST_HUMAN	xx66507.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE
558	13751	26778	2.09	3.0E-47	BE907634.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1]:
558	13751	26779	2.09	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
841	14019	27075	3.99	3.0E-47	N57483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
968	14141	27202	10.04	3.0E-47	AL163284.2	NT	y54b04.s1 Soares_multiple sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:277327 3'
3376	16548	29562	0.97	3.0E-47	4604116	NT	Homo sapiens chromosome 21 segment HS21C084
4073	17229		0.61	3.0E-47	U93181.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), mRNA
4482	17622	30603	1.14	3.0E-47	M12959.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1), mRNA, partial cds
6138	19315	32654	4.68	3.0E-47	AW408800.1	EST_HUMAN	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
6136	19315	32655	4.68	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-adv-d-07-0-J1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6894	19852		1.71	3.0E-47	A1222413.1	EST_HUMAN	UI-HF-BM0-adv-d-07-0-J1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
7540	20613	34089	0.88	3.0E-47	A1819755.1	EST_HUMAN	q104e07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
7540	20613	34090	0.88	3.0E-47	A1819755.1	EST_HUMAN	w111h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
9033	22112	35654	0.77	3.0E-47	AW963796.1	EST_HUMAN	w111h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
9033	22112	35655	0.77	3.0E-47	AW963796.1	EST_HUMAN	EST375869 MAGC resequences, MAGH Homo sapiens cDNA
152	13377	26409	1.21	2.0E-47	4505318	NT	EST375869 MAGC resequences, MAGH Homo sapiens cDNA
990	14162	27221	2.45	2.0E-47	AL163209.2	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
990	14162	27222	2.45	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1598	14751	27859	0.95	2.0E-47	A1968279.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
1623	14775	27859	1.61	2.0E-47	7662109	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
1712	14863	27852	4.49	2.0E-47	AA52514.1	EST_HUMAN	wq96602.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2478851 3'
4467	17607	30585	1.61	2.0E-47	4504866	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
4503	17643	30628	1.87	2.0E-47	AA569592.1	EST_HUMAN	hg43h12.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937607 3'
4503	17643	30629	1.87	2.0E-47	AA569592.1	EST_HUMAN	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4628	17764	30748	2.14	2.0E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R), mRNA
4833	18063	31048	1.25	2.0E-47	AW963166.1	EST_HUMAN	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5245	18366		0.71	2.0E-47	AI041126.1	EST_HUMAN	ov61h03.x1 Soares testis NIH-Homo sapiens cDNA clone IMAGE:1641845 3'
5904	19093	32407	0.8	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete cds
6097	19278	32607	1.32	2.0E-47	BE778476.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
6097	19278	32608	1.32	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
7878	25854		1.34	2.0E-47	L09731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
8151	21233	34753	1.96	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8151	21233	34754	1.98	2.0E-47	D87675.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
8916	21994	35533	1.76	2.0E-47	AF071771.1	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
9690	22739	36308	1.27	2.0E-47	11526138	NT	yR2e08.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:29966 3' similar to contains OFR repetitive element:
12357	26073	31653	3.36	2.0E-47	R42423.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
12394	26076		1.87	2.0E-47	AL163209.2	NT	q99h03.x1 Soares fetal lung Nhl-L19W Homo sapiens cDNA clone IMAGE:1631189 3'
1437	14590	27663	5.42	1.0E-47	AI833428.1	EST_HUMAN	601155321F1 NIH_MGC_27 Homo sapiens cDNA clone IMAGE:3138893 5'
3926	17085	30080	1.1	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_27 Homo sapiens cDNA clone IMAGE:3138893 5'
3926	17085	30081	1.1	1.0E-47	BE280477.1	EST_HUMAN	RC3-ST0197-130400-0174-02 ST0197 Homo sapiens cDNA
5187	18309	31275	2.4	1.0E-47	AW813906.1	EST_HUMAN	at19a08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22995
7189	20054	33484	10.76	1.0E-47	AI880886.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
9099	22148		4.24	1.0E-47	AW684848.1	EST_HUMAN	h84a11.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978672 3' similar to gb:M26326
10584	23599	37205	2.28	1.0E-47	L30115.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1643	14795	27879	3.84	9.0E-48	AF226391.1	NT	Papillohamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
3646	16909	29823	0.73	9.0E-48	BF359947.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5797	18987	32290	1.1	9.0E-48	BE888196.1	EST_HUMAN	CMV2-MT0100-310700-290-05 MT0100 Homo sapiens cDNA
5797	18987	32291	1.1	9.0E-48	BE888196.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
6226	19401	32751	0.57	9.0E-48	AI833168.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
6355	19525	32882	0.71	9.0E-48	AU123240.1	EST_HUMAN	at75h09.x1 Barstead cDNA HPLRB7 Homo sapiens cDNA clone IMAGE:2377889 3' similar to TR-O60844
11378	24439	36098	3.06	9.0E-48	BE393813.1	EST_HUMAN	O60844 HOMOLOG OF RAT ZYMOMEN GRANULE MEMBRANE PROTEIN. ;
1279	14436		1.75	8.0E-48	4501800	NT	AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM1000978 5'
1280	14436		1.65	8.0E-48	4501900	NT	601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
3205	16380	29390	5.72	8.0E-48	AW768477.1	EST_HUMAN	Homo sapiens aminocyclase 1 (ACY1), mRNA
							Homo sapiens aminocyclase 1 (ACY1), mRNA
							h61b03.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
							BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3205	16380	29391	5.72	8.0E-48	AW708477.1	EST_HUMAN	h161b03.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
4041	17197	30208	0.66	8.0E-48	4504116	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
503	13698		2.58	7.0E-48	AB033035.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
504	13698		18.69	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1627	14680	27761	1.96	7.0E-48	6912719	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1667	14819	27902	6.39	7.0E-48	5730038	NT	Homo sapiens tousel-like kinase 1 (TLK1), mRNA
6865	19843	33233	24.01	7.0E-48	1141683.1	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
12125	25105	39809	2.88	7.0E-48	R19623.1	EST_HUMAN	Homo sapiens histidyl-RNA synthetase (HARS), mRNA
3687	18650	29858	0.88	6.0E-48	A176111.1	EST_HUMAN	W37502.r1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:34747 5'
6183	18359	32707	0.84	6.0E-48	AB006955.1	NT	w69h03.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398613 3'
6924	20239	33674	0.93	6.0E-48	11420895	NT	Homo sapiens mRNA for AIE-75, complete cds
7628	25849	34172	0.78	6.0E-48	AB046844.1	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX), mRNA
7628	25949	34173	0.78	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9323	22399	35953	1.57	6.0E-48	AF026816.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9741	22806	36382	1.87	6.0E-48	11427428	NT	Homo sapiens putative oncogene protein mRNA, partial cds
9890	22830	36514	2.84	6.0E-48	AA189080.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
3384	18465	29608	1.48	5.0E-48	4826891	NT	zq45b08.s1 Streptococcus HNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
8774	21853	35395	1.04	5.0E-48	BE084410.1	EST_HUMAN	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
2829	15943	29053	1.02	4.0E-48	R45715.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
11200	24269	37905	3.11	4.0E-48	A1620420.1	EST_HUMAN	Hat 40-f Adult heart, Clontech Homo sapiens cDNA clone a140-f
12050	25031	38737	1.75	4.0E-48	BE084410.1	EST_HUMAN	lu47a02.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2254154 3'
1416	14570	27643	1.91	3.0E-48	AV690964.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
2032	15173	28282	31.61	3.0E-48	4885170	NT	AV690964 GKC Homo sapiens cDNA clone GKCDRE12 5'
2032	15173	28283	31.61	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3505	16672	29882	0.93	3.0E-48	AF172453.1	NT	Homo sapiens opidol growth factor receptor mRNA, complete cds
3721	16882	29888	0.9	3.0E-48	AW684531.1	EST_HUMAN	h14b12.x1 NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2972255 3' similar to SW:DCRB_HUMAN
4362	17505		0.63	3.0E-48	AA009541.1	EST_HUMAN	P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
6015	19189	32516	2.08	3.0E-48	BE084571.1	EST_HUMAN	Z04g03.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone IMAGE:429844 5'
7159	20262	33735	1.07	3.0E-48	AF087913.1	NT	MR4-BT0657-080400-201-e10 BT0657 Homo sapiens cDNA
8585	21668		3.73	3.0E-48	AA659930.1	EST_HUMAN	Human endogenous retrovirus HERV-P-T47D
							m03f05.s1 NCL CGAP_P22 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1 PTR5 repetitive element ;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4209	17358		0.98	0.0E+00	AA018975.1	EST_HUMAN	ze55e09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:362920 5' similar to contains Alu repetitive element
4218	17367	30356	5.32	0.0E+00	AF165527.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4227	14319	27373	0.7	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4227	14319	27374	0.7	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4234	17381	30369	1.32	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4234	17381	30370	1.32	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4236	18795	29812	0.84	0.0E+00	4508884	NT	Homo sapiens semenogelin II (SEMG2) mRNA
4238	17384	30372	0.91	0.0E+00	9922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4238	17384	30373	0.91	0.0E+00	9922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4244	17390	30377	0.85	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4252	17398	30386	5.57	0.0E+00	A1982597.1	EST_HUMAN	wa04d04.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2515975 3'
4252	17398	30387	5.57	0.0E+00	A1982597.1	EST_HUMAN	wa04d04.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2515975 3'
4255	17400	30389	1	0.0E+00	BE184856.1	EST_HUMAN	MRI-H10707-100500-001-a02 HT0707 Homo sapiens cDNA
4255	17400	30390	1	0.0E+00	BE184856.1	EST_HUMAN	MRI-H10707-100500-001-a02 HT0707 Homo sapiens cDNA
4259	17404		5.89	0.0E+00	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5'
4265	17410	30398	2.07	0.0E+00	5729725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4272	17417		5.76	0.0E+00	AW675599.1	EST_HUMAN	ba5104.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900095 3' similar to SW:TH12_BOVIN Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR
4277	17422	30410	1.12	0.0E+00	AW408788.1	EST_HUMAN	UHF-BM0-adv-c-02-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5'
4278	17423	30411	1.55	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4278	17423	30412	1.55	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4287	17432		2.35	0.0E+00	5174932	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
4300	17443	30429	1.07	0.0E+00	AB037739.1	NT	Homo sapiens mRNA for KIAA1318 protein, partial cds
4309	17452	30438	11.47	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element
4309	17452	30439	11.47	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element
4312	17455	30443	1.2	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4338	17481	30461	8.09	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4338	17481	30462	8.09	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4345	17483		0.86	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4388	17531	30512	5.01	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4038	17194	30205	1.14	0.0E+00	U85281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
4042	17198	30209	3.47	0.0E+00	BE378602.1	EST_HUMAN	601286666F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'
4043	17199	30210	1.2	0.0E+00	BE313146.1	EST_HUMAN	601153727F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508743 5'
4051	17207	30217	1.28	0.0E+00	AW580740.1	EST_HUMAN	PM3-LT0031-100-003-109 LT0031 Homo sapiens cDNA
4052	17208	30218	1.03	0.0E+00	5360215	NT	Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA
4077	17233	30238	0.8	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4077	17233	30239	0.8	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4077	17233	30240	0.8	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4084	17239	30244	9.31	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4084	17239	30245	9.31	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4093	17248		3.51	0.0E+00	M23910.1	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
4095	17250		7.25	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4104	17258	30258	2.63	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4112	17266	30268	2.13	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
4127	17281		111.8	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4134	17287		0.89	0.0E+00	AI657076.1	EST_HUMAN	U85g08.X1 NCJ_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2244734 3' similar to TR:060309 060309 KIAA0563 PROTEIN.
4137	17289	30284	1.91	0.0E+00	7862183	NT	Homo sapiens KIAA0568 gene product (KIAA0568), mRNA
4138	17290	30285	2.85	0.0E+00	U09366.1	NT	Human zinc finger protein ZNF133
4157	17308	30304	6	0.0E+00	AB015610.1	NT	Chirocebus aethiops mRNA for ribosomal protein S4X, complete cds
4168	17316		3.22	0.0E+00	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor RNA-associated antigenic protein (RNA48 gene)
4177	17327	30318	1.58	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4178	17328	30319	2.68	0.0E+00	AJ27276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
4178	17328	30320	2.68	0.0E+00	AJ27276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
4185	17335	30327	8.33	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4185	17335	30328	8.33	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4194	17344	30337	0.64	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
4202	17351	30343	6.02	0.0E+00	4885306	NT	phosphoribosylmethionine synthetase (GART) mRNA
4203	17352	30344	11.98	0.0E+00	AB006625.1	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4206	17355	30345	1.26	0.0E+00	4758807	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4207	17356	30346	7.08	0.0E+00	11419297	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4208	17357	30347	4.33	0.0E+00	AL066857.1	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
							Novel human mRNA from chromosome 1, which has similarities to BAT2 genes

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3943	17102	30099	1.78	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3946	17105	30101	1.62	0.0E+00	AF099601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3946	17105	30102	1.62	0.0E+00	AF099601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3951	17109	30107	1.02	0.0E+00	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3951	17109	30108	1.02	0.0E+00	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3952	17110	30109	0.9	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3957	17115	30117	6.96	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3957	17115	30118	6.96	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3959	17117	30121	4.85	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3960	17118	30122	1.12	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3963	17121	30124	1.23	0.0E+00	4626783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3966	17124	30127	1.44	0.0E+00	AF012615.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3967	17125	30128	2.87	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
3969	17127	30130	0.77	0.0E+00	AF099117.1	NT	Homo sapiens amphiphysin gene, partial cds
3979	17136	30140	3.22	0.0E+00	AB64727.1	EST_HUMAN	wk0101.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:O43340
3980	17137	30141	1.03	0.0E+00	AL163248.2	NT	O43340 R28830.2, contains element PTR7 repetitive element;
3983	17140	30145	18.17	0.0E+00	4506742	NT	Homo sapiens chromosome 21 segment HS21C048
3988	17145	30151	1.33	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3994	17151	30158	1.9	0.0E+00	6005887	NT	DKFZp434N0413.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0413 5'
3994	17151	30159	1.9	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3996	17153	30161	3.94	0.0E+00	4504138	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3997	17154	30164	2.26	0.0E+00	4505078	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
4001	17158	30164	0.97	0.0E+00	AF149412.1	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
4013	17170	30178	2.65	0.0E+00	4506758	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
4017	17174	30182	1.9	0.0E+00	4595842	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4026	17182	30191	5.14	0.0E+00	BF356295.1	EST_HUMAN	Homo sapiens zinc finger protein (KIAA0412) mRNA
4028	17184	30193	1.37	0.0E+00	AW888221.1	EST_HUMAN	RC3-HT0860-170800-011-a12 HT0860 Homo sapiens cDNA
4028	17184	30194	1.37	0.0E+00	AW888221.1	EST_HUMAN	NXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to NXRA5
4035	17191	30201	3.05	0.0E+00	AF129633.1	NT	Matrix remodeling associated gene 5
4038	17194	30204	1.14	0.0E+00	U66281.1	NT	NXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996720 similar to NXRA5

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3771	16932	29937	0.99	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
3771	16932	29938	0.99	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
3774	16935	29941	2.4	0.0E+00	AW851714.1	EST_HUMAN	MR2-CT0222-281099-005-e05 CT0222 Homo sapiens cDNA
3776	16937	29943	2.37	0.0E+00	5729928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3778	16939	29945	1.15	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
3780	16941	29947	0.74	0.0E+00	O14967	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3782	16943	29949	1.02	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3782	16943	29950	1.02	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3794	16955	29959	5.42	0.0E+00	AW288134.1	EST_HUMAN	UI-H-BWO-qls-e-12-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2733022 3'
3794	16955	29960	5.42	0.0E+00	AW288134.1	EST_HUMAN	UI-H-BWO-qls-e-12-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2733022 3'
3823	16963	29986	1.04	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen at chain, exon 6
3824	16984	29987	1.17	0.0E+00	AA463659.1	EST_HUMAN	aa06g01.1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to SW:KRBA_SHEEP_P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIB4. [1] :
3831	16991	29993	3.23	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3841	17000	30003	0.83	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3855	17015	30015	5.72	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3859	17019	30018	18.03	0.0E+00	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
3866	17025	30023	1.52	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3866	17025	30024	1.52	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3868	17028	30027	8.64	0.0E+00	4506594	NT	Homo sapiens plasminogen activator inhibitor, type II (arginine-serpin) (PAI2) mRNA
3922	17081	30077	1.96	0.0E+00	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
3924	17083		0.73	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3925	17084	30079	2.36	0.0E+00	AF179733.1	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3928	17087	30083	2.36	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3928	17087	30084	2.36	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3928	17088	30085	1.74	0.0E+00	AF020031.1	NT	Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cds
3935	17094	30092	1.05	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds
3935	17094	30093	1.05	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds
3936	17095	30094	1.29	0.0E+00	A1377699.1	EST_HUMAN	tc6210.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3937	17096		1	0.0E+00	AF152466.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3938	17097	30095	2.6	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPLI) (DSP) mRNA
3940	17099	30096	15.6	0.0E+00	S78685.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, complete cds
3942	17101	30098	2.14	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3623	16787	29803	0.68	0.0E+00	AA456282.1	EST_HUMAN	z889h04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3623	16787	29804	0.68	0.0E+00	AA456282.1	EST_HUMAN	z889h04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3630	16794	29811	1.45	0.0E+00	AV701869.1	EST_HUMAN	AY701869 ADB Homo sapiens cDNA clone ADBDAH06 5'
3631	16795	29812	4.48	0.0E+00	4506884	NT	Homo sapiens semogelin II (SEM32) mRNA
3633	16797		1.17	0.0E+00	AF078888.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3642	16806	29820	1.34	0.0E+00	AL132024.1	NT	Novel human gene mapping to chromosome X
3644	16807	29821	1.16	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3665	16828	29837	0.97	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3665	16828	29838	0.97	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3667	16830	29841	1.06	0.0E+00	6325483	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3672	16835		4.28	0.0E+00	AW852217.1	EST_HUMAN	QV0-CT0225-230300-169-e01 CT0225 Homo sapiens cDNA
3679	16842		1.28	0.0E+00	AF118846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds
3680	16843	29850	7.65	0.0E+00	BF676393.1	EST_HUMAN	602094583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248596 5'
3704	16866	29868	0.59	0.0E+00	BF672054.1	EST_HUMAN	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3704	16866	29869	0.59	0.0E+00	BF672054.1	EST_HUMAN	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3705	16866		0.99	0.0E+00	4826987	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3707	16868	29871	0.76	0.0E+00	AW664693.1	EST_HUMAN	h84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3707	16868	29872	0.76	0.0E+00	AW664693.1	EST_HUMAN	h84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3711	16872	29876	0.89	0.0E+00	4826763	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA
3713	16874	29878	0.93	0.0E+00	7662319	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
3720	16881	29886	0.74	0.0E+00	4557752	NT	Homo sapiens midline 1 (Optiz/BBB syndrome) (MID1) mRNA
3720	16881	29887	0.74	0.0E+00	4557752	NT	Homo sapiens midline 1 (Optiz/BBB syndrome) (MID1) mRNA
3737	16898	29901	2.35	0.0E+00	D87327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3741	16902		6.28	0.0E+00	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3757	16918	29920	3.98	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3759	16920	29922	1.06	0.0E+00	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
3761	16922	29923	5.16	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3761	16922	29924	5.16	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3767	16928	29932	32.49	0.0E+00	AA852743.1	EST_HUMAN	NHITBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHITBCae15g09
3767	16928	29933	32.49	0.0E+00	AA852743.1	EST_HUMAN	NHITBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHITBCae15g09
3770	16931	29935	1.95	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3770	16931	29936	1.95	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3493	16860	29672	1.26	0.0E+00	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-s isoform (CACNA1I) mRNA, complete cds
3498	16865		0.94	0.0E+00	AW867015.1	EST_HUMAN	MR1-SN0033-100400-001-c08 SN0033 Homo sapiens cDNA
3511	16877	29687	2.02	0.0E+00	7662401	NT	Homo sapiens KIAA0932 protein (KIAA0932), mRNA
3511	16877	29688	2.02	0.0E+00	7662401	NT	Homo sapiens KIAA0932 protein (KIAA0932), mRNA
3512	16878	29689	0.92	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3514	16880	29690	2.35	0.0E+00	5903067	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3523	15907	29015	3.08	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3528	16893	29703	2.46	0.0E+00	7657038	NT	Homo sapiens death receptor 5 (DR6), mRNA
3532	16897	29708	5.5	0.0E+00	K02380.1	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and IncA, IncB, and IncC incompatibility determinants
3535	16700	29711	1.38	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
3538	16703	29714	1.83	0.0E+00	4557748	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET) mRNA
3544	16709	29719	4.17	0.0E+00	A1835159.1	EST_HUMAN	wp14d10.x1 NCI CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634
3544	16709	29720	4.17	0.0E+00	A1835159.1	EST_HUMAN	wp14d10.x1 NCI CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634
3548	16713	29725	1.91	0.0E+00	AJ278120.1	NT	NEURAL CELL ADHESION MOLECULE ;
3555	16720	29734	5.38	0.0E+00	6552332	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3555	16720	29735	5.38	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3560	16725	29741	1.41	0.0E+00	M14123.1	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3566	16731	29747	5.78	0.0E+00	U43293.1	NT	Human endogenous retrovirus HERV-K10
3574	16739	29755	2.57	0.0E+00	AF045452.1	NT	Human MID5A (NML-7MDS1 fusion) mRNA, partial cds
3574	16739	29756	2.57	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3582	16747	29765	1.18	0.0E+00	AF231922.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3594	16758	29773	3.29	0.0E+00	BE304791.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
3594	16758	29774	3.29	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3597	16761	29777	1.04	0.0E+00	4926795	NT	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3600	16764	29780	0.8	0.0E+00	O14867	SWISSPROT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
3603	16787	29782	0.89	0.0E+00	A1884007.1	EST_HUMAN	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3621	16785	29801	0.6	0.0E+00	AB032978.1	NT	te35g12.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O00498
3621	16785	29802	0.6	0.0E+00	AB032979.1	NT	O00498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ;
							Homo sapiens mRNA for KIAA1153 protein, partial cds
							Homo sapiens mRNA for KIAA1153 protein, partial cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3298	16472	29493	0.76	0.0E+00	4758056	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3298	16472	29494	0.76	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3300	16474	29495	26.49	0.0E+00	AA71783.1	EST_HUMAN	aa87b11.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:371133 3'
3308	16482	29503	8.38	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3308	16482	29504	8.38	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3320	16493	29510	3.04	0.0E+00	4557590	NT	Homo sapiens fibrinogen (FBN1) mRNA
3326	16499	29517	1.01	0.0E+00	4507720	NT	Homo sapiens fibrinogen (FBN1) mRNA
3334	16507		10.18	0.0E+00	M65180.1	NT	Human connexin 43 processed pseudogene
3335	16508	29524	0.95	0.0E+00	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helixase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
3338	16511	29527	4.06	0.0E+00	AF055084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3348	16464	29535	1.34	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3348	16464	29538	1.34	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3363	16535	29549	3.56	0.0E+00	AF285208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3364	16536	29550	0.95	0.0E+00	8823624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3377	16549	29563	1.42	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3388	16558	29573	0.72	0.0E+00	4855312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3401	16571	29586	3.14	0.0E+00	AI589294.1	EST_HUMAN	tr5908.x2 NCI_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:222535 3' similar to SW:RL11_RAT
3404	16574	29589	9.94	0.0E+00	AW955400.1	EST_HUMAN	P25121 60S RIBOSOMAL PROTEIN L11, contains Alu repetitive element
3412	16581	29596	2.41	0.0E+00	AF128893.1	NT	EST367470 MAGE resequences, MAGD Homo sapiens cDNA
3412	16581	29597	2.41	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3413	16582	29598	1.03	0.0E+00	7657213	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3413	16582	29599	1.03	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3416	16585	29601	1.29	0.0E+00	4502582	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3416	16585	29602	1.29	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3419	16588	29604	11.92	0.0E+00	AF111163.1	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3421	16590	29606	1.02	0.0E+00	AB040940.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3428	16596	29612	0.79	0.0E+00	BE770399.1	EST_HUMAN	Homo sapiens pyrin (MEFV) gene, complete cds
3441	16609	29627	0.67	0.0E+00	AI632568.1	EST_HUMAN	Homo sapiens mRNA for KIAA1507 protein, partial cds
3483	16651	29667	10	0.0E+00	AU123654.1	EST_HUMAN	60146495F1 NIH_MGC_07 Homo sapiens cDNA clone IMAGE:3868246 5'
3492	16656	29671	1.16	0.0E+00	7706238	NT	wb10904.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR:Q91829 Q91829
							ZINC FINGER PROTEIN ;
							AU123654 NT2RM2 Homo sapiens cDNA clone NT2RM2000735 5'
							Homo sapiens neuroblastoma-amplified protein (LOC51694), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3114	16280		7.27	0.0E+00	AL359403.1	NT	isoform 2 of a novel human mRNA from chromosome 22
3119	16295	28309	1.88	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
							Homo sapiens transcription factor IGIM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
3122	16298		2.21	0.0E+00	AF196779.1	NT	Homo sapiens interleukin 2 receptor, beta (IL2RB) mRNA
3124	16300	28313	3.78	0.0E+00	4504664	NT	Human germline gene 16.1 for Ig lambda L-chain C region (IgL-C16.1)
3145	16321	28333	3.23	0.0E+00	XQ3529.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3151	16328		1.92	0.0E+00	AF199355.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3155	16330	28340	1.75	0.0E+00	AF084598.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3175	16350	28358	4.71	0.0E+00	AF265208.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3178	16351	28357	10.17	0.0E+00	AF149773.1	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3181	16355	28361	3.92	0.0E+00	7682139	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-6110 allele, partial cds
3182	16357	28362	1.29	0.0E+00	AF042075.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-6110 allele, partial cds
							X92H07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2664733 3' similar to SW:RNP_HYDHY P00677 RIBONUCLEASE PANCREATIC
3187	16362	28368	1.19	0.0E+00	AW188146.1	EST_HUMAN	
							Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3210	16384	28395	3.61	0.0E+00	4826783	NT	Human ferritin heavy chain mRNA, complete cds
3219	16393	29404	20.63	0.0E+00	L20941.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3222	16396	29407	1.05	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3222	16396	29408	1.05	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
							ye32f03.x1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:119483 3' similar to SP:S28639
3229	16403	29415	25.61	0.0E+00	T94870.1	EST_HUMAN	
							S28639 BASIC PROTEIN, 23K -
3244	16418	29433	0.93	0.0E+00	BF243336.1	EST_HUMAN	
							601878507F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4107433 5'
3245	16419	29434	1.22	0.0E+00	AI968086.1	EST_HUMAN	
							wu12h10.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2516803 3'
3250	16424	29441	5.36	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
3250	16424	29442	5.36	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
							U38909.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2253376 3' similar to SW:RASD_DICDI
3252	16426	29444	1.01	0.0E+00	AI685950.1	EST_HUMAN	
							P03967 RAS-LIKE PROTEIN RASD
3262	16436	29455	1.39	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3262	16436	29456	1.39	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3270	16444	29464	9.58	0.0E+00	4504658	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3288	16462	29482	4.54	0.0E+00	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
							Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3292	16466	29485	1.92	0.0E+00	4502098	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2995	16171	29190	6.2	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2996	16174	29193	3.31	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2998	16174	29194	3.31	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2999	16175	29195	4.93	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) homology), translocated to, 4 (MLL T4) mRNA
2999	16175	29196	4.93	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) homology), translocated to, 4 (MLL T4) mRNA
3003	16178	29199	1.29	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VNL1
3003	16178	29200	1.29	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VNL1
3011	16187	29211	3.91	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
3011	16187	29212	3.91	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
3019	16195	29218	1.51	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3022	16198	29221	0.98	0.0E+00	AB033034.1	NT	Homo sapiens mRNA for KIAA1208 protein, partial cds
3024	16200	29223	9.6	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (LT1c) gene, exon 6
3036	16214	29242	1.44	0.0E+00	A1149880.1	EST_HUMAN	q143f09.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1752809 3'
3045	16221	29243	0.71	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3045	16221	29243	0.71	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3046	16222	29244	0.92	0.0E+00	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
3047	16223	29245	2.81	0.0E+00	AB004684.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds
3057	16233	29252	1.85	0.0E+00	7662273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
3058	16234	29253	1.92	0.0E+00	AW612526.1	EST_HUMAN	hh03f08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2854055 3' similar to TR:O60407 O60407
3059	16235	29254	2.4	0.0E+00	5729755	NT	PAC CLONE DJ1168D11 FROM 7P21-P22, COMPLETE SEQUENCE ;
3059	16235	29255	2.4	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3067	16243	29263	1.17	0.0E+00	AF114488.1	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3067	16243	29264	1.17	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3091	16257	29285	0.61	0.0E+00	AL163246.2	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3093	16263	29285	1.29	0.0E+00	M74099.1	NT	Homo sapiens chromosome 21 segment HS21C046
3102	16276	29292	0.88	0.0E+00	4506882	NT	Human displacement protein (CCAAT) mRNA
3103	16285	29303	3.33	0.0E+00	AF195953.1	NT	Homo sapiens semenogelin I (SEMG1) mRNA
3112	16288	29303	4.9	0.0E+00	5579459	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3112	16288	29304	4.9	0.0E+00	5579459	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2919	16097	29110	1.3	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2921	16098	29111	15.94	0.0E+00	M88478.1	NT	Human transglutaminase mRNA, complete cds
2926	16103	29117	30.49	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2926	16103	29118	30.49	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2929	16106	29121	3.42	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2930	16107		6.12	0.0E+00	Y10658.1	NT	H. sapiens mRNA for nuclear DNA helicase II
2931	16108		1.13	0.0E+00	AF152303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2932	16109	29122	74.83	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2932	16109	29123	74.83	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2944	16121	29134	2.54	0.0E+00	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2947	16124	29138	1.19	0.0E+00	AL047599.1	EST_HUMAN	DKFZp586G0621.1 586 (synonym: huter) Homo sapiens cDNA clone DKFZp586G0621
2948	16125	29139	0.96	0.0E+00	7681883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2948	16125	29140	0.96	0.0E+00	7681883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2949	16126		2.44	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2952	16129	29142	5.16	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-H03 BT0636 Homo sapiens cDNA
2952	16129	29143	5.16	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-H03 BT0636 Homo sapiens cDNA
2958	16135	29151	0.77	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2958	16135	29152	0.77	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2961	16138	29156	2.3	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2961	16138	29157	2.3	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2962	16139	29158	1.3	0.0E+00	AA215579.1	EST_HUMAN	z96b11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE583517 3' similar to contains Alu repetitive element;
2969	16145		3.99	0.0E+00	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
2972	16148	29167	1.05	0.0E+00	4758278	NT	Homo sapiens EphA4 (EPHA4) mRNA
2974	16150	29170	26.96	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2975	16151	29171	1.15	0.0E+00	AI561002.1	EST_HUMAN	in18407.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2975	16151	29172	1.15	0.0E+00	AI561002.1	EST_HUMAN	in18407.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2977	16153	29174	1.18	0.0E+00	P52740	SWISSPROT	O16247 F44E7.2 PROTEIN;
2978	16154	29175	1.04	0.0E+00	AF152336.1	NT	ZINC FINGER PROTEIN 132
2984	16170	29187	3.4	0.0E+00	AB033093.1	NT	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2984	16170	29188	3.4	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2995	16171	29189	6.2	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2835	15949		1.67	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2841	15955	29062	1.08	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2841	15955	29063	1.08	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2842	15956	29064	5.05	0.0E+00	BF07694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
2848	15962	29072	1.33	0.0E+00	7427622	NT	Homo sapiens protein tyrosine phosphatase, receptor type, I (PTPR), mRNA
2852	15966	29075	17.21	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCOA03 5'
2852	15966	29076	17.21	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCOA03 5'
2854	15968		14.75	0.0E+00	A1879163.1	EST_HUMAN	au56d04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A:
2857	15971	29081	2.14	0.0E+00	BF530661.1	EST_HUMAN	602071957F1 NCL CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4214679 5'
2858	15972	29082	71.97	0.0E+00	BE872768.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854842 5'
2860	15974	29083	2.42	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2P3002672 5'
2860	15974	29084	2.42	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2P3002672 5'
2861	15975	29085	64.06	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2861	15975	29086	64.06	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2867	13415	26444	5.26	0.0E+00	S76830.1	NT	glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3068 nt]
2870	15982		1.64	0.0E+00	AB033281.1	NT	Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2876	13933	26978	1.89	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2876	13933	26979	1.89	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2880	14230	27287	2.04	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2880	14230	27288	2.04	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2897	16076	29094	3.73	0.0E+00	X85980.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene
2898	16077		1.26	0.0E+00	AF086624.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
2900	16079		1.91	0.0E+00	AB040980.1	NT	Homo sapiens mRNA for KIAA1827 protein, partial cds
2907	16085	29099	4.25	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2911	16089	29102	6.5	0.0E+00	M80902.1	NT	Human AHNK nucleoprotein mRNA, 5' end
2914	16092	29104	0.93	0.0E+00	BE154504.1	EST_HUMAN	PM0-HT0343-281289-003-e02 HT0343 Homo sapiens cDNA
2914	16092	29105	0.93	0.0E+00	BE154504.1	EST_HUMAN	PM0-HT0343-281289-003-e02 HT0343 Homo sapiens cDNA
2916	16094		2.05	0.0E+00	X73428.1	NT	H. sapiens l33 gene for HLH type transcription factor
2918	16086		2.6	0.0E+00	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
2919	16097	29108	1.3	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2919	16097	29109	1.3	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2700	15819	28935	2.52	0.0E+00	450468	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2710	15828		1.16	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2711	15829	28942	5.67	0.0E+00	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCY1B) gene, exon 1
2715	15833	28943	1.07	0.0E+00	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
2718	15836	28946	0.96	0.0E+00	AU133385.1	EST_HUMAN	Homo sapiens mRNA for KIAA0536 protein, partial cds
2721	15839	28949	1.15	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2721	15839	28950	1.16	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2724	15842	28953	1.66	0.0E+00	AW887015.1	EST_HUMAN	RC1-OT0086-220300-011-dC7 OT0086 Homo sapiens cDNA
2727	15845	28956	4.83	0.0E+00	BE383165.1	EST_HUMAN	60128714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
2728	15846		2.8	0.0E+00	BE531263.1	EST_HUMAN	601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610267 5'
2763	15878	28987	1	0.0E+00	AB037732.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
2785	15901		11.99	0.0E+00	AA316723.1	EST_HUMAN	EST168414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2789	15905	29013	4.04	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2791	15907	29015	3.72	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2792	15908	29016	2.32	0.0E+00	AB051826.1	NT	Homo sapiens hG28K mRNA for GTP-binding protein like 1, complete cds
2797	15912	29020	11.38	0.0E+00	BE796376.1	EST_HUMAN	60159193F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2800	16072	29024	17.3	0.0E+00	BE563433.1	EST_HUMAN	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5'
2801	15915		3.28	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE09 5'
2803	15917	29027	2.18	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2803	15917	29028	2.18	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2804	15918	29029	2.21	0.0E+00	AF290195.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2805	15919		47.74	0.0E+00	AV651086.1	EST_HUMAN	AV651068 GLC Homo sapiens cDNA clone GLCCLD07 3'
2806	15920	29030	5.84	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2806	15920	29031	5.84	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2810	15924	29034	1.15	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2810	15924	29035	1.15	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2813	15927	29039	21.96	0.0E+00	BE747193.1	EST_HUMAN	601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928472 5'
2814	15928	29040	1.05	0.0E+00	N44974.1	EST_HUMAN	y935h10.1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR-A45773
2816	15930	29042	1.15	0.0E+00	BE176836.1	EST_HUMAN	A45773 kelch protein, long form - fruit fly
2827	15941		1.13	0.0E+00	AL163201.2	NT	RC4-HT0587-170300-072-d11 HT0587 Homo sapiens cDNA
2828	15942	29052	3.19	0.0E+00	BF514110.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001 UIH-BW1-amiw-e-07-0-UJ.s1 NC1_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2550	15775	28798	3.03	0.0E+00	AW501010.1	EST_HUMAN	UI-HF-BP0p-els-c-07-0-UIr1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2575	15700		2.02	0.0E+00	AW813853.1	EST_HUMAN	RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA
2578	15704	28824	7.28	0.0E+00	BE795542.1	EST_HUMAN	601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2579	15135	28241	1.12	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
2580	15705	28825	1.44	0.0E+00	BF509482.1	EST_HUMAN	UI-H-BI4-acz-b-08-0-UIr1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2583	15708	28827	2.21	0.0E+00	Z32884.2	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2585	15710		5.17	0.0E+00	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGRL) mRNA
2587	15712	28830	1.07	0.0E+00	BE910378.1	EST_HUMAN	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'
2588	15713	28831	2.38	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2589	15714	28832	3.09	0.0E+00	U93238.1	NT	Human Sec62 (Sec62) mRNA, complete cds
2605	15720	28838	1.96	0.0E+00	BE808490.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909886 5'
2608	15722	28842	13.07	0.0E+00	BE875511.1	EST_HUMAN	601488241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2609	15723	28844	13.07	0.0E+00	BE875511.1	EST_HUMAN	601488241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2616	15740	28852	1.83	0.0E+00	AF245505.1	EST_HUMAN	Homo sapiens adican mRNA, complete cds
2623	15746	28860	3.66	0.0E+00	AU143277.1	EST_HUMAN	601064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2624	15747	28862	1.25	0.0E+00	BE292896.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2624	15747	28863	1.25	0.0E+00	BE292896.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2625	15748	28864	1.04	0.0E+00	BF223041.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887955 5'
2628	15751	28865	8.3	0.0E+00	AF245505.1	NT	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887955 5'
2664	15000	28901	2.18	0.0E+00	AB037836.1	NT	7q27h12.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:3000246 000246
2684	15000	28902	2.18	0.0E+00	AB037836.1	NT	HYPOTHETICAL 9.3 KD PROTEIN ;
2685	15786		2.35	0.0E+00	BF613835.1	EST_HUMAN	Homo sapiens adican mRNA, complete cds
2676	15795	28912	32.6	0.0E+00	BF204131.1	EST_HUMAN	Homo sapiens mRNA for KIAA1415 protein, partial cds
2675	15795	28913	32.6	0.0E+00	BF204131.1	EST_HUMAN	Homo sapiens mRNA for KIAA1415 protein, partial cds
2678	15798	28915	2.15	0.0E+00	AB037742.1	NT	UI-H-BW1-emp-4-12-0-UIr1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2679	15799	28916	2.52	0.0E+00	5032150	NT	601869073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2681	15801	28918	8.53	0.0E+00	AB037859.1	EST_HUMAN	601869073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2682	15802	28919	1.16	0.0E+00	BE795445.1	EST_HUMAN	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 28KD (TAF21)
2682	15802	28920	1.16	0.0E+00	BE795445.1	EST_HUMAN	mRNA
2682	15802	28920	1.16	0.0E+00	BE795445.1	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
2680	15810		2.75	0.0E+00	BE792472.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2680	15810		2.75	0.0E+00	BE792472.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2680	15810		2.75	0.0E+00	BE792472.1	EST_HUMAN	601584930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2399	15530	28657	1.5	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2402	15533	28659	2.22	0.0E+00	7582401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2402	15533	28660	2.22	0.0E+00	7582401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2405	15536	28663	3.83	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2405	15536	28664	3.83	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2424	15553	28679	3.04	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2428	15556	28683	3.56	0.0E+00	AU131142.1	EST_HUMAN	Homo sapiens cDNA clone NT2RP3002064 5'
2429	15557	28684	9.82	0.0E+00	BE794026.1	EST_HUMAN	90158843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2430	15558	28684	3.96	0.0E+00	7562017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2431	15559	28685	1.39	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2431	15559	28686	1.39	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2432	15560		7.14	0.0E+00	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; and cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2434	15562	28698	10.61	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2434	15562	28699	10.61	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2434	15562	28699	10.61	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2452	15580		1.03	0.0E+00	BE814424.1	EST_HUMAN	MRO-BN0070-090600-029-d12 BN0070 Homo sapiens cDNA
2485	15612	28735	1.14	0.0E+00	AU119632.1	EST_HUMAN	AU119632 HEMBA1 Homo sapiens cDNA clone HEMBA1008155 5'
2487	15614		4.63	0.0E+00	AI042035.1	EST_HUMAN	ox60b02.x1 Soares NHMMPu_S1 Homo sapiens cDNA clone IMAGE:1660583 3' similar to TR:008662
2489	15616	28737	0.94	0.0E+00	8923620	NT	O08662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE
2492	15619		1.35	0.0E+00	BE895605.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20683 (FLJ20683), mRNA
2503	15630		2.22	0.0E+00	AB005622.1	EST_HUMAN	601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2505	15632	28752	6.05	0.0E+00	6006002	NT	AB005622 HeLa cDNA (T.Noma) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2510	15636	28756	1.99	0.0E+00	D85606.1	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2510	15636	28757	1.99	0.0E+00	D85606.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
2520	15646	28769	2.42	0.0E+00	AF106275.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
2524	15649	28773	0.96	0.0E+00	BF345274.1	EST_HUMAN	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
2530	15655	28780	3.64	0.0E+00	5729777	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 8
2538	15663	28786	1.02	0.0E+00	U13666.1	NT	602018058F1 NCL_CGAP_Brr67 Homo sapiens cDNA clone IMAGE:4133670 5'
2538	15663	28787	1.02	0.0E+00	U13666.1	NT	Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA
2539	15664	28788	28.11	0.0E+00	BF569144.1	EST_HUMAN	Human G protein-coupled receptor (GPR1) gene, complete cds
2547	15672	28786	4.18	0.0E+00	AW46822.1	EST_HUMAN	Human G protein-coupled receptor (GPR1) gene, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2272	15405	28533	5.56	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2272	15405	28534	5.56	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2276	16059	28539	4.08	0.0E+00	BF313617.1	EST_HUMAN	601900261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128622 5'
2279	15411	28542	3.13	0.0E+00	BE018750.1	EST_HUMAN	b58-4e02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-J-RELATED PROTEIN;
2281	15413	28544	1.68	0.0E+00	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486340 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN);
2281	15413	28545	1.68	0.0E+00	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486340 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN);
2289	15421	28553	3.08	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21O004
2289	15421	28554	3.06	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21O004
2290	15422	28555	3.72	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2290	15422	28556	3.72	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2295	15427	28561	2.34	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2296	15428	28561	1.02	0.0E+00	AA282281.1	EST_HUMAN	zk12b10.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712891 5'
2313	15445	28579	7.92	0.0E+00	4557558	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2313	15445	28584	2.63	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2327	15458	28592	3.44	0.0E+00	BE895281.1	EST_HUMAN	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5'
2331	15463	28596	1.51	0.0E+00	BE805683.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2331	15463	28597	1.51	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2333	15464	28599	1.83	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2375	15506	28632	4.35	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 5 (DEF6), mRNA
2375	15506	28633	4.35	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 5 (DEF6), mRNA
2376	15507	28634	2.67	0.0E+00	AD76404.1	EST_HUMAN	oz09c07.x1 Soares_fetal_liver_spleen_NFLS_ST Homo sapiens cDNA clone IMAGE:1674828 3'
2378	15509	28636	2.95	0.0E+00	AA429001.1	EST_HUMAN	zk78a11.1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2378	15509	28637	2.95	0.0E+00	AA429001.1	EST_HUMAN	zk78a11.1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2380	15511	28639	1.82	0.0E+00	BF347039.1	EST_HUMAN	602021846F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4157339 5'
2385	15516	28645	1.33	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2385	15516	28646	1.33	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2386	15517	28647	2.34	0.0E+00	6325466	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2393	15524	28653	2.36	0.0E+00	BE978095.1	EST_HUMAN	7122a02.x1 NCI_CGAP_OLL1 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:O84939 O94939
2396	15527	28655	5.46	0.0E+00	AF044571.1	NT	KIAA0857 PROTEIN;
2397	15528	28656	2.6	0.0E+00	AI625542.1	EST_HUMAN	Homo sapiens phosphotyrosine kinase alpha subunit (PHK2) gene, exon 32 y57c08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2283182 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2128	15264		1.48	0.0E+00	4585863	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rod, alpha (PDE8A), mRNA
2129	15265	28384	2.9	0.0E+00	Z42399.1	EST_HUMAN	HSC01C021 normalized infant brain cDNA Homo sapiens cDNA clone c-01c02
2131	15267		2.38	0.0E+00	A1244247.1	EST_HUMAN	q40008.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element;
2136	15272	28393	4.37	0.0E+00	BE877225.1	EST_HUMAN	601485146F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3887747 5'
2138	15274	28395	2.25	0.0E+00	BF315325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2138	15274	28396	2.25	0.0E+00	BF315325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2144	15280	28404	3.6	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2144	15280	28405	3.6	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2152	15288	28414	3.43	0.0E+00	LO0820.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2152	15288	28415	3.43	0.0E+00	LO0820.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2153	15289	28416	1.11	0.0E+00	AJ297709.1	NT	Homo sapiens mRNA for GDC2L6 protein kinase, (GDC2L6 gene), isoform 1
2158	15294	28420	1.16	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2162	15298	28423	1.94	0.0E+00	BE500695.1	EST_HUMAN	7634-02.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3220610 3' similar to SW:DTD_HUMAN
2182	15317		3.17	0.0E+00	BE787864.1	EST_HUMAN	P0443 SULFATE TRANSPORTER
2183	15318		1.26	0.0E+00	AF018993.1	NT	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2185	15320	28446	4.64	0.0E+00	BF027562.1	EST_HUMAN	Homo sapiens X-linked juvenile retinoschisis protein (XLR51) gene, exon 6 and complete cds
2186	15321	28447	1.5	0.0E+00	BE072624.1	EST_HUMAN	601672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3054785 5'
2188	15323	28448	1.29	0.0E+00	AF240786.1	NT	PMO-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA
2180	15325	28450	3.41	0.0E+00	AW752708.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2192	15327	28452	6.48	0.0E+00	AI804640.1	EST_HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2192	15327	28453	6.48	0.0E+00	AI804640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2225	15359		1.08	0.0E+00	7657262	NT	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2249	15382		1.52	0.0E+00	L14787.1	NT	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNNB3L), mRNA
2259	15392	28518	1.26	0.0E+00	BE274696.1	EST_HUMAN	Human DNA-binding protein mRNA, 3' end
2261	15394	28521	0.94	0.0E+00	DB7685.1	NT	Human mRNA for KIAA0244 gene, partial cds
2262	15395	28522	23.12	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBND08 5'
2262	15395	28523	23.12	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBND08 5'
2264	15397	28525	2.57	0.0E+00	AA931591.1	EST_HUMAN	6032801.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1667896 3'
2268	15401	28529	24.38	0.0E+00	BF344434.1	EST_HUMAN	602014829F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150734 5'
2269	15402	28530	40.14	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2005	15145	28250	1.3	0.0E+00	BE018068.1	EST_HUMAN	b573f11.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048045 5'
2011	15151	28255	1.69	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
2011	15151	28256	1.69	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
2024	15165		1.04	0.0E+00	AL163262.2	NT	Homo sapiens chromosome 21 segment HS21C062
2026	15167	28272	1.41	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
2026	15167	28273	1.41	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
2027	15168	28274	12.98	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2027	15168	28275	12.98	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2037	15178	28288	2.11	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2037	15178	28289	2.11	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2043	15184	28293	1.93	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
2043	15184	28294	1.93	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
2045	15186	28295	3.24	0.0E+00	AW193024.1	EST_HUMAN	xl89b01.x1 NCL CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2679913 3'
2045	15186	28296	3.24	0.0E+00	AW193024.1	EST_HUMAN	xl89b01.x1 NCL CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2679913 3'
2046	15187	28297	9.68	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2046	15187	28298	9.68	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2048	15189	28300	1.53	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2049	15190	28301	1.09	0.0E+00	Z47558.1	NT	H sapiens genes for semenogelin I and semenogelin II
2049	15190	28302	1.09	0.0E+00	Z47558.1	NT	H sapiens genes for semenogelin I and semenogelin II
2056	15197	28311	5.04	0.0E+00	AB040843.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
2078	15218	28337	1.85	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2078	15218	28338	1.85	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2109	15247	28368	1.53	0.0E+00	8394548	NT	Homo sapiens chromosome 21 open reading frame 7 (YG81), mRNA
2112	15250	28370	0.98	0.0E+00	7706742	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2117	15255	28374	35.36	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2117	15255	28375	35.36	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2119	15257	28376	1.02	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia B) (F9) mRNA
2121	15258	28378	57.93	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
2122	14612	27694	0.97	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2122	14612	27695	0.97	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2124	15260	28380	2.59	0.0E+00	AA075589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2124	15260	28381	2.59	0.0E+00	AA075589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2126	15262		3.79	0.0E+00	7637468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1853	14939	28105	24.99	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1870	15015	28124	3.11	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1870	15015	28125	3.11	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1881	15025	28131	7.19	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1881	15025	28132	7.19	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1892	15036	28143	1.84	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1892	15036	28144	1.84	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1895	15038	28148	3.59	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1895	15038	28147	3.59	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1896	15039	28148	7.35	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1896	15039	28149	7.35	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1899	15042	28152	2.3	0.0E+00	AW207280.1	EST_HUMAN	U1H-B11-efh-4-07-Q.U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1899	15042	28153	2.3	0.0E+00	AW207280.1	EST_HUMAN	U1H-B11-efh-4-07-Q.U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1924	15067	28171	3.22	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1924	15067	28172	3.22	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1943	15086	28187	1.04	0.0E+00	BE006292.1	EST_HUMAN	RC2-BN0128-200300-012-b04 BN0128 Homo sapiens cDNA
1972	15115	28215	1.62	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1972	15115	28216	1.62	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1975	15118	28218	3.14	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1975	15118	28219	3.14	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1981	15124	28228	1.29	0.0E+00	AB037783.1	NT	Homo sapiens mRNA for KIAA1367 protein, partial cds
1985	15128		1.64	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1986	16051	28230	57.92	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1986	16051	28231	57.92	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1991	16133	28238	3.19	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1991	15133	28239	3.19	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1994	15135	28241	2.41	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
1996	15137		6.39	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2001	15142		5.28	0.0E+00	M55632.1	NT	Human topoisomerase I pseudogene 1
2003	16052	28248	1.84	0.0E+00	5901805	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1714	14855	27955	1.08	0.0E+00	BE222374.1	EST_HUMAN	hu11405.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3162281 3' similar to TR:095147 095147
1716	14856	27957	3.2	0.0E+00	4557610	NT	MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1719	14859	27960	4.3	0.0E+00	H30132.1	EST_HUMAN	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA yc6e08.r1 Soares broad 3NbrHst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64089
1719	14859	27960	4.3	0.0E+00	H30132.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1719	14859	27960	4.3	0.0E+00	H30132.1	EST_HUMAN	yc69408.r1 Soares breast 3NbrHst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099
1719	14859	27960	4.3	0.0E+00	H30132.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1721	14871	27963	10.28	0.0E+00	Z80780.1	NT	qf4309.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
1722	14872	27964	10.28	0.0E+00	Z80780.1	NT	Hi.sapiens H2B/h gene
1725	14875	27976	21.3	0.0E+00	6031748	NT	Hi.sapiens H2B/h gene
1734	14883	27978	6.13	0.0E+00	8923841	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1737	14886	27979	1.83	0.0E+00	5453855	NT	Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1741	14890	27983	1.95	0.0E+00	M75990.1	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1741	14890	27984	1.95	0.0E+00	M75990.1	NT	Human hepatocyte growth factor gene, exon 15
1744	14893	27988	1.11	0.0E+00	4826973	NT	Human hepatocyte growth factor gene, exon 15
1747	14896	27990	2.54	0.0E+00	M75980.1	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1747	14896	27991	2.54	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1751	14900	27997	6.57	0.0E+00	AB026542.1	NT	Human hepatocyte growth factor gene, exon 15
1753	14902	28006	2.64	0.0E+00	S94400.1	NT	Human hepatocyte growth factor gene, exon 15
1762	14911	28006	5.29	0.0E+00	4557568	NT	Human hepatocyte growth factor gene, exon 15
1784	14933	28027	3.33	0.0E+00	AF273841.1	NT	Human hepatocyte growth factor gene, exon 15
1826	16047	28073	41.96	0.0E+00	4508718	NT	Human hepatocyte growth factor gene, exon 15
1830	14978	28074	3.2	0.0E+00	4557556	NT	Human hepatocyte growth factor gene, exon 15
1830	14978	28078	2.47	0.0E+00	U63963.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1837	16048	28083	7.55	0.0E+00	4505332	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1839	14985	28085	1.7	0.0E+00	AA113030.1	EST_HUMAN	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1850	14996	28099	24.06	0.0E+00	U14967.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1852	14998	28102	9	0.0E+00	AB002331.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1853	14999	28103	24.99	0.0E+00	4502264	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1853	14999	28104	24.99	0.0E+00	4502264	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1579	16042		32.23	0.0E+00	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1580	14732	27813	27.68	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1592	14746	27828	1.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1592	14745	27829	1.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1594	14747	27830	13.85	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melenoma-associated) (CSPG4), mRNA
1602	14755		3.25	0.0E+00	D00333.1	NT	human c-yes-2 gene
1611	14764	27844	11.38	0.0E+00	Z83738.1	NT	H. sapiens FH25/c gene
1612	14765	27845	2.55	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1612	14765	27846	2.55	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1613	14766	27847	11.09	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1613	14766	27848	11.09	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1616	16043	27851	2.1	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1618	14770	27852	1.88	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1620	14772	27855	6.83	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1620	14772	27856	6.83	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1622	14774	27857	56.88	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1622	14774	27858	56.88	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1624	14776	27860	1.53	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1639	14791	27876	6.29	0.0E+00	H26973.1	EST_HUMAN	y076c05.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:183848 3'
1648	14801	27887	1.87	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1648	14801	27888	1.87	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1688	14820	27903	1.66	0.0E+00	AW444637.1	EST_HUMAN	UL-H-B13-ajw-c-04-U1.s1 NCI CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2733284 3'
1698	14850	27936	2.12	0.0E+00	BE144364.1	EST_HUMAN	MR0-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA
1698	14850	27937	2.12	0.0E+00	BE144364.1	EST_HUMAN	MR0-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA
1702	14854	27941	1.3	0.0E+00	A1768104.1	EST_HUMAN	wg81b07.x1 Soares NSF F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q82788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN. ;
1703	14855	27942	1.71	0.0E+00	4758513	NT	Homo sapiens hematopoietic-derived zinc finger protein (HD-ZNF1) mRNA
1704	14856	27943	2.8	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1708	14859	27947	2.1	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1708	14859	27948	2.1	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1710	14861	27950	64.4	0.0E+00	4557687	NT	Homo sapiens keratin 18 (KRT18) mRNA
1711	14862	27951	2.42	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1714	14865	27954	1.08	0.0E+00	BE222374.1	EST_HUMAN	hu11d05.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O65147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE. ;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1440	14593	27688	1.03	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cyd gene
1449	14902	27680	13.57	0.0E+00	6042206	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1457	14310	27680	0.97	0.0E+00	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1457	14310	27691	0.97	0.0E+00	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1459	14512	27694	1.99	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1459	14512	27695	1.99	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1462	14615	27697	29.09	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Altu repeat elements
1471	14625	27709	4.63	0.0E+00	AF039280.1	NT	Homo sapiens alpha1-6fucosyltransferase (alpha1-6fucT) gene, exon 7
1490	14643	27724	4.2	0.0E+00	AL132669.1	NT	Novel human gene on chromosome 20
1491	14644	27725	1.37	0.0E+00	AL137764.1	NT	Novel human gene mapping to chromosome 1
1495	14648	27730	1.73	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1498	14651	27733	8.24	0.0E+00	6912457	NT	Homo sapiens calchectin binding protein 1 (KIAA0330), mRNA
1500	14653	27735	2.28	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1500	14653	27736	2.28	0.0E+00	7661966	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1501	14654	27738	3.74	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1507	14660	27742	6.62	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1507	14660	27743	6.62	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1541	14693	27772	2.61	0.0E+00	7709434	NT	Homo sapiens hHDG for homolog of Drosophila headcase (LOC51896), mRNA
1555	14708	27786	2.66	0.0E+00	AA481172.1	EST_HUMAN	Homo sapiens CGAP_G0B1 Homo sapiens cDNA clone IMAGE:815116 5'
1562	14715	27792	27.8	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1562	14715	27793	27.8	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1564	14717	27796	1.55	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGC resequences, MAGN Homo sapiens cDNA
1564	14717	27797	1.55	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGC resequences, MAGN Homo sapiens cDNA
1565	14718	27798	1.03	0.0E+00	D10884.1	NT	Bovine mRNA for neurocalcin
1567	14720		3.2	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FIP3 (FIP3) genes, complete cds
1568	14721	27801	26.69	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1568	14721	27802	26.69	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1570	14723	27804	3.85	0.0E+00	7662405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1571	14724	27810	9.78	0.0E+00	7666972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1578	14729	27810	64.77	0.0E+00	M88478.1	NT	Human transglutaminase mRNA, complete cds
1578	14731	27811	0.97	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1578	14731	27812	0.97	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1236	14395		1.28	0.0E+00	7657336	NT	Homo sapiens mult. (E. coli) homolog 3 (MLH3), mRNA
1250	14409	27471	0.94	0.0E+00	8922583	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
1254	14413	27475	2.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1254	14413	27476	2.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1254	14413	27477	3.33	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1255	14414	27478	2.46	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1256	14432	27478	4.88	0.0E+00	AF264750.1	NT	Homo sapiens chromosome 3 subtelomeric region
1275	14432	27503	1.87	0.0E+00	AF109718.1	NT	Homo sapiens chondroin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1276	14433	27504	0.69	0.0E+00	4503098	NT	Homo sapiens prefoldin 4 (PF4N4), mRNA
1286	14442	27510	1.38	0.0E+00	4505740	NT	Homo sapiens NF2 gene
1295	14451		29.86	0.0E+00	Y18000.1	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
1303	14459	27525	2.96	0.0E+00	4505718	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSOR9), mRNA, complete cds
1310	14465	27534	1.63	0.0E+00	AF084479.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1316	14472	27538	1.63	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1316	14472	27539	3.28	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1328	14485	27552	3.28	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1328	14485	27553	3.28	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1328	14485	27554	3.28	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1329	14486		2.16	0.0E+00	AF06156.1	NT	Homo sapiens protein phosphatase 2A, BR gamma subunit gene, exon 5
1339	16034	27566	1.2	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1339	16034	27567	1.2	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1345	15991	27573	1.4	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1346	14501	27574	1.86	0.0E+00	5803148	NT	Homo sapiens zinc finger protein 173 (ZNF173), mRNA
1347	14502	27575	0.83	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173), mRNA
1349	14504	27576	1.7	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1350	14505	27577	1.55	0.0E+00	5803148	NT	Homo sapiens zinc finger protein 173 (ZNF173), mRNA
1351	14506	27578	0.71	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173), mRNA
1353	14508	27580	4.44	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1354	14508	27581	1.34	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1355	14510	27582	4.99	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1356	14511	27583	3.83	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1356	14511	27584	3.83	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1356	14511	27587	1.36	0.0E+00	IM14123.1	NT	Human endogenous retrovirus HERV-K10
1368	14522	27597	1.02	0.0E+00	BE257955.1	EST_HUMAN	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'
1428	14563	27656	1.02	0.0E+00	BE257955.1	EST_HUMAN	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'
1429	14563	27657	1.02	0.0E+00	BE257955.1	EST_HUMAN	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1055	14221	27280	0.97	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated Nf- κ B activator (TANK) mRNA
1058	14224		3.27	0.0E+00	8922933	NT	Homo sapiens hypothetical protein FLJ11198 (FLJ11198), mRNA
1072	14238	27295	1.51	0.0E+00	4758669	NT	Homo sapiens heat shock 70kD protein 98 (hsp98) mRNA
1090	14255	27310	1.51	0.0E+00	4926672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1090	14255	27311	1.51	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1094	14259	27315	2.74	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1094	14259	27316	2.74	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1095	14260	27317	13.57	0.0E+00	8923624	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1097	14262		0.92	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1099	14264	27321	2.81	0.0E+00	5174384	NT	Homo sapiens alkylation repair, alkB homolog (ABH), mRNA
1106	14271	27330	2.04	0.0E+00	4788117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1120	14285	27364	1.91	0.0E+00	BE005208.1	EST_HUMAN	MR0-BN0116-200300-003-R08 BN0115 Homo sapiens cDNA
1143	14308	27364	3.82	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1143	14308	27365	3.82	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1155	14319	27373	0.82	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1155	14319	27374	0.82	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1156	14320	27375	9.35	0.0E+00	4506712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1156	14322	27377	1.2	0.0E+00	8923280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1161	14325	27380	3.95	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1163	14327	27381	19.6	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1164	14328	27382	4.52	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1164	14328	27383	4.52	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1168	14331	27386	1.44	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
1169	14332	27387	0.71	0.0E+00	X68826.1	NT	H sapiens ART4 gene
1169	14332	27388	0.71	0.0E+00	X68826.1	NT	H sapiens ART4 gene
1170	14333	27389	1.15	0.0E+00	AI147850.1	EST_HUMAN	qb22d10.x1 Soares, pregnant, uterus, NbHPU Homo sapiens cDNA clone IMAGE:1687011 3'
1172	14335	27391	1.62	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1181	14344	27400	1.22	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1181	14344	27401	1.22	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1182	14345	27402	1.32	0.0E+00	9668844	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1195	14357	27415	2.19	0.0E+00	7305076	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1195	14357	27415	2.19	0.0E+00	7305076	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1198	14360	27419	1.09	0.0E+00	AB037835.1	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1205	14367	27428	8.64	0.0E+00	4957887	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
					4957887	NT	Homo sapiens keratin 18 (KRT18) mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
973	14146	27205	0.93	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
974	14147	27206	9.11	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
975	14148	27207	0.79	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
976	14149	27208	1.24	0.0E+00	4507430	NT	Homo sapiens thyroidal embryonic factor (TEF), mRNA
978	14149	27209	1.24	0.0E+00	4507430	NT	Homo sapiens thyroidal embryonic factor (TEF), mRNA
984	16027	27216	3.95	0.0E+00	A1001948.1	EST_HUMAN	os98403.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
984	16027	27217	3.95	0.0E+00	A1001948.1	EST_HUMAN	os98403.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
986	14158	27219	14.34	0.0E+00	7657268	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
987	14168	27229	1.76	0.0E+00	AB030563.1	NT	Homo sapiens mRNA for PSP24, complete cds
1006	14177	27236	43.62	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1006	14177	27237	43.62	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1006	14177	27238	43.62	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1008	14179	27241	2.02	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1008	14179	27242	2.02	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1017	14188	27249	3.97	0.0E+00	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL), mRNA
1029	14199	27257	1.07	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1030	14200	27258	5.81	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1031	14200	27258	9.09	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1034	14203		4	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MITG8 (CBFA2T1) gene, partial cds
1035	14203		29.56	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MITG8 (CBFA2T1) gene, partial cds
1039	14207	27264	0.96	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1040	14207	27264	4.66	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1041	14207	27264	1.3	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1042	14208	27265	1.18	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1045	14211	27268	2.11	0.0E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1049	14216	27272	1.27	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (IMMT), mRNA
1051	14217		1.39	0.0E+00	AA458880.1	EST_HUMAN	aa88g07.s1 Strabagene fetal retina 937/202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW:PR88_HUMAN P47210 28S PROTEASE REGULATORY SUBUNIT 8;
1064	14220	27277	2.43	0.0E+00	N43182.1	EST_HUMAN	EST15124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1054	14220	27278	2.43	0.0E+00	N43182.1	EST_HUMAN	EST15124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1055	14221	27279	0.97	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
856	14033	27094	2.19	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
856	14033	27095	2.19	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
857	14034	27096	1.45	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
862	14039	27101	2.85	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
866	14042	27106	1.37	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
866	14042	27107	1.37	0.0E+00	4507500	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
873	14049		2.07	0.0E+00	AF027153.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
877	14053	27118	5.27	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
877	14053	27119	5.27	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
878	14054	27120	11.32	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
879	14055	27121	4.03	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
880	14056	27122	3.87	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
884	14060	27125	1.54	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
884	14060	27126	1.54	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
885	14061	27127	1.82	0.0E+00	AA533272.1	EST_HUMAN	U68407.s1 NCJ_CGAP_P10 Homo sapiens cDNA clone IMAGE:997453
885	14061	27128	1.82	0.0E+00	AA533272.1	EST_HUMAN	U68407.s1 NCJ_CGAP_P10 Homo sapiens cDNA clone IMAGE:997453
886	14062		8.41	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
890	14066	27129	1.4	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
890	14066	27130	1.4	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
891	14067	27131	2.54	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
891	14067	27132	2.54	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
891	14067	27133	2.54	0.0E+00	7657213	NT	Homo sapiens chromosome 21 segment HS21C003
914	14089	27155	0.98	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
921	14096	27160	1.93	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 B70703 Homo sapiens cDNA
921	14096	27161	1.93	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 B70703 Homo sapiens cDNA
931	14106	27170	2.7	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
941	14115		9.06	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
943	14115		9.89	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
944	14117	27176	1.42	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antitrypsin precursor, mRNA, partial cds
945	14118	27177	0.69	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
945	14118	27178	0.69	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
945	14118	27179	0.69	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
946	14119	27180	1.62	0.0E+00	L28101.1	NT	Homo sapiens kallistatin (P4) gene, exons 1-4, complete cds
949	14122	27183	0.71	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
949	14122	27184	0.71	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
705	13888	26920	4.84	0.0E+00	AB029012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
715	13897	26935	3.83	0.0E+00	7667468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
727	13909	20949	13.13	0.0E+00	AA614537.1	EST_HUMAN	np-49d01.a1 NCL CGAP_Br1.1 Homo sapiens cDNA clone IMAGE:1129633 3' similar to gb:X57932
731	13913	26953	6.4	0.0E+00	M60675.1	NT	INTERFERON-INDUCIBLE PROTEIN 1-8J (HUMAN);
731	13913	26954	6.4	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
741	13923	26963	1.35	0.0E+00	5032192	NT	Human von Willebrand factor gene, exons 23 through 34
747	13928	26969	4.62	0.0E+00	AF264750.1	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
747	13928	26970	4.62	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
749	13930	26973	9.17	0.0E+00	11545800	NT	Homo sapiens ALR-like protein mRNA, partial cds
755	13938	26981	2.26	0.0E+00	BE241577.1	EST_HUMAN	Homo sapiens hypodermal protein FLJ21634 (FLJ21634), mRNA
776	13955	27005	1.19	0.0E+00	AF226990.2	NT	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Bay/or-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0779
776	13955	27006	1.19	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
778	13958	27009	8.92	0.0E+00	J03764.1	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
778	13958	27010	8.92	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
781	13961	27011	0.96	0.0E+00	AB037760.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
782	13962	27012	2.07	0.0E+00	6912749	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
784	16022	27014	2.36	0.0E+00	D30612.1	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
785	13964	27015	3.55	0.0E+00	BE869735.1	EST_HUMAN	Homo sapiens mRNA for repressor protein, partial cds
790	13969	27021	4.04	0.0E+00	R46915.1	EST_HUMAN	601445847F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3849803 5'
791	13970	27022	2.85	0.0E+00	5032088	NT	y69g08.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154046 5'
800	13979	27031	1.64	0.0E+00	AB011399.1	NT	Homo sapiens splicing factor 3a, subunit 1, 120KD (SF3A1), mRNA
803	13983	27035	3.01	0.0E+00	7661963	NT	Homo sapiens gene for AF-6, complete cds
815	13994	27048	1.24	0.0E+00	D80006.1	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
816	13994	27049	1.24	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
820	13999	27053	2.74	0.0E+00	X89772.1	NT	Human mRNA for KIAA0184 gene, partial cds
824	14003	27057	3.25	0.0E+00	AB020717.1	NT	H sapiens mRNA for interferon alpha/beta receptor (long form)
824	14003	27058	3.25	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0610 protein, partial cds
829	14007	27064	13.47	0.0E+00	5174476	NT	Homo sapiens mRNA for KIAA0610 protein, partial cds
830	14008	27065	11.09	0.0E+00	4507500	NT	Homo sapiens perlecanin (PONT) mRNA
847	14025	27085	1.65	0.0E+00	7657213	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
848	14026	27086	2.46	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
850	14026	27088	1.84	0.0E+00	4557686	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
							Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNE1) mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
612	13801		7.14	0.0E+00	J04068.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
615	13804	26824	1.87	0.0E+00	BF104898.1	EST_HUMAN	601822627F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
617	13806	26826	0.95	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
617	13806	26827	0.95	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
618	13806	26828	0.77	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
618	13806	26827	0.77	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
619	13806	26826	0.72	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
619	13806	26827	0.72	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
624	13809	26830	0.64	0.0E+00	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
629	13814	26837	1.93	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
639	13824	26847	2.19	0.0E+00	AF221712.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
641	13828	26850	0.93	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
643	13828	26851	1.99	0.0E+00	8806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
644	13829	26852	2.34	0.0E+00	8806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
644	13829	26853	2.34	0.0E+00	8806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
645	13830	26854	0.98	0.0E+00	8806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
645	13830	26855	0.98	0.0E+00	8806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
652	13838	26865	1.42	0.0E+00	AA399486.1	EST_HUMAN	460c07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726732 5'
656	13842	26869	6.57	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
660	13846	26872	4.28	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
660	13846	26873	4.28	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
663	13849	26873	3.58	0.0E+00	4885526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
670	13856	26885	2.16	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
672	13858	26888	1.25	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
675	13861	26892	1.88	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
679	13865	26895	1.07	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
679	13865	26896	1.07	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
685	13870	26901	5.11	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
685	13870	26902	5.11	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
691	16018		1.8	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
700	13883	26915	3.92	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
445	13641	26679	4.23	0.0E+00	AF183607.1	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
457	13652		1.45	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
459	13654	26692	4.44	0.0E+00	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
464	13659		0.75	0.0E+00	BE264447.1	EST_HUMAN	60111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
480	13675	26706	3.38	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
480	13675	26707	3.38	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
486	13680	26715	21.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
486	13680	26716	21.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
496	13691	26722	4.1	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
497	13692	26723	5.9	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
497	13692	26724	5.9	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
509	13700	26729	4.25	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
508	13702	26731	1.81	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4-000837 5'
516	13710	26737	1.66	0.0E+00	BE385144.1	EST_HUMAN	60127495F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815756 5'
517	16014	26738	1.7	0.0E+00	AW938825.1	EST_HUMAN	PMO-DT0065-130400-002-008 DT0065 Homo sapiens cDNA
520	13713	26740	1.82	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
521	13714	26741	0.95	0.0E+00	8923958	NT	Homo sapiens PCS26 protein (PCS26), mRNA
525	13718		1.9	0.0E+00	BF373403.1	EST_HUMAN	IL2-FT0159-070800-120-F07 FT0159 Homo sapiens cDNA
532	13725	26751	4.43	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
539	16015	26755	1.57	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-105 BT0635 Homo sapiens cDNA
544	13737	26761	1.15	0.0E+00	BF028005.1	EST_HUMAN	60176485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3696998 5'
550	13743	26763	1.57	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
553	13746	26771	8.39	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
554	13747	26772	4.53	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein) alpha 11 (Gq class) (GNA11) mRNA
554	13747	26773	4.53	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein) alpha 11 (Gq class) (GNA11) mRNA
556	13749	26775	0.73	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
557	13750	26776	0.63	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
557	13750	26777	0.63	0.0E+00	8923831	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
562	13754		4.82	0.0E+00	AF003528.1	NT	UI-H-B1-acb-1-0-0-UI:st NCI_CGAP Sub3 Homo sapiens cDNA clone IMAGE:2713651 3'
570	13762	26786	1.39	0.0E+00	AW136324.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
580	13772		5.31	0.0E+00	DT10083.1	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCORF51), nuclear gene
589	13789	26810	1.85	0.0E+00	5174742	NT	encoding mitochondrial protein, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
366	13576	26607	2.75	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
366	13576	26608	2.75	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
367	16011	26609	2.53	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
369	13578	26611	1.01	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
372	13581	26615	1.59	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
373	13582	26616	2	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
374	13582	26616	1.43	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
376	13584	26618	0.86	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
387	13593	26629	3.37	0.0E+00	AU134953.1	EST_HUMAN	AU134953 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
398	13635	26673	7.59	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
399	13636	26674	1.08	0.0E+00	AI363014.1	EST_HUMAN	qy61M05.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb:X54199
407	13603	26638	1.32	0.0E+00	AW754180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (HUMAN);
407	13603	26639	2.24	0.0E+00	4503680	NT	RC2-CT0320-300100-016-a09 CT0320 Homo sapiens cDNA
408	13604	26640	2.34	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
408	13604	26641	2.34	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
409	13605	26642	2.18	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
410	13606	26643	1.42	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
411	13607	26645	1.98	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
412	13608	26646	2.55	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
413	13609	26647	2.14	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
414	13610	26648	0.96	0.0E+00	X74870.1	NT	H sapiens gene for RNA pol II largest subunit, exons 23-29
414	13610	26649	0.96	0.0E+00	X74870.1	NT	H sapiens gene for RNA pol II largest subunit, exons 23-29
415	13610	26648	1.07	0.0E+00	X74870.1	NT	H sapiens gene for RNA pol II largest subunit, exons 23-29
415	13610	26649	1.07	0.0E+00	X74870.1	NT	H sapiens gene for RNA pol II largest subunit, exons 23-29
419	13614		18.46	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
433	13233	26233	1.49	0.0E+00	R17706.1	EST_HUMAN	yp09a02.r1 Scars infant brain IN1B Homo sapiens cDNA clone IMAGE:31652 5'
441	13637	26675	1.39	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
442	13638		3.85	0.0E+00	4506728	NT	phosphoribosylaminimidazole synthetase (GART) mRNA
443	13639	26676	2.82	0.0E+00	AB028942.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
444	13640	26677	17.7	0.0E+00	4507152	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
444	13640	26678	17.7	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA

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237	13459	26485	0.99	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project;TCBA Homo sapiens
245	13467	26496	1.17	0.0E+00	AB018301.1	NT	cDNA clone TCBAP4486
245	13467	26497	1.17	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
246	13468	26501	7.54	0.0E+00	5453806	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
250	13471		3.79	0.0E+00	AL163201.2	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
257	13476	26507	4.65	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 segment HS21 C001
259	13478	26510	1.22	0.0E+00	X89772.1	NT	Homo sapiens chromosome 21 unknown mRNA
267	13488		6.96	0.0E+00	AF231919.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
280	13498	26528	1.37	0.0E+00	4507600	NT	Homo sapiens chromosome 21 unknown mRNA
280	13498	26530	1.37	0.0E+00	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
282	13500	26532	1.9	0.0E+00	7706028	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
283	13510		0.96	0.0E+00	D83327.1	NT	Homo sapiens hypothetical protein (LOC51250), mRNA
284	13511	26545	1.2	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
284	13511	26546	1.2	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
285	13512		1.41	0.0E+00	AW845283.1	EST_HUMAN	Homo sapiens DORR1 mRNA, partial cds
304	13520	26553	5.65	0.0E+00	4557028	NT	IL2-CT0031-181199-020-B03 CT0031 Homo sapiens cDNA
304	13520	26554	5.65	0.0E+00	4557028	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
315	13531	26564	5.16	0.0E+00	AB028942.1	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
316	13532	26565	4.28	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
317	16010		8.13	0.0E+00	4506728	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
318	13533		1.42	0.0E+00	AA480002.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8), mRNA
319	13534	26566	19.55	0.0E+00	4507162	NT	zr1806.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:753994 5'
320	13534	26566	24.65	0.0E+00	4507162	NT	Homo sapiens SON DNA binding protein (SON) mRNA
324	13538	26570	1.59	0.0E+00	AF114488.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
337	13550	26579	1.15	0.0E+00	O14867	SWISSPROT	Homo sapiens intersechin short isoform (ITSN) mRNA, complete cds
337	13550	26580	1.15	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
338	13551	26581	4.14	0.0E+00		SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
339	13551	26581	1.82	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
354	13565	26593	4.38	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
355	13568	26594	0.74	0.0E+00	4505256	NT	Homo sapiens moesin (MSN), mRNA
358	13569	26598	4.58	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
361	13572	26603	0.96	0.0E+00	U71600.1	NT	Human zinc finger protein zfp31 (zfp31) mRNA, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
170	13394	26421	2.4	0.0E+00	W73973.1	EST_HUMAN	z62b05.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to gb:X16282 cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);
171	13395	26422	0.79	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
171	13395	26423	0.79	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
172	13396	26424	4.73	0.0E+00	AF244098.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
175	13399	26427	26.75	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
175	13399	26428	26.75	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
185	13407	26435	6.75	0.0E+00	BE018970.1	EST_HUMAN	bb24a12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
185	13407	26435	6.75	0.0E+00	BE018970.1	EST_HUMAN	bb24a12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
185	13407	26436	6.75	0.0E+00	BE018970.1	EST_HUMAN	CE22631.1
190	13412	26439	2.4	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
190	13412	26440	2.4	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	13413	26441	1.68	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	13413	26442	1.68	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
199	13422	26453	57.89	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
204	13427	26458	3.13	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
204	13427	26459	3.13	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
208	13428	26461	7.71	0.0E+00	AF167174.1	NT	Homo sapiens chromosome XMSL3-2 protein mRNA, complete cds
206	13428	26462	7.71	0.0E+00	AF167174.1	NT	Homo sapiens chromosome XMSL3-2 protein mRNA, complete cds
216	16007	26489	12	0.0E+00	AI587308.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN);
216	16007	26470	12	0.0E+00	AI587308.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN);
218	13440	26472	1.93	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
221	13443		11.48	0.0E+00	4508832	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
222	13444		6.53	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
228	13450	26478	1.48	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
229	13450	26478	1.34	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
230	13451	26479	2.02	0.0E+00	6678444	NT	Mus musculus testis-specific protein, Y-encoded-like (Tspv), mRNA
237	13459	26483	0.89	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
237	13459	26484	0.89	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
69	13306		23.72	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
77	13313	26339	2.1	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
77	13313	26340	2.1	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
80	13313	26339	1.06	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
80	13313	26340	1.06	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
83	13318	26346	0.62	0.0E+00	AA953770.1	EST_HUMAN	cn89e04.s1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1563870 3' similar to SW:TMOD_HUMAN P28288 TROPOMODULIN.1
84	13319	26347	16.99	0.0E+00	4501860	NT	Homo sapiens amiloride binding protein 1 (amlino oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
85	13320	26347	12.3	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
94	13329	26356	23.92	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
97	13332	26359	40.86	0.0E+00	U89277.1	NT	Human polyomelic 1 homolog (HPH1) mRNA, partial cds
103	13339	26366	2.4	0.0E+00	AI114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
104	13340	26367	0.9	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
110	13343	26371	0.68	0.0E+00	X91213.1	NT	H. sapiens nct1 gene (exon 2)
118	13350	26377	0.68	0.0E+00	AI623701.1	EST_HUMAN	ts38b05.x1 NCJ CGAP_U4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.1
119	13350	26377	1.58	0.0E+00	AI623701.1	EST_HUMAN	ts38b05.x1 NCJ CGAP_U4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.1
120	15980	26378	1.92	0.0E+00	N36040.1	EST_HUMAN	W01109.r1 Soares melanocyte 2Nbl-IM Homo sapiens cDNA clone IMAGE:270017 5'
120	15980	26379	1.92	0.0E+00	N36040.1	EST_HUMAN	W01109.r1 Soares melanocyte 2Nbl-IM Homo sapiens cDNA clone IMAGE:270017 5'
123	13353	26384	1.63	0.0E+00	4505458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
133	13359	26392	3.65	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
133	13359	26393	3.65	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
141	13609	26647	1.9	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
143	13367	26400	0.7	0.0E+00	T56945.1	EST_HUMAN	ya83g04.i2 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5'
143	13367	26401	0.7	0.0E+00	T56945.1	EST_HUMAN	ya83g04.i2 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5'
157	13382		12.8	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
161	13386	26416	2.06	0.0E+00	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3853803 5'
163	13388		96.39	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
166	13391	26419	12.6	0.0E+00	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
168	13393	26420	1.03	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529884 5'
169	13393	26420	0.79	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529884 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5208	18329	31300	1.49	1.0E-130	AW363299.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
5208	18329	31301	1.49	1.0E-130	AW363299.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
6960	20188	33612	1.03	1.0E-130	AW843875.1	EST_HUMAN	GM0-CN0045-170200-228-g03 CN0045 Homo sapiens cDNA
6960	20188	33613	1.03	1.0E-130	AW843875.1	EST_HUMAN	GM0-CN0045-170200-228-g03 CN0045 Homo sapiens cDNA
6975	20203	33630	0.65	1.0E-130	11425446	NT	Homo sapiens estrogen-responsive B box protein (EBBP), mRNA
7404	20482	33949	1.85	1.0E-130		NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7508	20660	34052	0.63	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7508	20660	34053	0.63	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8881	21960		0.53	1.0E-130	AF008551.1	NT	Homo sapiens aurora-related kinase 1 (ARK1) mRNA, complete cds
9018	22098	35638	2.06	1.0E-130	AW06242.1	EST_HUMAN	EST368312 IMAGE sequences, MAGD Homo sapiens cDNA
9415	22488	36054	1.82	1.0E-130	AB037766.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
10137	23175		0.63	1.0E-130	AW103454.1	EST_HUMAN	z68c04.11 NC1_CGAP_Oic23 Homo sapiens cDNA clone IMAGE:259587.4 3'
4	13243	26243	2.52	0.0E+00	AA228126.1	EST_HUMAN	z68c04.11 Soares_NHMPu_ST Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G2222811
4	13243	26244	2.52	0.0E+00	AA228126.1	EST_HUMAN	G2222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
8	13246	26248	1.14	0.0E+00	4885136	NT	G2222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
16	13254	26254	3.34	0.0E+00	8923349	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
16	13254	26255	3.34	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
23	13261	26262	3.17	0.0E+00	D83327.1	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
23	13261	26263	3.17	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
27	13265	26267	9	0.0E+00	AF141349.1	NT	Homo sapiens DORR1 mRNA, partial cds
35	13273	26277	0.62	0.0E+00	5802997	NT	Homo sapiens beta-tubulin mRNA, complete cds
37	13275	26280	0.89	0.0E+00	M58600.1	NT	Homo sapiens Odc42 effector protein 2 (OEP2), mRNA
41	13279	26285	4.6	0.0E+00	6857825	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
58	13296	26312	1.77	0.0E+00	Y17151.2	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
58	13296	26313	1.77	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	13298	26317	1.45	0.0E+00	D78804.1	EST_HUMAN	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	13298	26318	1.45	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (T Fujiwara) Homo sapiens cDNA clone GEN:516H08 5'
61	13299	26319	9.83	0.0E+00	L16558.1	NT	HUM516H08B Human placenta polyA+ (T Fujiwara) Homo sapiens cDNA clone GEN:516H08 5'
63	13301	26322	16.36	0.0E+00	AW069534.1	EST_HUMAN	Human ribosomal protein L7 (RPL7) mRNA, complete cds
63	13301	26323	16.36	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC cr48e07 3'
67	13304	26327	2.48	0.0E+00	M630376.1	NT	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC cr48e07 3'
							Human von Willebrand factor pseudogene corresponding to exons 23 through 34

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4395	17538	30518	2.32	1.0E-129	AW755264.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
6216	19391	32739	3.77	1.0E-129	AJ006345.1	NT	Cardiomyopathy associated gene 5
6654	19813	33201	0.61	1.0E-129	BE888334.1	EST_HUMAN	Homo sapiens KVLQT1 gene
7277	20360	33814	3.89	1.0E-129	AJ006345.1	NT	601513891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915350 5'
7340	20420	33882	4.03	1.0E-129	11420850	NT	Homo sapiens KVLQT1 gene
7697	20762	34245	1.04	1.0E-129	AF041056.1	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
7697	20762	34246	1.04	1.0E-129	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
8513	21594		3.57	1.0E-129	AB014634.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
10284	23319	36920	1.03	1.0E-129	11437282	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
10284	23319	36921	1.03	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10730	23763	37370	0.52	1.0E-129	AH199117.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10730	23763	37371	0.52	1.0E-129	AH199117.1	EST_HUMAN	q140d08.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:1858958 3' similar to TR:Q14840 Q14840
11497	24555	38230	3.32	1.0E-129	AA625628.1	EST_HUMAN	MITOGEN INDUCIBLE GENE MIG-2;
11578	20420	33882	5.01	1.0E-129	11420850	NT	q140d08.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:1858958 3' similar to TR:Q14840 Q14840
12387	25273		4.28	1.0E-129	H83155.1	EST_HUMAN	MITOGEN INDUCIBLE GENE MIG-2;
12817	25844		1.97	1.0E-129	AL120739.1	EST_HUMAN	q140d08.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:1047589 5'
78	13314	26341	1.01	1.0E-130	7705530	NT	SP-B48150 B48150 HP-25-HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS=ASIAN;
1197	14359	27418	0.64	1.0E-130	AB037635.1	NT	Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
1700	14852	27939	22.97	1.0E-130	BE275192.1	EST_HUMAN	Homo sapiens RET finger protein-like 1 antisense transcript, partial
1700	14852	27940	22.97	1.0E-130	BE275192.1	EST_HUMAN	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
2040	15181		2.63	1.0E-130	X04092.1	NT	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
2830	15944		7.23	1.0E-130	AJ010230.1	NT	Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
2943	16120	29132	1.36	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2943	16120	29133	1.36	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3668	16831	26842	1.03	1.0E-130	AF240698.1	NT	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3864	16120	29132	6.31	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH), complete cds
3864	16120	29133	6.31	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
4047	17203	30213	1.8	1.0E-130	AW503580.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
4184	17334	30326	0.91	1.0E-130	M97710.1	NT	UI-HF-BNO-aky-g-06-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4660	17796	30782	9.77	1.0E-130	AW843993.1	EST_HUMAN	Human T-cell receptor (V alpha 22.1, J alpha 1) mRNA
							CM4-CN0045-180200-511-402 CN0045 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2283	15415	28547	37.91	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2516	15642		1.11	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3481	16648	29664	1.17	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4768	17621	30909	7.27	1.0E-128	11426873	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5662	18956	32139	0.76	1.0E-128	X69339.1	NT	H. sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exon 12
6548	19710	33086	1.5	1.0E-128	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
7070	20123	33538	6.26	1.0E-128	BF224345.1	EST_HUMAN	7q86b10.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE: 3'
8746	21824	35360	0.67	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8745	21824	35361	0.67	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
10341	23376	36987	1.29	1.0E-128	AA630198.1	EST_HUMAN	nc04at1.1 NCI CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182620 similar to TR:G951338 G951338
10949	24031	37666	3.54	1.0E-128	11425254	NT	CHROMOSOME SEGREGATION GENE HOMOLOG CAS.;
10957	24038	37873	3.51	1.0E-128	AA926959.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
11210	24279	37918	1.98	1.0E-128	BE887554.1	EST_HUMAN	om68H08.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1552383 3' similar to gb.X54941 CYCLIN
12402	25282		4.26	1.0E-128	AW955290.1	EST_HUMAN	DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
124	13621	26663	1.93	1.0E-128	S37722.1	NT	EST 367360 MAGE resequences, MAGC Homo sapiens cDNA
428	13621	26663	1.65	1.0E-128	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1756	14905	27999	3.74	1.0E-129	AL096880.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1761	14910	28004	1.66	1.0E-129	AF240786.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1761	14910	28005	1.66	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1894	15037	28145	4.07	1.0E-129	11418522	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2838	15952	29059	2.93	1.0E-129	4505682	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
2838	15952	29059	2.93	1.0E-129	4505682	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
3198	16373	29380	1.43	1.0E-129	Q14585	SWISSPROT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
3198	16373	29381	1.43	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3198	16373	29382	1.43	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4279	17424	30413	2.37	1.0E-129	AB040892.1	NT	ZINC FINGER PROTEIN HZF10
4395	17538	30517	2.32	1.0E-129	AW756254.1	EST_HUMAN	Homo sapiens mRNA for KIAA1459 protein, partial cds
							CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
							Cardiomyopathy associated gene 5

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4795	17830	30916	4.38	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
5824	18014	32320	1.57	1.0E-127	W03547.1	EST_HUMAN	z01a10.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:291268 5' similar to SW:PIP6_RAT P10688 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1;
5834	19044	32351	0.91	1.0E-127	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM), mRNA
5923	19110	32423	4.18	1.0E-127	X85764.1	NT	H.sapiens NOS2 gene, exon 6
6291	19464	32816	2.23	1.0E-127	X84060.1	NT	H.sapiens TCF11 gene, exon 3-6
6451	19818	32981	5.73	1.0E-127	4504778	NT	Homo sapiens integrin, beta 8 (ITGB8), mRNA
6797	19952	33352	1.09	1.0E-127	11421595	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA
7208	20073	33485	0.81	1.0E-127	4826977	NT	Homo sapiens redin (RELN), mRNA
7894	21014	34526	1.31	1.0E-127	11421914	NT	Homo sapiens Pentred syndrome (PDS), mRNA
7964	21014	34526	1.31	1.0E-127	11421914	NT	Homo sapiens Pentred syndrome (PDS), mRNA
7973	21023	34536	0.63	1.0E-127	BF671355.1	EST_HUMAN	602151232F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292575 5'
8088	22167	35713	0.81	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9088	22167	35714	0.81	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9840	22880	36462	3.73	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9840	22880	36463	3.73	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10077	23115	36718	0.86	1.0E-127	A1298932.1	EST_HUMAN	q094h09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896449 3'
10551	23586	37194	0.99	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
11426	24487	38150	5.64	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
11426	24487	38151	5.64	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
11927	24913	38614	1.55	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
11927	24913	38615	1.55	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
12539	13400	26429	3.03	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12539	13400	26430	3.03	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12763	25507	32037	1.74	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
13170	26044		1.64	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
472	13667	26700	1.56	1.0E-128	BE385617.1	EST_HUMAN	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3818822 5'
1178	14342	27396	0.96	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1179	14342	27397	0.96	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2132	15268	28387	18.07	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2132	15268	28388	18.07	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8177	21259	34781	2.42	1.0E-126	X16609.1	NT	Human mRNA for ankyrin (variant 2.1)
8377	21458	34982	0.8	1.0E-126	AA483368.1	EST_HUMAN	ne74b12.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909983 similar to SW:TSG6_HUMAN
10000	20308	36829	0.57	1.0E-126	4505424	EST_HUMAN	P88066 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR;
11099	24172	37607	2.01	1.0E-126	BF683175.1	EST_HUMAN	Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), splice variant 1, mRNA
11808	24796	38494	2.2	1.0E-126	BE261680.1	EST_HUMAN	602139138F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4288240 5'
12823	18500	31536	6.48	1.0E-126	BE743922.1	EST_HUMAN	601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502129 5'
176	13400	26429	2.92	1.0E-127	AB024597.1	NT	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926885 5'
176	13400	26430	2.92	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
177	13400	26429	2.75	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
177	13400	26430	2.75	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
284	13502	26536	2.14	1.0E-127	D87675.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
284	13502	26536	2.14	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
904	14079	27145	1.17	1.0E-127	AF114488.1	NT	Homo sapiens intersein short isoform (ITSN) mRNA, complete cds
939	14113	27174	4.81	1.0E-127	U72621.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1726	14876	27967	2.22	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 9 (USP9) mRNA
2127	15263	28392	1.97	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2127	15263	28393	1.97	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2273	15408	28535	17.46	1.0E-127	4506620	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2418	15547	28676	3.12	1.0E-127	AF245505.1	NT	Homo sapiens adican mRNA, complete cds
2674	15704	28911	21.46	1.0E-127	X12881.1	NT	Human mRNA for cytokerin 18
3781	16942	29948	0.61	1.0E-127	AF114488.1	NT	Homo sapiens intersein short isoform (ITSN) mRNA, complete cds
3913	17072	30070	0.7	1.0E-127	AW161297.1	EST_HUMAN	eu0606.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to
4232	17379	30368	0.59	1.0E-127	AF135188.1	NT	TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;contains element MER22
4368	17511	30491	24.93	1.0E-127	7706239	NT	repetitive element;
4368	17511	30492	24.93	1.0E-127	7706239	NT	Homo sapiens delayed rectifier potassium channel subunit isK mRNA, complete cds
4318	17755	30737	0.83	1.0E-127	AF252297.1	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4725	17860	30842	6.74	1.0E-127	4506384	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4755	17890		2.69	1.0E-127	AL163288.2	NT	Homo sapiens cytochrome P450 rethoid metabolizing protein P450RAL2 mRNA, complete cds
							Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
							Homo sapiens chromosome 21 segment HS21C068

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9881	22723	38298	1.06	1.0E-125	AI565998.1	EST_HUMAN	hms2b03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2171981 3' similar to TR:Q14089 Q14089
10670	23704	37313	0.72	1.0E-125	BE794576.1	EST_HUMAN	HYPOTHETICAL PROTEIN;
10712	23745	37351	1.06	1.0E-125	AB002288.1	NT	601590345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944631 5'
10921	24004	37639	3.03	1.0E-125	AF043458.1	NT	Human mRNA for KIAA0300 gene, partial cds
11091	24165	37802	1.34	1.0E-125	11425570	NT	Homo sapiens IREL gene, exon 5
11357	24419	38076	2.42	1.0E-125	AL040655.1	EST_HUMAN	Homo sapiens ryanodine receptor 1 (skeletal) (RYR1), mRNA
11401	24462	38126	3.35	1.0E-125	AB014567.1	NT	DKFZp434N2414.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N2414 5'
11538	24594		1.63	1.0E-125	R61450.1	EST_HUMAN	Homo sapiens mRNA for KIAA0667 protein, partial cds
11568	24623	38303	2.13	1.0E-125	7693505	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
11575	24630	38309	5.32	1.0E-125	AF026029.1	NT	YH15a12.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:37663 5'
11686	24685	38375	2.27	1.0E-125	AW812899.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
11763	24783	38479	4.71	1.0E-125	BE074267.1	EST_HUMAN	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
11783	24783	38480	4.71	1.0E-125	BE074267.1	EST_HUMAN	Homo sapiens CDC-like kinase (CLK) mRNA
795	13974	27027	2.16	1.0E-126	4758007	NT	Homo sapiens B1 chain gene, exon 20
798	13977	27030	1.74	1.0E-126	M61938.1	NT	Human laminin B1 chain gene, exon 3
942	14116	27175	1.53	1.0E-126	X68735.1	NT	H. sapiens gene for alpha1-antichymotrypsin, exon 3
2663	15785	28900	4.55	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3140	16316	29329	8.12	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Sitelagene pancreas (#837208) Homo sapiens cDNA clone IMAGE:592420 5'
3140	16316	29330	8.12	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Sitelagene pancreas (#837208) Homo sapiens cDNA clone IMAGE:592420 5'
3719	18880	29885	0.87	1.0E-126	X53941.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogene
3745	18906	29910	2.52	1.0E-126	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
4908	18038	31026	1.08	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4908	18038	31027	1.08	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4956	18086	31082	1.81	1.0E-126	N34078.1	EST_HUMAN	yx78cd06.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:267850 5'
5820	18010	32316	0.68	1.0E-126	T68998.1	EST_HUMAN	y452b12.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:68527 3'
6362	19532	32891	2.91	1.0E-126	AA460075.1	EST_HUMAN	z666d03.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:68527 3'
6419	19588	32951	4.33	1.0E-126	AB040958.1	NT	TR:G1145880 G1145880 TITN ;
6419	19588	32952	4.33	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7669	20735	34212	0.9	1.0E-126	AF257737.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7669	20735	34213	0.9	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8062	21144	34662	0.73	1.0E-126	AB037715.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8062	21144	34663	0.73	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1023	14194	27252	1.54	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1177	14340	27394	1.73	1.0E-125	7662270	NT	Homo sapiens KIAA0744 gene product, histone deacetylase 7 (KIAA0744), mRNA
1707	18045	27946	1.44	1.0E-125	7661887	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1854	15000	28106	5.91	1.0E-125	AF015450.1	NT	Homo sapiens Usurin-alpha mRNA, complete cds
1854	15000	28107	5.91	1.0E-125	AF015450.1	NT	Homo sapiens Usurin-alpha mRNA, complete cds
2433	15561	28687	4.81	1.0E-125	AA011278.1	EST_HUMAN	z01g09.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429568 5'
2573	15698	28820	0.96	1.0E-125	AA042813.1	EST_HUMAN	zk63c07.s1 Soares_pregnant_uterus_NdrHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to
2661	15783	28898	2.34	1.0E-125	4504686	NT	gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2661	15783	28899	2.34	1.0E-125	4504686	NT	Homo sapiens inhibin, alpha (INH) mRNA
3661	17119	30123	1.33	1.0E-125	AA042813.1	EST_HUMAN	Homo sapiens inhibin, alpha (INH) mRNA
4672	17607	30796	1.82	1.0E-125	11425114	NT	zk63c07.s1 Soares_pregnant_uterus_NdrHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to
4672	17607	30797	1.82	1.0E-125	11425114	NT	gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
4739	17874	30857	0.85	1.0E-125	BE315412.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5877	19067	32375	0.65	1.0E-125	BF683645.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5994	19179	32501	1.39	1.0E-125	11436448	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
6013	19197	32514	1.2	1.0E-125	BE175169.1	EST_HUMAN	602139874F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300770 5'
6054	19236	32561	3.53	1.0E-125	BE892660.1	EST_HUMAN	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
6096	19777	32606	0.85	1.0E-125	AI679904.1	EST_HUMAN	QV2-HT0577-010500-165-506 HT0577 Homo sapiens cDNA
6412	19881	32942	0.72	1.0E-125	BE736055.1	EST_HUMAN	601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'
6711	19869	33259	3.71	1.0E-125	BE562526.1	EST_HUMAN	tu67c07.x1 NOI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2256108 3' similar to WP:C45G9.2
6711	19869	33260	3.71	1.0E-125	BE562526.1	EST_HUMAN	CE01854
7207	20072	33483	4.06	1.0E-125	X03427.1	NT	601305670F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640097 5'
7207	20072	33484	4.06	1.0E-125	X03427.1	NT	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
7700	20765	34249	1.56	1.0E-125	BE278823.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
7933	20983	34491	0.59	1.0E-125	11425672	NT	Homo sapiens IQF-II gene, exon 5
8743	21822	35357	1.49	1.0E-125	U90288.1	NT	Homo sapiens IQF-II gene, exon 5
8743	21822	35358	1.49	1.0E-125	U90288.1	NT	Homo sapiens IQF-II gene, exon 5
9318	22394	35945	4.15	1.0E-125	BE181640.1	EST_HUMAN	601159076F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505603 5'
9318	22394	35946	4.15	1.0E-125	BE181640.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
							Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
							Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
							Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
							QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
							QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7287	20370	33825	0.94	1.0E-124	BE271295.1	EST_HUMAN	G0094377.F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966585 5'
7725	20789	34278	2.38	1.0E-124	AA630331.1	EST_HUMAN	sacDh05.s1 Stratiogene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:855897 3'
8453	21634	35064	2.73	1.0E-124	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
8857	21737	35277	1.24	1.0E-124	AW612108.1	EST_HUMAN	hg94a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:O95162
8857	21737	35278	1.24	1.0E-124	AW612108.1	EST_HUMAN	O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE ;
9383	22438	35986	0.88	1.0E-124	AJ799884.1	EST_HUMAN	hg94a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:O95162
9383	22438	35987	0.88	1.0E-124	AJ799884.1	EST_HUMAN	O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE ;
9891	22740	36309	1.72	1.0E-124	AV645633.1	EST_HUMAN	wc43g03.x1 NCI_CGAP_P228 Homo sapiens cDNA clone IMAGE:2321428 3'
9891	22740	36310	1.72	1.0E-124	AV645633.1	EST_HUMAN	wc43g03.x1 NCI_CGAP_P228 Homo sapiens cDNA clone IMAGE:2321428 3'
9808	22848	36426	7.77	1.0E-124	AJ767133.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
9808	22848	36427	7.77	1.0E-124	AJ767133.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
10075	23113	36717	1.46	1.0E-124	AW503755.1	EST_HUMAN	wf93t02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
11302	24368	38009	1.57	1.0E-124	U94776.1	NT	wf93t02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
11617	24688	38356	3.9	1.0E-124	AW695863.1	EST_HUMAN	UH-F-BND-akz-b-04-0.U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078846 5'
11781	23947	37575	2.18	1.0E-124	AI446455.1	EST_HUMAN	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17
11781	23947	37576	2.18	1.0E-124	AI446455.1	EST_HUMAN	tj05c08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2980906 3'
12310	13891	26926	4.6	1.0E-124	AA397551.1	EST_HUMAN	tj05a03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662
12310	13891	26927	4.6	1.0E-124	AA397551.1	EST_HUMAN	YKRS PROTEIN ;
12780	25522	32004	1.89	1.0E-124	AB028016.1	EST_HUMAN	tj05a03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662
13080	26038	31680	2.36	1.0E-124	11417862	NT	YKRS PROTEIN ;
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	tj05a03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens mRNA for KIAA1093 protein, partial cds
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080	26038	31681	2.36	1.0E-124	11417862	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13080							

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
279	13497	26527	1.02	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
279	13497	26528	1.02	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
285	13503		1.49	1.0E-124	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
498	13693	26725	2.26	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
709	13891	26926	4	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
709	13891	26927	4	1.0E-124	AA397551.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) :
777	13957	27008	3.72	1.0E-124	AF155954.1	NT	z81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
831	14009	27065	2.06	1.0E-124	4507500	NT	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) :
927	14102	27165	2.67	1.0E-124	7705448	NT	Human putative ribosomal protein S1 mRNA
1343	14499	27572	0.66	1.0E-124	11419092	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1377	14532	27605	6.42	1.0E-124	AF274892.1	NT	Homo sapiens ring finger protein (RNF), mRNA
1377	14532	27606	6.42	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1858	15004	28111	4.06	1.0E-124	AJ131712.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
2123	15259	28379	2.16	1.0E-124	BE879524.1	EST_HUMAN	Homo sapiens mRNA for nuclear RNA-helicase (nclh51 gene)
2528	15653	28777	0.98	1.0E-124	AB024039.1	NT	601491715F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893954 5'
3579	16744	29761	1.06	1.0E-124	S78684.1	NT	Homo sapiens gene for B120, exon 11
3579	16744	29762	1.06	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3739	16900	29904	1.24	1.0E-124	X13794.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
4006	17163	30170	0.64	1.0E-124	4507500	NT	H.sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS)
4179	17329	30321	0.69	1.0E-124	4504116	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4187	17337	30330	0.98	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4868	17999	30983	2.51	1.0E-124	AB024039.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
6050	18178		15.32	1.0E-124	M18178.1	NT	Homo sapiens gene for B120, exon 11
5205	18326	31296	0.74	1.0E-124	AW983390.1	EST_HUMAN	Homo sapiens gene extra type III repeat (EDII), exon xt-1
5412	18614	31588	10.49	1.0E-124	8922337	NT	EST375463 MAGe sequences, MAGH Homo sapiens cDNA
5789	18981	32284	1.2	1.0E-124	4506788	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6008	19193	32511	6.89	1.0E-124	BF696135.1	EST_HUMAN	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
6298	19471	32828	0.8	1.0E-124	AV711283.1	EST_HUMAN	60212464F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281635 5'
							AV711283 Cu Homo sapiens cDNA clone CuaADF07 5'
6563	19725	33103	1.12	1.0E-124	11420854	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
7152	20286	33728	3.15	1.0E-124	Y11717.1	NT	M.musculus mRNA for hoxa3 gene.
7287	20370	33824	0.94	1.0E-124	BE271286.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2968585 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1267	1424	27492	3.83	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
2035	15176	28288	0.94	1.0E-123	11422479	NT	Homo sapiens similar to sex comb on midleg (Drosophila)-like 2 (H. sapiens) (LOC63782), mRNA
2166	15301	28427	3.21	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2166	15301	28428	3.21	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2166	15301	28429	3.21	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2389	15520		4.21	1.0E-123	7706982	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
3322	16495	29512	0.71	1.0E-123	6912617	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutamyl cyclase) (QPCT), mRNA
5563	18760	31789	1.62	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5563	18760	31800	1.62	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5569	18693	32185	1.76	1.0E-123	BE799746.1	EST_HUMAN	601591108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945433 5'
6598	19758	33146	1.93	1.0E-123	AU118435	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
7143	20278	33718	0.91	1.0E-123	H53193.1	EST_HUMAN	y84403.1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:202444 5' similar to SP:YAK1_YEAST P14680 PROTEIN KINASE YAK1;
7156	20290	33733	1.39	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
7344	20424	33887	0.71	1.0E-123	U55258.1	NT	Human hBRAVO/Nr-CAM precursor (hBRAVO/Nr-CAM) gene, complete cds
7562	20634	34109	0.83	1.0E-123	11525833	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HSST2), mRNA
7820	20875	34374	1.31	1.0E-123	11436439	NT	Homo sapiens 2'-5'-oligoadenylate synthetase 2 (OAS2), mRNA
7829	20884	34388	2.22	1.0E-123	BE283001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509162 5'
7836	20891	34393	0.6	1.0E-123	11437202	NT	Homo sapiens hypothetical protein FLJ20184 (FLJ20184), mRNA
7976	21025	34538	0.6	1.0E-123	N35941.1	EST_HUMAN	y89d11.1 Soares melanocyte 2Nb-IM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611 S49611 protein Kinase PtkpA - Phycomyces blakesleeanus;
7975	21025	34539	0.6	1.0E-123	N35941.1	EST_HUMAN	y89d11.1 Soares melanocyte 2Nb-IM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611 S49611 protein Kinase PtkpA - Phycomyces blakesleeanus;
8100	21182	34701	0.79	1.0E-123	AU131881.1	EST_HUMAN	AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5'
8100	21182	34702	0.79	1.0E-123	AU131881.1	EST_HUMAN	AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5'
8732	21812		0.7	1.0E-123	AW371924.1	EST_HUMAN	RC4-BT0311-251189-012-ae7 BT0311 Homo sapiens cDNA
9569	22711	36279	2.07	1.0E-123	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9705	22734	36325	18.77	1.0E-123	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefaz2) mRNA, complete cds
12020	25004	38705	4.91	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
12020	25004	38706	4.91	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
12114	25094	38788	2.71	1.0E-123	AW450931.1	EST_HUMAN	U1H-B18-alk-f-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737281 3'
12114	25094	38799	2.71	1.0E-123	AW450931.1	EST_HUMAN	U1H-B18-alk-f-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737291 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
368	13577	26610	2.56	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
905	14080	27146	3.34	1.0E-122	AF114488.1	NT	Homo sapiens intersechin short isoform (ITSN), mRNA, complete cds
1247	14406	27468	5.19	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1728	14378	27969	18.7	1.0E-122	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1750	14899	27995	1.61	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1750	14899	27996	1.61	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1857	15003	28110	6.92	1.0E-122	BE806024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3893368 5'
2560	15685	28810	7.43	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2560	15685	28811	7.43	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2901	16080	29096	4.87	1.0E-122	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4971	18100	31076	3.81	1.0E-122	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
5104	18232		1.41	1.0E-122	AW504645.1	EST_HUMAN	UI-HF-BND-ali-a-03-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078948 5'
5681	18875	32164	1.2	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
6896	18875	32164	6.8	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
7363	20442	33904	0.64	1.0E-122	AA868671.1	EST_HUMAN	ek49h06.s1 Soares, Basilis, NHT Homo sapiens cDNA clone IMAGE:1409339 3'
8996	22075	38614	0.8	1.0E-122	AJ276801.1	NT	Homo sapiens mRNA for doublesex and mab-3 related transcription factor 1 (DMRT1)
9228	22306	35849	1.17	1.0E-122	11424216	NT	Homo sapiens lethal giant larvae (Drosophila) homolog 2 (LGL2), mRNA
9524	22589	36159	0.96	1.0E-122	AI359618.1	EST_HUMAN	q32h07.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW-MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.
9524	22589	36160	0.96	1.0E-122	AI359618.1	EST_HUMAN	q32h07.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW-MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.
10338	23373	36983	0.64	1.0E-122	AL117234.1	NT	Novel human gene mapping to chromosome X, isoform of dhl (proto-oncogene)
11233	24302	37939	2.12	1.0E-122	AW955834.1	EST_HUMAN	EST367904 MAGE sequences, MAGD Homo sapiens cDNA
11667	24744	38436	1.83	1.0E-122	AB024068.1	NT	Homo sapiens gene for B120, exon 10
12231	25178		5.28	1.0E-122	11418187	NT	Homo sapiens phosphomannomutase 1 (PMM1), mRNA
789	13968	27019	1.53	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153670 5'
789	13968	27020	1.53	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153670 5'
1038	14206	27263	6.18	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1047	14213	27270	3.36	1.0E-123	5903114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1267	14424	27491	3.83	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2023	15164	28269	1	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107KD (INPP4A), splice variant a, mRNA
2023	15164	28270	1	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107KD (INPP4A), splice variant a, mRNA
2169	15304	28431	1.22	1.0E-121	L78631.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
2643	15766	28880	1.07	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4150286 5'
2843	15766	28881	1.07	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4150286 5'
3150	16325	26336	6.8	1.0E-121	Y18208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3150	16325	26337	5.8	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3626	16790	29807	1.23	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3626	16790	29808	1.23	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3768	16229	26934	8.25	1.0E-121	AF155156.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
4450	17690	30671	1.76	1.0E-121	AI263294.1	EST_HUMAN	q57601.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3'
5091	18219	31188	3.42	1.0E-121	X91937.1	NT	H.sapiens ECE-1 gene (exon 17)
5382	18594	31453	0.84	1.0E-121	BE222250.1	EST_HUMAN	hu09f08.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166119 3'
5679	18873	32161	0.73	1.0E-121	BE271424.1	EST_HUMAN	601140485F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049820 5'
6757	19913	33308	0.64	1.0E-121	M91463.1	NT	Human glucose transporter (GLUT4) gene, complete cds
7028	20164	31483	0.96	1.0E-121	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
7102	18529	31483	0.79	1.0E-121	AW890086.1	EST_HUMAN	RC3-NN0066-270400-011-402 NN0066 Homo sapiens cDNA
7102	18529	31484	0.79	1.0E-121	AW890086.1	EST_HUMAN	RC3-NN0066-270400-011-402 NN0066 Homo sapiens cDNA
8123	21205	34725	1.07	1.0E-121	11436217	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
8127	21209	34729	2.51	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
8127	21209	34730	2.51	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
10062	23100	36702	1.02	1.0E-121	AW563858.1	EST_HUMAN	la05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:O75457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.
10062	23100	36703	1.02	1.0E-121	AW563858.1	EST_HUMAN	la05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:O75457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.
11015	24094	37733	3.45	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
11023	24102	37740	1.94	1.0E-121	AF064200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds
11211	24280	37919	5.74	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
11243	24312	37950	1.93	1.0E-121	N59624.1	EST_HUMAN	y74c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248448 3'
278	13496	26526	2.64	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
346	13557	26585	2.33	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1631	14763	27869	11.19	1.0E-120	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds
1849	14995	28098	6.58	1.0E-120	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2174	15309	28437	1.83	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2174	15309	28438	1.83	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3382	13528	26561	1.61	1.0E-120	4507334	NT	Homo sapiens synaptobrevin 1 (SYN1), mRNA
4477	17617	30598	2.05	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4477	17617	30599	2.05	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4784	17919	30906	3.11	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
4784	17919	30907	3.11	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
5853	19043	32349	16.08	1.0E-120	BF598222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
5853	19043	32350	16.08	1.0E-120	BF598222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
7746	20806	34295	1.84	1.0E-120	D34619.1	NT	Human TBXAS1 gene for thromboxane synthase, exon 7
8078	21160	34677	1.38	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8078	21160	34678	1.38	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8527	21608	35147	2.31	1.0E-120	BF337599.1	EST_HUMAN	602035352F1 NCJ_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4183333 5'
8599	21880	35218	0.9	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8599	21880	35219	0.9	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8603	21884	35221	1.94	1.0E-120	AB007984.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8647	21727	35284	1.31	1.0E-120	AB007934.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
9701	22750	36319	4.67	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
9701	22750	36320	4.67	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
9946	22985	36578	3.54	1.0E-120	BF306541.1	EST_HUMAN	601888966F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122878 5'
9962	23001	36597	6.7	1.0E-120	AU133205.1	EST_HUMAN	AU133205 NT2RP4 Homo sapiens cDNA clone NT25P4001541 5'
9979	23018	36612	1.02	1.0E-120	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10096	23134		0.55	1.0E-120	AB04151.1	EST_HUMAN	CM-BT043-060289-075 BT043 Homo sapiens cDNA
10281	23316	36918	3.4	1.0E-120	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
11391	24452	38118	8.66	1.0E-120	BE296387.1	EST_HUMAN	601176727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632015 5'
11625	24705	38397	2.12	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3847281 5'
11625	24705	38398	2.12	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3847281 5'
12657	25436	32049	1.42	1.0E-120	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0390), mRNA
75	13311	26337	0.62	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
369	13595	26631	1.35	1.0E-121	AU194963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
742	16020	26964	1.31	1.0E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5468	18668	31645	15.48	1.0E-119	M88914.1	NT	Human neurofibromin (NF1) gene, complete cds
5470	18670	31650	3.28	1.0E-119	BE593121.1	EST_HUMAN	RC1-NN0073-250800-018-g06 NN0073 Homo sapiens cDNA
5550	18747	31782	1.81	1.0E-119	AV693731.1	EST_HUMAN	AV693731 GKC Homo sapiens cDNA clone GKCDH603 5'
5707	18900	32194	0.86	1.0E-119	AL134503.1	EST_HUMAN	DKFZp762M0710.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
5707	18900	32195	0.86	1.0E-119	AL134503.1	EST_HUMAN	DKFZp762M0710.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
6255	19429	32775	6.7	1.0E-119	AI150703.1	EST_HUMAN	cb77c09.x1 Soares fetal heart NbhH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02835 KERATIN, TYPE I CYTOSKELETAL 10
6414	19583	32944	0.71	1.0E-119	AF315683.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6414	19583	32945	0.71	1.0E-119	AF315683.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6461	19628	32989	1.22	1.0E-119	AI476732.1	EST_HUMAN	Im23f10.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157451 3'
6589	19750	33133	2.39	1.0E-119	X06282.1	NT	Human c-fos/pro proto-oncogene
6601	19761	33149	4.01	1.0E-119	AW974193.1	EST_HUMAN	EST396296 MAGC resequences, MAGM Homo sapiens cDNA
7688	20840	34116	0.83	1.0E-119	BE5615150.1	EST_HUMAN	601592005F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946081 5'
8862	21941	35476	0.93	1.0E-119	BE5615150.1	EST_HUMAN	601280564F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622526 5'
9957	22866	36592	0.46	1.0E-119	11645921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5) mRNA
10111	23149	36750	0.96	1.0E-119	11036643	NT	Homo sapiens KIAA0477 gene product (KIAA0477), mRNA
10311	23346	36952	0.61	1.0E-119	AI149796.1	EST_HUMAN	qf43a11.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1752764 3' similar to TR:Q13458
10452	23487	37095	2.29	1.0E-119	AA465124.1	EST_HUMAN	Q13458 GUANINE NUCLEOTIDE EXCHANGE FACTOR PROTEIN TRIO. ;
10722	23755	37361	1.13	1.0E-119	AJ297701.1	NT	aa32105.r1 NOI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814977 5'
10766	23799	37420	0.77	1.0E-119	11425837	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 18-17
10766	23799	37421	0.77	1.0E-119	11425837	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10844	23877	37497	0.59	1.0E-119	BE561967.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10849	23882	37502	0.73	1.0E-119	AB032261.1	NT	601347190F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687887 5'
11308	24373	38015	1.58	1.0E-119	AJ297701.1	NT	Homo sapiens Scl mRNA for stearoyl-CoA desaturase, complete cds
11308	24373	38016	1.58	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 18-17
11479	24538		6.62	1.0E-119	BF569571.1	EST_HUMAN	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 18-17
12490	26098		5.48	1.0E-119	AW847519.1	EST_HUMAN	602186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310833 5'
12845	25882		3.03	1.0E-119	X89211.1	NT	RC3-CT0212-240959-011-f03 CT0212 Homo sapiens cDNA
247	13468	26500	0.68	1.0E-120	AB018301.1	NT	H. sapiens DNA for endogenous retroviral like element
312	13528	26561	0.97	1.0E-120	4507334	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
1066	14232	27290	2.74	1.0E-120	AF248540.1	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1066	14232	27291	2.74	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1456	14609	27689	3.26	1.0E-120	N44873.1	EST_HUMAN	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
							yy40g12.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:273766 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7246	20329	33775	1	1.0E-118	AL043761.1	EST_HUMAN	DKFZp434O0127_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434O0127 5'
7776	20833	34324	4.7	1.0E-118	11491050	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
7760	20846	34339	0.72	1.0E-118	L46590.1	NT	Homo sapiens very long chain acyl-CoA dehydrogenase gene, exons 1-20, complete cds
8159	21241	34761	1.95	1.0E-118	BE787223.1	EST_HUMAN	601469159F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:3872247 5'
8577	21658	35198	7	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
8577	21658	35199	7	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
8583	21664	35204	1.1	1.0E-118	AA443024.1	EST_HUMAN	z88407.r1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8583	21664	35205	1.1	1.0E-118	AA443024.1	EST_HUMAN	z88407.r1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8873	21952	35498	0.94	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8873	21952	35489	0.94	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8916	21997	35536	1.94	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8916	21997	35537	1.94	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9236	22313	35855	5.15	1.0E-118	BE263134.1	EST_HUMAN	601144863F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502 5'
9256	22343	35894	0.55	1.0E-118	AL048474.2	EST_HUMAN	DKFZp586K1824_r1 586 (synonym: hufet1) Homo sapiens cDNA clone DKFZp586K1824
9792	22832	36411	1.07	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
10541	23576	37184	1.23	1.0E-118	BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10541	23576	37185	1.23	1.0E-118	BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10586	23621	37228	1.75	1.0E-118	BF195407.1	EST_HUMAN	7n17e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3564785 3' similar to SW_ZP3A_HUMAN
10752	23785	37399	0.59	1.0E-118	AW296351.1	EST_HUMAN	P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR ; UIH-BW0-aip-a-07-0-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729772 3'
11555	24610	38290	3.75	1.0E-118	AA315007.1	EST_HUMAN	EST188814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light chain 1, cytoplasmic
11855	24843	38539	2.92	1.0E-118	BE908876.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11855	24843	38540	2.62	1.0E-118	BE908876.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
12071	25052	38761	1.81	1.0E-118	BE218235.1	EST_HUMAN	h36a06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176474 3' similar to TR-Q9Z2H4
776	13956	27007	2.46	1.0E-119	AF170492.1	NT	Q9Z2H4 G PROTEIN-COUPLED RECEPTOR LGR4. ; Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
1082	16029	27284	0.93	1.0E-119	7705607	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA
1987	15129	28232	2.96	1.0E-119	AB023147.1	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3171	16346	29353	1.01	1.0E-119	8922205	NT	Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
3312	18485		2.17	1.0E-119	AA816760.1	EST_HUMAN	on10b05.s1 NCI_CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1556241 3' similar to WP.E04F6.2 CE01214 ;
4053	17219	30227	1.22	1.0E-119	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5453	18953	31632	3.96	1.0E-119	AU133399.1	EST_HUMAN	AU133399 NT2RP4 Homo sapiens cDNA clone NT2RP4001991 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2142	15278	28401	1.13	1.0E-115	BE745489.1	EST_HUMAN	601579338F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2150	15286	28411	1.1	1.0E-115	AB007902.1	NT	Homo sapiens KIAA0442 mRNA, partial cds
2374	15505	28631	1.11	1.0E-115	AF231124.1	NT	Homo sapiens testican-1 mRNA, complete cds
2372	15090		1.03	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-150-b08 UM0094 Homo sapiens cDNA
3184	13359	29365	2.88	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3184	13359	29366	2.88	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3561	16726	29742	1.8	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4153	17305	30299	4.2	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4521	17680	30647	2.49	1.0E-115		NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4557	17695	30874	4.28	1.0E-115	6912859	NT	Homo sapiens EphA4 (EPHA4) mRNA
4797	17932	30918	2.86	1.0E-115	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4797	17932	30919	2.86	1.0E-115	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
5028	18156	31132	2.89	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5028	18155	31133	2.89	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5044	18172	31149	1.01	1.0E-115	Y19215.1	NT	Homo sapiens putative pshHbc pseudogene for hair keratin, exons 1 to 9
5304	18421	31391	1.23	1.0E-115	4504658	NT	Homo sapiens Interleukin 1 receptor, type I (IL1R1) mRNA
5347	18460	31425	0.92	1.0E-115	AB018311.1	NT	Homo sapiens mRNA for KIAA0788 protein, partial cds
5463	18683	31642	2.8	1.0E-115	AW070335.1	EST_HUMAN	EST382416 IMAGE resequences, MAGK Homo sapiens cDNA
5540	18737	31754	0.97	1.0E-115	BF665387.1	EST_HUMAN	602119346F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4276738 5'
5659	18853	32139	1.74	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5659	18853	32137	1.74	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5908	18898	32304	1.15	1.0E-115	AI928799.1	EST_HUMAN	au84g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb.L07807
5908	18898						DYNAMIN-1 (HUMAN);
5908	18898	32305	1.15	1.0E-115	AI928799.1	EST_HUMAN	au84g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb.L07807
6391	19560	32919	0.88	1.0E-115	11426786	NT	DYNAMIN-1 (HUMAN);
6391	19560	32920	0.88	1.0E-115	11426786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6525	19690	33084	9.49	1.0E-115	11426038	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63436), mRNA
6558	19817	33204	1.68	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product, Helicase (KIAA0054), mRNA
6558	19817	33205	1.68	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product, Helicase (KIAA0054), mRNA
7074	20127	33543	0.75	1.0E-115	T86774.1	EST_HUMAN	ydb5b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115095 5' similar to
7428	20505	33975	1.24	1.0E-115	AI076598.1	EST_HUMAN	SP'DPOG_YEAST P15801 DNA POLYMERASE GAMMA ;
7428	20505	33976	1.24	1.0E-115	AI076598.1	EST_HUMAN	oz31a06.x1 Soares_total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1676914 3'
							oz31a06.x1 Soares_total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1676914 3'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9384	22459	36022	0.87	1.0E-114	BF109832.1	EST_HUMAN	7189g12.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3528847 3' similar to TR:Q9JHN6 Q9JHN6 TRANSMEMBRANE PROTEIN 2 ;
9614	22669		1.3	1.0E-114	AW327455.1	EST_HUMAN	dq0305.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 5'
9662	21104	34621	2.67	1.0E-114	AF07754.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
9748	22812		1.36	1.0E-114	M13536.1	NT	Human ceruloplasmin mRNA
10343	23378	36989	1.02	1.0E-114	BE870004.1	EST_HUMAN	6071449752F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853500 5'
10364	23399	37010	1.11	1.0E-114	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10762	23795	37415	1.18	1.0E-114	BE171984.1	EST_HUMAN	MRO-HT0559-250200-002-007 HT0559 Homo sapiens cDNA
11027	24106						ba73g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906086 5' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
11466	24525	38197	4.31	1.0E-114	BE302986.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
11466	24525	38198	8.11	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
11842	24631	38522	6.28	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
11842	24631	38523	6.28	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
12643	26187		4.63	1.0E-114	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12936	25616	31975	2.75	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
12936	25616	31976	2.75	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
24	13262	26264	3.06	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
132	13358	26391	1.09	1.0E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
136	13362		18.42	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
303	13519	26562	2.02	1.0E-115	AW804759.1	EST_HUMAN	QV4-JM0094-300300-156-508 UM0094 Homo sapiens cDNA
549	13742	26766					q106f01.x1 NCL CGAP GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536
549	13742	26767	1.68	1.0E-115	AI339206.1	EST_HUMAN	TTF-I INTERACTING PEPTIDE 5 ;
809	13988	27041	3	1.0E-115	AI339206.1	EST_HUMAN	q106f01.x1 NCL CGAP GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536
809	13988	27042	3	1.0E-115	5174702	NT	TTF-I INTERACTING PEPTIDE 5 ;
811	13990	27044	15.24	1.0E-115	4503794	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
1590	14742	27823	1.15	1.0E-115	AF229180.1	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
1590	14742	27824	1.15	1.0E-115	AF229180.1	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1888	15032	28140	1.31	1.0E-115	U78027.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
2142	15278	28400	1.13	1.0E-115	BE745469.1	EST_HUMAN	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
							Homo sapiens Brubn's lysine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
							601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928632 5'

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
59	13297	26315	0.75	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
59	13297	26316	0.75	1.0E-114	Y17161.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
662	13948	26876	7.46	1.0E-114	T70551.1	EST_HUMAN	yt15c01.a1 Sacchar fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element
1098	14261	27318	2.54	1.0E-114	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1341	14497	27569	4.05	1.0E-114	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1673	14825	27909	1.9	1.0E-114	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
1706	14858	27945	5.08	1.0E-114	6878073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2145	15281	28408	2.52	1.0E-114	BE171684.1	EST_HUMAN	MRO-HT0559-250200-002-d07 HT0559 Homo sapiens cDNA
2330	15462	28595	0.99	1.0E-114	AB002374.1	NT	Human mRNA for KIAA0376 gene, partial cds
2865	13293	26290	0.6	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2865	13293	26291	0.6	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3201	16376	29386	2.6	1.0E-114	X04068.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3240	16414	29429	1.03	1.0E-114	BF206374.1	EST_HUMAN	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
4124	17278	30275	3.27	1.0E-114	AF149773.1	NT	601869932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
4510	17649	30637	0.7	1.0E-114	J03171.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
5282	18401	31370	1.1	1.0E-114	AW294203.1	EST_HUMAN	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
5516	16714	31727	1.68	1.0E-114	4506880	NT	UIH-B12-ehc-d01-Q-U1a1 NC1 CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726424 3'
5516	16714	31728	1.68	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5712	18905	32200	0.9	1.0E-114	9257201	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
7224	20088		0.71	1.0E-114	AB041533.1	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1), transcript variant 2, mRNA
7388	20466	33831	1.09	1.0E-114	AU134187.1	EST_HUMAN	Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds
7388	20466	33932	1.09	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7434	20511	33983	8.2	1.0E-114	Y18000.1	NT	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7434	20511	33984	8.2	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
8075	21157	34675	1.94	1.0E-114	4557600	NT	Homo sapiens NF2 gene
8360	21441	34963	1.85	1.0E-114	AI036199.1	EST_HUMAN	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
8360	21441	34964	1.85	1.0E-114	AI036199.1	EST_HUMAN	qy68d06.x1 NC1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
8898	21977	35516	2.99	1.0E-114	U63041.1	NT	qy68d06.x1 NC1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
8866	22045	35589	5.81	1.0E-114	AB011133.1	NT	Human neural cell adhesion molecule CD56 mRNA, complete cds
8866	22045	35590	5.81	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
8866	22045	35590	5.81	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1993	15994	28240	1.63	1.0E-113	AF240775.1	NT	Homo sapiens eIF-4E-transporter mRNA, complete cds
2161	15297	28422	1.49	1.0E-113	BF515218.1	EST_HUMAN	U1-H-BW1-ant-f-03-0-U1.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876 3'
3200	16375	29385	2.06	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5178	18300	31263	36.66	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5178	18300	31264	36.66	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5359	25930		2.4	1.0E-113	BE780858.1	EST_HUMAN	601469465F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872536 5'
5610	18803	31870	6.37	1.0E-113	AU127214.1	EST_HUMAN	AU127214 NT25P2 Homo sapiens cDNA clone NT2RP2000807 5'
6045	19228	32552	3.54	1.0E-113	AU140291.1	EST_HUMAN	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'
6072	19264	32583	1.02	1.0E-113	AF016535.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6195	19371	32722	2.57	1.0E-113	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
6285	19458	32809	0.8	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6285	19458	32810	0.8	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6446	19613	32976	0.68	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
6446	19613	32977	0.68	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7474	20549	34021	0.63	1.0E-113	BE262161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
7474	20549	34022	0.63	1.0E-113	BE262161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
9093	22172	35717	0.5	1.0E-113	8922819	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
9296	22372	35921	2.91	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
9296	22372	35922	2.91	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
9601	22656	36674	0.62	1.0E-113	BE772987.1	EST_HUMAN	RC1-F10134-280600-021-d02 F10134 Homo sapiens cDNA
10036	23074	36674	1.27	1.0E-113	11429367	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
10256	23291	36888	1.01	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10256	23291	36889	1.01	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10842	23875	37495	0.47	1.0E-113	AW500517.1	EST_HUMAN	U1-HF-BNO-aq-b-10-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077322 5'
11385	24446	38107	1.89	1.0E-113	AW500519.1	EST_HUMAN	U1-HF-BNO-aq-b-12-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077326 5'
11396	24457	38119	5.42	1.0E-113	AW630291.1	EST_HUMAN	h181a09.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869176 5' similar to TR:O60327 O60327 KIAA0594 PROTEIN ;
11396	24457	38120	5.42	1.0E-113	AW630291.1	EST_HUMAN	h181a09.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869176 5' similar to TR:O60327 O60327 KIAA0594 PROTEIN ;
11540	24996	38272	2.91	1.0E-113	BE282968.1	EST_HUMAN	KIAA0584 PROTEIN ;
59	13297	26314	0.75	1.0E-114	Y17151.2	NT	601105529F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988366 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6773	19928	33323	0.83	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505608 5'
6773	19928	33324	0.83	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505608 5'
6981	20209	33637	1.51	1.0E-112	BF574235.1	EST_HUMAN	602131405F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270921 5'
7305	20387	33847	0.68	1.0E-112	AL043298.1	EST_HUMAN	DKFZp434M0523_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M0523 5'
7491	20566	34037	1.49	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7491	20566	34038	1.46	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8887	21488	34995	1.79	1.0E-112	AU118051.1	EST_HUMAN	AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'
9158	22236	35781	2.64	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
9158	22236	35782	2.64	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
10097	23135	36736	2.97	1.0E-112	BF111413.1	EST_HUMAN	T330g07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to TR:Q9VW35 Q9VW35 CG8743 PROTEIN ;
11017	24086	37735	16.73	1.0E-112	AW683327.1	EST_HUMAN	MIR3-SN0009-100400-106-b12 SN0009 Homo sapiens cDNA
11103	24175	37810	1.31	1.0E-112	T63567.1	EST_HUMAN	Yd56d10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN ;
11103	24175	37811	1.31	1.0E-112	T63567.1	EST_HUMAN	Yd56d10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN ;
11191	24260	37896	3.14	1.0E-112	AJ249900.1	NT	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
11359	24421	38077	2.24	1.0E-112	BE280479.1	EST_HUMAN	601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138989 5'
11428	24489	38153	2.28	1.0E-112	A1792603.1	EST_HUMAN	qk24c08.y6 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
11428	24489	38154	2.28	1.0E-112	A1792603.1	EST_HUMAN	qk24c08.y6 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
11460	24519	38188	4.78	1.0E-112	AW377670.1	EST_HUMAN	PMO-CT0237-1410399-001-H02 CT0237 Homo sapiens cDNA
12096	25076	38783	1.66	1.0E-112	A1792603.1	EST_HUMAN	qk24c08.y6 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
12096	25076	38784	1.66	1.0E-112	A1792603.1	EST_HUMAN	qk24c08.y6 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
12727	25484	26967	1.31	1.0E-112	AF106856.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
761	13942	26967	6.82	1.0E-113	A1365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
761	13942	26968	6.82	1.0E-113	A1365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
965	27199	27199	2.93	1.0E-113	M11955.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1572	14725	27805	3.23	1.0E-113	A1365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10355	23390	37000	1.56	1.0E-111	AA504160.1	EST_HUMAN	aa58902.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825170 3' similar to gb:U09235
10383	23418		1.04	1.0E-111	D10083.1	NT	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
10479	23514	37127	5.58	1.0E-111	AA131248.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
10955	24074	37707	1.34	1.0E-111	AW298467.1	EST_HUMAN	Z31801.r1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:503545 5'
11299	24365	38008	3.29	1.0E-111	U68159.1	NT	UI-H-BW0-qlq-07-0-J1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2730276 3'
12167	25130	38828	4.07	1.0E-111	114717901	NT	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
12741	25492	32028	4.72	1.0E-111	AV708482.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
12881	25888	31855	4.82	1.0E-111	W22562.1	EST_HUMAN	AV708482 ADC Homo sapiens cDNA clone ADCAO808 5'
13041	18504	31539	1.27	1.0E-111	AB033556.1	NT	72C9 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
625	13808	26829	2.71	1.0E-112	4501864	NT	Homo sapiens mRNA for neurixin 1-alpha protein, complete cds
625	13810	26832	4.84	1.0E-112	U29103.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
625	13810	26832	4.84	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
649	13834	26860	1.82	1.0E-112	BF509039.1	EST_HUMAN	UI-H-B14-aot-g-04-0-J1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
649	13834	26861	1.82	1.0E-112	BF509039.1	EST_HUMAN	UI-H-B14-aot-g-04-0-J1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1026	14197	27255	33.06	1.0E-112	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1087	14253	27308	1.49	1.0E-112	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
1718	14868	27958	7.1	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1718	14868	27959	7.1	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1863	15009	28115	1.11	1.0E-112	AF248540.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
2577	15703	28823	2.83	1.0E-112	BE86859.1	EST_HUMAN	601442674F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846858 5'
3147	16323		0.76	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3444	16612	29630	0.61	1.0E-112	A1826511.1	EST_HUMAN	wk45b12.x1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2418335 3' similar to gb:M81650_ma1
3960	17147	30153	0.63	1.0E-112	BE076073.1	EST_HUMAN	SEMNOCGELIN 1 PROTEIN PRECURSOR (HUMAN);
4726	17861	30843	0.68	1.0E-112	4504116	NT	MR2-BT0590-090300-113-09 BT0590 Homo sapiens cDNA
4875	18007	30990	5.87	1.0E-112	AB037832.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4875	18007	30991	5.87	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5784	18976	32282	38.7	1.0E-112	N46046.1	EST_HUMAN	Homo sapiens mRNA for KIAA1411 protein, partial cds
6201	19376	32727	1.33	1.0E-112	AF149773.1	NT	W35d07.r1 Soares_melanocyte 2bHM Homo sapiens cDNA clone IMAGE:273229 5'
6273	19447	32785	0.66	1.0E-112	AW502437.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6273	19447	32786	0.66	1.0E-112	AW502437.1	EST_HUMAN	UI-HF-BR0p-qls-g-06-0-J1.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6379	19548	32904	0.93	1.0E-112	BE741666.1	EST_HUMAN	UI-HF-BR0p-qls-g-06-0-J1.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076658 5'
6588	19749	33132	0.7	1.0E-112	BF672815.1	EST_HUMAN	60169471F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948557 5'
							602192649F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293420 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
201	13424	26455	1.64	1.0E-111	4788807	NT	Homo sapiens res GTPase activating protein-like (NGAP) mRNA
753	13934		1.99	1.0E-111	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
762	13943	26989	4.13	1.0E-111	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
950	14123	27185	2.5	1.0E-111	M25142.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
4286	17431	30419	1.15	1.0E-111		NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
4449	17589	30570	4.59	1.0E-111	K02268.1	NT	Human enkephalin B (enkeB) gene, exon 4 and 3' flank and complete cds
5593	18798	31835	0.75	1.0E-111	AA151017.1	EST_HUMAN	247007.1 Soares_pregnant_uterus_NihHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5593	18788	31836	0.75	1.0E-111	AA151017.1	EST_HUMAN	247007.1 Soares_pregnant_uterus_NihHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5749	18941	32242	0.88	1.0E-111	BE867909.1	EST_HUMAN	601443690F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847655 5'
5802	19052	32359	0.86	1.0E-111	U19989.1	NT	Human two-handed zinc finger protein ZEB mRNA, partial cds
6156	19332	32678	2.09	1.0E-111	A1344679.1	EST_HUMAN	qp09g12.x1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gb:M28993 RAS-RELATED PROTEIN RAL-A (HUMAN);
6818	19971	33379	0.96	1.0E-111	AL040762.1	EST_HUMAN	DKFZP434C1815.1 434 (synonym: hlae3) Homo sapiens cDNA clone DKFZP434C1815 5'
6945	20258	33697	1.31	1.0E-111	AW294648.1	EST_HUMAN	U1-H-BW0-ai1-d-03-0-U1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729825 3'
7605	20675	34149	3.04	1.0E-111	BF366228.1	EST_HUMAN	IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA
7704	20769	34254	0.7	1.0E-111	A1761228.1	EST_HUMAN	wf68d01.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398465 3' similar to gb:J04813 CYTOCHROME P450 IIA5 (HUMAN);
7791	20847	34340	0.83	1.0E-111	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8286	21368	34988	0.8	1.0E-111	AA278988.1	EST_HUMAN	zs79g03.r1 NCL CGAP_GC81 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410
8286	21368	34889	0.8	1.0E-111	AA278988.1	EST_HUMAN	G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR, ;
8383	21464	34989	0.83	1.0E-111	11431896	NT	G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR, ;
8435	21616	35047	3.58	1.0E-111	U66533.1	NT	Homo sapiens protein x 0001 (LOC51185), mRNA
8878	21957	35492	0.96	1.0E-111	AK024453.1	NT	Human beta4-integrin (ITGB4) gene, exon 13
8975	22054	35597	0.64	1.0E-111	BF214902.1	EST_HUMAN	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
9008	22087		8.43	1.0E-111	X17033.1	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
9085	22164	35708	15.93	1.0E-111	X17033.1	NT	601847132F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078303 5'
9085	22164	35709	15.93	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
9289	22385	35914	3.37	1.0E-111	AF091395.1	NT	Homo sapiens Trlo isoform mRNA, complete cds
9518	22583	36152	0.54	1.0E-111	BF333210.1	EST_HUMAN	Homo sapiens QV2-B10817-270900-398-e06 B10817 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4758	17893	30872	2.04	1.0E-110	AI017213.1	EST_HUMAN	ou32b10.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627963 3' similar to SW:N121_RAT P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
4777	17912	30897	3.01	1.0E-110	AU117812.1	EST_HUMAN	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
5088	18216		2.28	1.0E-110	7882441	NT	Homo sapiens KIAA11002 protein (KIAA11002), mRNA
5409	18611	31583	2.23	1.0E-110	BE290406.1	EST_HUMAN	60111870F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029539 5'
5843	19033	32339	0.78	1.0E-110	BE821069.1	EST_HUMAN	60149367F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895795 5'
5860	19050	32388	8.61	1.0E-110	11418323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5860	19050	32357	8.61	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6858	25935	33421	5.43	1.0E-110	M55112.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
7179	20311	33754	0.59	1.0E-110	BE251406.1	EST_HUMAN	601108388F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350277 5'
7251	20334	33782	0.85	1.0E-110	U08898.1	NT	Human GS2 gene, exon 2
7251	20334	33783	0.85	1.0E-110	U08888.1	NT	Human GS2 gene, exon 2
7477	20552	34025	0.78	1.0E-110	AI580289.1	EST_HUMAN	t12408.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167407 3' similar to SW:ETV1_HUMAN P50549 ETS TRANSLOCATION VARIANT 1 ;
7583	20655	34131	16.19	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
7583	20655	34132	16.19	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
7613	20683	34159	2.87	1.0E-110	AB020675.1	NT	Homo sapiens mRNA for KIAA0898 protein, partial cds
7743	20804	34293	0.86	1.0E-110	AU137923.1	EST_HUMAN	AU137923 PLACE1 Homo sapiens cDNA clone PLACE1007511 5'
9536	22801	36174	1.09	1.0E-110	BE302594.1	EST_HUMAN	ba68f01.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905551 5' similar to TR:O77258 O77258 EG-114D9.2 PROTEIN. ;
9777	22817	36395	2.46	1.0E-110	AW838394.1	EST_HUMAN	QV2-LT0053-020400-119-e04 LT0053 Homo sapiens cDNA
10529	23564	37171	3.38	1.0E-110	11432732	NT	Homo sapiens galactokinase 2 (GALK2), mRNA
10986	24065	37700	3.2	1.0E-110	Y12337.1	NT	Homo sapiens mRNA for myotonic dystrophy protein kinase like protein
11209	24278	37916	3.64	1.0E-110	BE734357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11209	24278	37917	3.64	1.0E-110	BE734357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11608	24661	38347	1.89	1.0E-110	M10051.1	NT	Human insulin receptor mRNA, complete cds
11728	23914	37539	1.7	1.0E-110	AA446529.1	EST_HUMAN	zw67g02.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:781298 5' similar to TR:G1145816 G1145816 FKBP54 ;
12211	25164		2.47	1.0E-110	BE897218.1	EST_HUMAN	601439784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5'
12341	25246		2.86	1.0E-110	AW062258.1	EST_HUMAN	IL0-BT0163-040899-094-g10 BT0163 Homo sapiens cDNA
12594	25400		2.98	1.0E-110	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12746	26113		6.01	1.0E-110	BF364546.1	EST_HUMAN	PM3-NN1082-140900-009-f12 NN1082 Homo sapiens cDNA
13071	15286		1.16	1.0E-110	BF508898.1	EST_HUMAN	UI-H-BI4-aos-b-05-0-U1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
179	13402		14.92	1.0E-111	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9550	22615	36184	0.64	1.0E-109	BE397068.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
9550	22615	36185	0.64	1.0E-109	BE397068.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
9685	22734	36304	1.37	1.0E-109	F06804.1	EST_HUMAN	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-1ec12
11013	24092	37730	1.8	1.0E-109	BE540909.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449589 5'
11013	24092	37731	1.8	1.0E-109	BE540909.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449589 5'
11046	24123	37757	19.68	1.0E-109	BF694831.1	EST_HUMAN	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5'
11387	24448	38109	1.57	1.0E-109	AU121370.1	EST_HUMAN	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002690 5'
11651	24730	38422	2.18	1.0E-109	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
11693	24691	38382	4.5	1.0E-109	W18510.1	EST_HUMAN	z508b12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to PIR:S43969 S43969 p54-beta stress-activated protein kinase - rat;
11884	24872	38569	1.64	1.0E-109	BE045560.1	EST_HUMAN	h23105.x1 NCI CGAP_L124 Homo sapiens cDNA clone IMAGE:2955869 3' similar to TR:Q9Z124 Q9Z124
11884	24934	38636	1.5	1.0E-109	AL110824.1	EST_HUMAN	YGR163W MRNA HOMOLOGUE, COMPLETE CDS. ;
11884	24969	38673	1.31	1.0E-109	11418618	NT	DKFZp7611124_r1781 (synonym: ham2) Homo sapiens cDNA clone DKFZp7611124 5'
12126	25106	38810	2.26	1.0E-109	AB007892.1	NT	Homo sapiens single-minded (Drosophila) homolog 1 (SIM1), mRNA
12397	15457	28589	2.32	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
12636	15457	28589	3.2	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
12762	25506	32036	8.36	1.0E-109	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3	13242	26242	1.4	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
38	13276	26281	3.96	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
38	13276	26282	3.96	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
112	13242	26242	1.83	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
305	13521	26555	1.31	1.0E-110	D87291.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
540	13733	28757	1.04	1.0E-110	U84550.1	NT	Human dystrobrevin (DTN) gene, exon 20
1207	14369	27429	0.89	1.0E-110	5031620	NT	Homo sapiens calcitonin receptor-like (CALCRL) mRNA
1308	14464	27532	1.02	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1973	15116	28217	1.51	1.0E-110	BE379477.1	EST_HUMAN	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609663 5'
2118	15256		1.68	1.0E-110	BF508896.1	EST_HUMAN	UIH-B14-eos-b-05-D-J1.st1NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
2803	16081		7.19	1.0E-110	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3156	16331		1.48	1.0E-110	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
3264	16438	29457	2.68	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3264	16438	29458	2.66	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
4320	17463	30449	1.09	1.0E-110	M15918.1	NT	Human autoimmune antigen small nuclear ribonucleoprotein E pseudogene

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2688	15808	28925	2.88	1.0E-109	4504208	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
3125	16301	28314	3.37	1.0E-109	N95190.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3475	16642	29681	2.08	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA
3475	16642	29682	2.08	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA
3608	16770	29785	1.1	1.0E-109	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3945	17104		1.31	1.0E-109	BE146144.1	EST_HUMAN	MRO-HT0209-110400-108-a04 HT0209 Homo sapiens cDNA
4264	17409	30395	4.35	1.0E-109	AI655417.1	EST_HUMAN	ts98608.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP.F53A2.8 OE16100
4524	17663	30650	2.57	1.0E-109	4504208	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
4722	17857	30839	1.7	1.0E-109	7882083	NT	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
5165	18287	31252	0.72	1.0E-109	BE293673.1	EST_HUMAN	601189922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2856636 5'
5165	18287	31253	0.72	1.0E-109	BE293673.1	EST_HUMAN	601189922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2856636 5'
5361	18584	31480	0.87	1.0E-109	AU137282.1	EST_HUMAN	AU137282 PLACE1 Homo sapiens cDNA clone PLACE1006159 5'
5374	18571	31445	0.92	1.0E-109	BF673718.1	EST_HUMAN	602136446F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272922 5'
5428	18628	31604	2.92	1.0E-109	5174622	NT	Homo sapiens placental protein 11 (serine proteinase) (PT1) mRNA
5724	18917		1.23	1.0E-109	BE179356.1	EST_HUMAN	RC1-HT0615-200400-022-d04 HT0615 Homo sapiens cDNA
6050	25817	32556	1.23	1.0E-109	BF379688.1	EST_HUMAN	CM1-UT0035-060900-399-H07 UT0038 Homo sapiens cDNA
6119	18917		1.41	1.0E-109	BE179356.1	EST_HUMAN	RC1-HT0615-200400-022-d04 HT0615 Homo sapiens cDNA
6721	19878	33269	0.85	1.0E-109	AI221385.1	EST_HUMAN	qg86108.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842111 3'
6907	20222	33651	0.69	1.0E-109	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
6907	20222	33652	0.69	1.0E-109	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
7389	20467	33953	0.67	1.0E-109	AB046811.1	NT	Homo sapiens mRNA for KIAA1561 protein, perital cds
7738	20799	34288	3.75	1.0E-109	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7740	20801	34290	4.91	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
7740	20801	34291	4.91	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8366	21447	34970	1.35	1.0E-109	AL049784.1	NT	Novel human gene mapping to chromosome 13
8480	21591	35096	1.39	1.0E-109	AW749130.1	EST_HUMAN	PMO-BT0340-091299-002-e05 BT0340 Homo sapiens cDNA
8857	21636		2.84	1.0E-109	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
8932	22011	35549	4.36	1.0E-109	BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
8932	22011	35550	4.36	1.0E-109	BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
9177	22255	35797	0.57	1.0E-109	BE145672.1	EST_HUMAN	IL0-HT0205-071199-142-g01 HT0205 Homo sapiens cDNA
9439	22513	36077	1.05	1.0E-109	HB4890.1	EST_HUMAN	ys90g08.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP:A53491 A53491 BUMETANIDE-SENSITIVE NA-K-C1 COTRANSPORTER - SPINX;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10904	21037	34549	2.09	1.0E-108	BE535227.1	EST_HUMAN	601058769F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445361 5'
11066	18501	31537	2.67	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Gq11-associated microtubule-binding protein (GMAP-210)
11319	24382	38027	1.35	1.0E-108	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11549	24605	38283	3.46	1.0E-108	AW966185.1	EST_HUMAN	EST1378258 MAGI resequences, MAGI Homo sapiens cDNA
11605	24658	38343	1.71	1.0E-108	AV708790.1	EST_HUMAN	AV708790 ADG Homo sapiens cDNA clone ADCAEE03 5'
11605	24658	38344	1.71	1.0E-108	AV708790.1	EST_HUMAN	AV708790 ADG Homo sapiens cDNA clone ADCAEE03 5'
11652	24731		2.77	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
11688	15538	28665	2.99	1.0E-108	AI686040.1	EST_HUMAN	tt91e10.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
11698	15538	28666	2.99	1.0E-108	AI686040.1	EST_HUMAN	PROTEOGLYCAN II PRECURSOR (HUMAN);
11712	24752	38446	1.72	1.0E-108	D63539.1	NT	PROTEOGLYCAN II PRECURSOR (HUMAN);
12499	25344	32064	4.15	1.0E-108	AK024447.1	NT	Homo sapiens COL4A3 gene for a6(V) collagen, exon 23
12940	25618		5.09	1.0E-108	BF346336.1	EST_HUMAN	Homo sapiens mRNA for FLJ00037 protein, partial cds
43	13281	26287	1.01	1.0E-109	AW803116.1	EST_HUMAN	602018571F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154297 5'
66	13303	26326	1.17	1.0E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds
225	13447	26475	3.34	1.0E-109	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
235	13456	26482	2.77	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
479	13674	26705	2.28	1.0E-109	4507712	NT	Homo sapiens letrictopeptide repeat domain 2 (TTC2) mRNA
611	13800	26820	14.77	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
611	13800	26821	14.77	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1037	14205	27262	1.62	1.0E-109	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1229	14389	27451	8.5	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1230	14389	27451	6.38	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1573	14726	27806	0.89	1.0E-109	BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2969636 5'
1573	14726	27807	0.99	1.0E-109	BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2969636 5'
1923	15068	28170	2.3	1.0E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2314	15446	28580	5.46	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2326	15457	28589	3.65	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2687	15907	28923	19.35	1.0E-109	AI022328.1	EST_HUMAN	ow95a01.x1 Soares fetal liver spleen _INFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN.;
2687	15907	28924	19.35	1.0E-109	AI022328.1	EST_HUMAN	ow95a01.x1 Soares fetal liver spleen _INFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN.;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4273	17418	30406	1.57	1.0E-108	AW664438.1	EST_HUMAN	h12a11.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE
4647	17783	30765	2.62	1.0E-108	U72961.1	NT	P55194 SH3-BINDING PROTEIN 3BP-1;
4647	17783	30766	2.62	1.0E-108	U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4927	18057	31040	3.37	1.0E-108	7661979	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
5037	18165	31141	0.63	1.0E-108	AW504799.1	EST_HUMAN	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5063	18191	31166	3.18	1.0E-108	AJ008005.1	NT	U1-HF-BNO-ah-e-04-U1,r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080168 5'
5598	18791	31839	1.24	1.0E-108	AW384094.1	EST_HUMAN	Homo sapiens PSN1 gene, alternative transcript
5644	18838	31816	2.56	1.0E-108	BE869016.1	EST_HUMAN	RCO-H10372-241199-031-c03 HT0372 Homo sapiens cDNA
5644	18838	31917	2.56	1.0E-108	BE869016.1	EST_HUMAN	601444922F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3848980 5'
6049	19232		0.66	1.0E-108	AF012623.1	NT	601444922F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3848980 5'
6125	19304	32644	0.74	1.0E-108	BF334851.1	EST_HUMAN	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 20
6267	19441	32789	6.14	1.0E-108	AF264717.1	NT	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6267	19441	32780	6.14	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6392	19581	32921	1.22	1.0E-108	AJ133269.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6489	19304	32644	1.09	1.0E-108	BF334851.1	EST_HUMAN	Homo sapiens cavedin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6753	19909	33302	0.64	1.0E-108	AF016706.1	NT	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6753	19909	33303	0.64	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7308	20390	33850	4.52	1.0E-108	11431857	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7597	20667	34143	2.12	1.0E-108	4758333	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), mRNA
7646	20715	34193	1.32	1.0E-108	BE252607.1	EST_HUMAN	Homo sapiens delta-6 fatty acid desaturase (FADS6) mRNA
7674	20739	34218	0.73	1.0E-108	BF528912.1	EST_HUMAN	601113471F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354084 5'
7674	20739	34219	0.73	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181037 5'
8254	21336		1.72	1.0E-108	AF083500.1	NT	602043384F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181037 5'
8306	21388	34910	0.61	1.0E-108	AF083500.1	EST_HUMAN	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8306	21388	34911	0.61	1.0E-108	AF083500.1	EST_HUMAN	U1-HF-BMO-ads-e-12-0-U1,r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
8247	22324	35869	0.77	1.0E-108	AF203977.1	NT	U1-HF-BMO-ads-e-12-0-U1,r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
9287	22363	35912	0.46	1.0E-108	N44974.1	EST_HUMAN	Homo sapiens ETS-family transcription factor EHF (EHF) mRNA, complete cds
10847	23880	37500	1.08	1.0E-108	11428155	NT	y95h10.r1 Soares melanocyte 2Nbr-IM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR:A45773
							A45773 kelch protein, long form - fruit fly;
							Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H, sapiens) (LOC63446), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3931	17090	30087	4.89	1.0E-107	AF020671.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
5742	18935	32235	0.64	1.0E-107	AW969038.1	EST_HUMAN	EST381115 IMAGE resequences, MAGK Homo sapiens cDNA
5986	19171	32493	2.71	1.0E-107	BE867469.1	EST_HUMAN	601442558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846484 5'
7520	20593	34067	1.33	1.0E-107	AW503913.1	EST_HUMAN	U1-HF-BND-alf-c-08-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
7520	20593	34068	1.33	1.0E-107	AW503913.1	EST_HUMAN	U1-HF-BND-alf-c-08-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
7698	20763	34247	1.36	1.0E-107	AW603978.1	EST_HUMAN	wt58h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384791 3'
7909	20981	34487	0.59	1.0E-107	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9) gene
7909	20981	34488	0.59	1.0E-107	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9) gene
6587	22729	36299	0.99	1.0E-107	AU122469.1	EST_HUMAN	AU122469 MAMMA1 Homo sapiens cDNA clone MAMMA1002433 5'
10889	23973	37604	1.92	1.0E-107	BE168728.1	EST_HUMAN	QV1-HT0516-140300-107-c10 H70516 Homo sapiens cDNA
10944	24026	37682	2.96	1.0E-107	AI392850.1	EST_HUMAN	ig10d06.x1 NCI_CGAP_Q11.1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICD1
11189	24258	37894	1.58	1.0E-107	L49141.1	NT	P05095 ALPHA-ACTININ 3, NON MUSCULAR
11202	24271	37907	2.3	1.0E-107	BF66611.1	EST_HUMAN	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
11803	24659	38341	3.91	1.0E-107	BE540550.1	EST_HUMAN	602123863F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281039 5'
11678	23504	37526	4.29	1.0E-107	11419701	NT	601066681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5'
11876	23904	37527	4.29	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
12322	26100		7.14	1.0E-107	AA001415.1	EST_HUMAN	Homo sapiens HSPC049 protein (HSPC049), mRNA
13211	25780	31920	1.24	1.0E-107	BE798189.1	EST_HUMAN	Homo sapiens HSPC049 protein (HSPC049), mRNA
977	14160	27210	1.72	1.0E-108	BE29042.1	EST_HUMAN	2e45e01.s1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1
1294	14450	27515	2.41	1.0E-108	Y18000.1	NT	THR repetitive element
2140	15278	28398	1.02	1.0E-108	BF026728.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
2407	15538	28665	12.11	1.0E-108	AI688040.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
2407	15538	28666	12.11	1.0E-108	AI688040.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
2496	15926	28746	11.96	1.0E-108	BE206694.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
3025	16201	28224	0.64	1.0E-108	6006979	NT	PROTEOGLYCAN II PRECURSOR (HUMAN);
3430	16598	29814	0.64	1.0E-108	AF032897.1	NT	PROTEOGLYCAN II PRECURSOR (HUMAN);
3430	16598	29815	0.64	1.0E-108	AF032897.1	NT	PROTEOGLYCAN II PRECURSOR (HUMAN);
							b625b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963899 3' similar to gb:X53777 60S
							RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
							Homo sapiens Kruppel-like factor 8 (KLF8) mRNA
							Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
							Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar: (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptör
10497	23532	37141	0.66	1.0E-108	11438432	NT	Homo sapiens multimierin (MMRN), mRNA
10497	23532	37142	0.66	1.0E-108	11438432	NT	Homo sapiens multimierin (MMRN), mRNA
10678	23712	37320	0.66	1.0E-108	AL039886.1	EST_HUMAN	DKFZp434F0712_1 434 (synonym: huc3) Homo sapiens cDNA clone DKFZp434F0712 5'
10807	23840	37484	4.20	1.0E-106	AL163202.2	NT	DKFZp434F0712_1 434 (synonym: huc3) Homo sapiens cDNA clone DKFZp434F0712 5'
11135	24207	37832	4.81	1.0E-106	BF032755.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
11135	24207	37833	4.81	1.0E-108	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
11317	24380	38025	2.06	1.0E-106	J05200.1	NT	601453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
11317	24380	38026	2.06	1.0E-108	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
11694	24692	38383	1.35	1.0E-106	BE257383.1	EST_HUMAN	Human ryanodine receptor mRNA, complete cds
11837	24826	38514	1.89	1.0E-108	BE010882.1	EST_HUMAN	601109219F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349997 5'
11837	24826	38515	1.89	1.0E-106	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
12253	25946	4.3	1.0E-106	AW470405.1	EST_HUMAN	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
12484	25336	32059	1.97	1.0E-106	BE894483.1	EST_HUMAN	f005h11.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961644 5'
12484	25336	32060	1.97	1.0E-108	BE894483.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12717	25477	3.71	1.0E-106	BE969505.1	EST_HUMAN	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
244	13466	4.52	1.0E-107	AJ271736.1	NT	NT	RC1-C10249-090800-024-d05 CT0249 Homo sapiens cDNA
275	13493	1.03	1.0E-107	X60459.1	NT	NT	Homo sapiens Xa pseudocytoskeletal region; segment 1/2
637	13922	1.03	1.0E-107	4828883	NT	NT	Human IFNAR gene for Interferon alpha/beta receptor
647	13832	26868	2.34	1.0E-107	AF155103.1	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM), mRNA
836	14014	27059	1.02	1.0E-107	X60459.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
909	14084	27149	1.38	1.0E-107	X60459.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
991	14163	27223	9.71	1.0E-107	AF154121.1	NT	Human IFNAR gene for Interferon alpha/beta receptor
1307	14463	27531	1.06	1.0E-107	AB032253.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1600	14763	27836	3.81	1.0E-107	BF087405.1	EST_HUMAN	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1791	14940	28033	5.42	1.0E-107	AF136275.1	NT	QV2-HT05-40-120900-358-a05 HT0540 Homo sapiens cDNA
1887	15031	28138	1.52	1.0E-107	AB007922.2	NT	Homo sapiens caldespin Z precursor (C1SZ) gene, exon 3
1887	15031	28139	1.52	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2282	15414	28546	3.77	1.0E-107	U13729.1	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2435	15563	28691	4.03	1.0E-107	AW842451.1	EST_HUMAN	Homo sapiens dipeptidyl peptidase IV (CD26) gene, exon 20
2435	15563	28692	4.03	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3072	16248	29268	6.14	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3072	16248	29269	6.14	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3169	16344	29352	2.9	1.0E-107	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast homolog 2 (SMT3H2), mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6336	19507	32864	0.81	1.0E-108	BE897112.1	EST_HUMAN	601439870F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924841 5'
6526	19507	32864	0.66	1.0E-108	BE897112.1	EST_HUMAN	601439870F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924841 5'
6549	19711	33087	15.91	1.0E-108	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6549	19711	33088	15.91	1.0E-108	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
7528	20601	34075	5.69	1.0E-106	AA663779.1	EST_HUMAN	aa72a07.st Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:989732 3' similar to gb:X65873
7582	20654	34130	4.17	1.0E-108	11429817	NT	KINESIN HEAVY CHAIN (HUMAN)
7672	20738	34216	1.64	1.0E-106	BE292722.1	EST_HUMAN	Homo sapiens XPMC2 protein (LOC57108), mRNA
7787	20843	34335	8.06	1.0E-108	11425503	NT	601105736F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988345 5'
7894	21044	34598	0.6	1.0E-108	AU116850.1	EST_HUMAN	Homo sapiens sorting nexin 11 (SNX11), mRNA
8173	21255	34776	3.62	1.0E-106	BE741408.1	EST_HUMAN	AU116850 HEMBA1 Homo sapiens cDNA clone IMAGE:3948463 5'
8173	21255	34777	3.62	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8388	21449	34972	2.21	1.0E-108	AI523066.1	EST_HUMAN	af68a07.x1 Barsiad acia HPLR86 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X06233
8830	21909	35447	0.64	1.0E-106	BE387950.1	EST_HUMAN	CALGRANULIN B (HUMAN)
8830	21909	35448	0.64	1.0E-106	BE387950.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
8903	21982	35522	2.77	1.0E-108	AI654123.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
9252	22329	35876	0.83	1.0E-106	AW838831.1	EST_HUMAN	ly62a05.x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN
9348	22424	35978	2.34	1.0E-108	AA825307.1	EST_HUMAN	C05084 69 KD ISLET CELL AUTOANTIGEN ;
9348	22424	35979	2.34	1.0E-106	AA825307.1	EST_HUMAN	GM4-L T0059-150200-086-e08 L10059 Homo sapiens cDNA
9486	22543	36108	0.77	1.0E-106	AI750447.1	EST_HUMAN	cc87e08.st NCL_CGAP_G081 Homo sapiens cDNA clone IMAGE:1354790 3'
9829	22684	36255	1.94	1.0E-106	AI479559.1	EST_HUMAN	cc87e08.st NCL_CGAP_G081 Homo sapiens cDNA clone IMAGE:1354790 3'
9829	22684	36256	1.94	1.0E-106	AI479559.1	EST_HUMAN	cn03a04.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn03a04 random
10205	23241	36832	0.6	1.0E-106	BE389234.1	EST_HUMAN	tm41102.x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.t3
10289	23324	36926	1.09	1.0E-108	BF027310.1	EST_HUMAN	TAR1 PTR5 repetitive element;
10289	23324	36927	1.09	1.0E-108	BF027310.1	EST_HUMAN	tm41102.x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.t3
10446	23481	37088	10.7	1.0E-106	AA604417.1	EST_HUMAN	TAR1 PTR5 repetitive element;
10446	23481	37089	10.7	1.0E-106	AA604417.1	EST_HUMAN	601282367F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604217 5'
10492	23527	37136	1.83	1.0E-106	AW363299.1	EST_HUMAN	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
							601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
							np57b10.st NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
							np57b10.st NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
							RC00-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1736	14885	27978	7.83	1.0E-106	U48724.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1757	14906	28000	1.33	1.0E-106	U04510.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
1846	14932	28083	5.51	1.0E-106	AA527148.1	EST_HUMAN	hg41cd05.s1 NCI_GGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element
1846	14992	28094	5.51	1.0E-106	AA527446.1	EST_HUMAN	hg41cd05.s1 NCI_GGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element
2191	15326	28451	1.94	1.0E-106	BE144286.1	EST_HUMAN	MRO-HT0165-140200-008-j10 HT0165 Homo sapiens cDNA
2391	15522	28651	3.62	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2574	15699	28821	2.19	1.0E-106	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2667	15788	28904	1.93	1.0E-106	U04875.2	NT	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds
2689	15790	28906	2.01	1.0E-106	BE260201.1	EST_HUMAN	801149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502461 5'
2815	15929	29041	8.05	1.0E-106	AI278526.1	EST_HUMAN	q176h10.x1 Sources_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3'
2886	16177	27700	1.84	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2886	16177	27701	1.84	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2939	16116	29128	1.18	1.0E-106	BE384296.1	EST_HUMAN	801272875F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3613818 5'
3007	16182	29204	5.7	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3007	16182	29205	5.7	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3248	16422	29438	2.5	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3248	16422	29439	2.5	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3461	16628	29648	1.04	1.0E-106	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3527	16692	29701	1.07	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3527	16692	29702	1.07	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4149	17301	30293	9.2	1.0E-106	AW074650.1	EST_HUMAN	EST386875 MAGe resequences, MAGN Homo sapiens cDNA
4149	17301	30294	9.2	1.0E-106	AW074650.1	EST_HUMAN	EST386875 MAGe resequences, MAGN Homo sapiens cDNA
4723	17858	30840	2.27	1.0E-106	BE144286.1	EST_HUMAN	MRO-HT0165-140200-008-j10 HT0165 Homo sapiens cDNA
5485	18684	31701	2.95	1.0E-106	AA781155.1	EST_HUMAN	g24b09.s1 Sources_testis_NHT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN PHPS1-2 (HUMAN)
5976	19161	32480	0.95	1.0E-106	AU130113	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
5976	19161	32481	0.95	1.0E-106	AU130113	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6026	19209	32529	0.61	1.0E-106	AA434168.1	EST_HUMAN	2w28d12.s1 Sources ovary tumor NbhOT Homo sapiens cDNA clone IMAGE:770615 3'
6116	19298	32631	1	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6116	19298	32632	1	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6227	19402	32762	8.39	1.0E-106	BF679574.1	EST_HUMAN	602154012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285067 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5053	18181		5.34	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5259	18378	31344	1.08	1.0E-105	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
5445	18645	31623	1.18	1.0E-105	AF016704.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 2
5513	18711		1.12	1.0E-105	11420134	NT	Homo sapiens Redra-derived POU-domain factor-1 (RPF-1), mRNA
7045	20098	33513	1.44	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7045	20098	33514	1.44	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7121	18547	31458	3.78	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7121	18547	31458	3.78	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7167	20300	33743	0.72	1.0E-105	BE602616.1	EST_HUMAN	EST363089 IMAGE resequences, MAGB Homo sapiens cDNA
7436	20513	33986	0.72	1.0E-105	BE602616.1	EST_HUMAN	EST363089 IMAGE resequences, MAGB Homo sapiens cDNA
8043	21126	34647	0.83	1.0E-105	X12556.1	NT	Human mRNA for dbl proto-oncogene
8217	21299	34820	11.05	1.0E-105	T05087.1	EST_HUMAN	EST02975 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBRCR32
8592	21673	35211	1.63	1.0E-105	AW007194.1	EST_HUMAN	ws50c10.x1 NCL CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2500628 3' similar to
9128	22207	35750	0.82	1.0E-105	AW840817.1	EST_HUMAN	SW_ACSA_PENCH P36333 ACETYL-COENZYME A SYNTHETASE ;
9250	22327	35874	2.51	1.0E-105	AW016879.1	EST_HUMAN	RG1-CN0008-070100-011-e05 CN0008 Homo sapiens cDNA
9404	22478	36041	0.83	1.0E-105	AW882372.1	EST_HUMAN	UI-H-B10p-abb-b-12-0-J1.e1 NCL CGAP_Sub2 Homo sapiens cDNA
9404	22478	36042	0.83	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-009 OT0062 Homo sapiens cDNA
9767	22764	36333	0.75	1.0E-105	BE807793.1	EST_HUMAN	QV2-OT0062-140300-083-009 OT0062 Homo sapiens cDNA
9767	22764	36334	0.75	1.0E-105	BE807793.1	EST_HUMAN	QV2-OT0062-140300-083-009 OT0062 Homo sapiens cDNA
11173	24243	37876	4.82	1.0E-105	AF254822.1	NT	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
11506	24564	38241	1.42	1.0E-105	D63548.1	NT	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
11559	24614	38280	1.85	1.0E-105	77056936	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
11887	24875	38572	2.52	1.0E-105	AW027554.1	EST_HUMAN	Homo sapiens COL4A6 gene for a6(IV) collagen, exon 31
11972	24957	38659	1.48	1.0E-105	BF430921.1	EST_HUMAN	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
12111	25081	38784	1.3	1.0E-105	AF218896.1	EST_HUMAN	wv74f07.x1 Scores, thymus_NHFT Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87892
155	13380	26464	0.86	1.0E-106	AW503208.1	EST_HUMAN	P87892 PROTEASE ;
210	13433	26464	5.14	1.0E-106	AW503208.1	EST_HUMAN	7a18c10.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3574281 3' similar to TR:P97680 P97680
555	13748	26774	1.89	1.0E-106	AW585556.1	EST_HUMAN	RIN1. ;
620	13807	26828	0.8	1.0E-106	J00146.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 8
621	13807	26828	1.13	1.0E-106	J00146.1	NT	UI-HF-BNO-elt-g-07-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
1554	14707	27787	8.84	1.0E-106	AF145712.1	NT	iq78c01.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2215008 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9641	21084	34597	4.14	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
9641	21084	34598	4.14	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
9655	22984	36589	0.92	1.0E-104	AW103948.1	EST_HUMAN	xd76d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116
9655	22984	36590	0.92	1.0E-104	AW103948.1	EST_HUMAN	Q24116 HYPOTHETICAL 29.4 KD PROTEIN. ;
10153	23190	36787	0.49	1.0E-104	AF113514.1	NT	Q24116 HYPOTHETICAL 29.4 KD PROTEIN. ;
10296	23333	36987	3.15	1.0E-104	BE791713.1	EST_HUMAN	Homo sapiens histone acetyltransferase MORF mRNA, complete cds
10296	23333	36988	3.15	1.0E-104	BE791713.1	EST_HUMAN	Homo sapiens histone acetyltransferase MORF mRNA, complete cds
10611	23645	37253	1.49	1.0E-104	AV728070.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10657	23691	37301	4.47	1.0E-104	AU130765.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10757	23790	37407	0.54	1.0E-104	AA931321.1	EST_HUMAN	AV728070 HTC Homo sapiens cDNA clone HTCBYA07 5'
10757	23790	37408	0.54	1.0E-104	AA931321.1	EST_HUMAN	AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001398 5'
10774	23807	37430	5.4	1.0E-104	U66535.1	NT	6006a10.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1565370 3'
10791	23824	37430	0.74	1.0E-104	U66535.1	NT	6006a10.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1565370 3'
11577	24632	38310	44.85	1.0E-104	BE720191.1	EST_HUMAN	Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25
11577	24632	38311	44.86	1.0E-104	BE720191.1	EST_HUMAN	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11611	24663	38350	4.1	1.0E-104	BF684288.1	EST_HUMAN	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
12082	25062	38768	46.12	1.0E-104	11434729	NT	RCO-HT0885-310700-021-609 HT0885 Homo sapiens cDNA
13073	25702		1.32	1.0E-104	BE333892.1	EST_HUMAN	RCO-HT0885-310700-021-609 HT0885 Homo sapiens cDNA
289	15981	26541	2.57	1.0E-105	4502160	NT	602141215F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302507 5'
438	13738	26238	6.69	1.0E-105	4505150	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RP-S6KA5), mRNA
607	13798	26815	2.51	1.0E-105	AF032897.1	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
607	13798	26816	2.51	1.0E-105	AF032897.1	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
1865	15011	28118	10.24	1.0E-105	AL163280.2	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1979	15122	28223	2.39	1.0E-105	D50918.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
2263	15398	28524	3.06	1.0E-105	AA318369.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2388	15529		1.18	1.0E-105	BE891766.1	EST_HUMAN	Human mRNA for KIAA0128 gene, partial cds
2794	15900		0.98	1.0E-105	AA584608.1	EST_HUMAN	EST20609 Spleen 1 Homo sapiens cDNA 5' end similar to autoimmunity antigen Ku, p70/p80 subunit
3071	16247		2.79	1.0E-105	AJ228041.1	NT	601434491F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919511 5'
3432	16600	29618	0.86	1.0E-105	7304922	NT	no10405.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265 3'
3432	16600	29619	0.86	1.0E-105	7304922	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22: segment 1/3
4213	17362	30350	2.23	1.0E-105	AW661688.1	EST_HUMAN	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
							Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
							Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
							EST1373761 IMAGE: resequences, MAGG Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2287	15400	28528	33.28	1.0E-104	AA132973.1	EST_HUMAN	z022c06.s1 Stragatene colon (#937204) Homo sapiens cDNA clone IMAGE:587628 3' similar to gb:Z14116.mai1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2277	15409	28540	4.55	1.0E-104	BE744628.1	EST_HUMAN	501577460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926438 5'
2442	15570	28698	9.73	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 C10248 Homo sapiens cDNA
2442	15570	28699	9.73	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 C10249 Homo sapiens cDNA
2506	15633	28753	2	1.0E-104	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homologue (ACTR2), mRNA
2834	16111	29125	17.99	1.0E-104	M34671.1	NT	Human lymphocyte antigen CD59/MEIM43 mRNA, complete cds
2983	16159		2.15	1.0E-104	Y1151.1	NT	H. sapiens gene encoding phenylpyruvate tautomerase II
3337	16510	29526	0.99	1.0E-104	AU133928.1	EST_HUMAN	AU133928 OVARC1 Homo sapiens cDNA clone OVARC1000936 5'
3478	16945		2.33	1.0E-104	AA319436.1	EST_HUMAN	EST12658 Adrenal gland tumor Homo sapiens cDNA 5' end
3690	16852	29860	0.65	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3690	16852	29861	0.65	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
4053	17209	30219	0.71	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4248	17394	30393	0.71	1.0E-104	F11745.1	EST_HUMAN	HSC31A07.1 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4498	17638	30618	33.95	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4732	17867	30849	1.2	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4732	17867	30850	1.2	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
6061	19243	32567	1.05	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6061	19243	32568	1.05	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6108	19288	32623	0.93	1.0E-104	AB017332.1	NT	Homo sapiens aik3 mRNA for Aurora/ipl-related kinase 3, complete cds
6396	19756	33142	8.5	1.0E-104	AI768797.1	EST_HUMAN	w03b12.x1 NCI CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN, contains element LTR7 repetitive element;
6596	19756	33143	8.5	1.0E-104	AI768797.1	EST_HUMAN	w03b12.x1 NCI CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN, contains element LTR7 repetitive element;
6786	19941	33338	0.74	1.0E-104	7708512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6942	20255	33692	3.39	1.0E-104	BE314182.1	EST_HUMAN	501150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6942	20255	33693	3.39	1.0E-104	BE314182.1	EST_HUMAN	501150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
7373	20482	33917	2.01	1.0E-104	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
7896	21875	35414	0.87	1.0E-104	BF508244.1	EST_HUMAN	UI-H-B14-ssw-b-09-q-U1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086176 3'
9388	22443	36004	2.41	1.0E-104	BF448230.1	EST_HUMAN	ncad18g11.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365948 3'
9463	22520	36082	0.46	1.0E-104	AA682308.1	EST_HUMAN	z93605.s1 Soares fetal liver spliced INFLS_S1 Homo sapiens cDNA clone IMAGE:462897 3'
9484	22541		1.03	1.0E-104	174219.1	EST_HUMAN	yc8302.2.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22440 5'
9515	22580	36146	5	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9515	22580	36147	5	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8484	21565	35101	0.59	1.0E-103	T31080.1	EST_HUMAN	EST127193 Human Brain Homo sapiens cDNA 5' and similar to None
8822	21901	35440	1.05	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8822	21901	35441	1.05	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8900	21979	35518	1.34	1.0E-103	BF109244.1	EST_HUMAN	706003.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525964 3' similar to
9307	22383	35934	3.18	1.0E-103	6005921	NT	SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;
9307	22383	35935	3.18	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9349	22425	35980	0.97	1.0E-103	AA581086.1	EST_HUMAN	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
10263	23298	36896	2.04	1.0E-103	Z37976.1	NT	PROTEASE SUBUNIT 4 (HUMAN);
10304	23339	36944	2.07	1.0E-103	AW963676.1	EST_HUMAN	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
10443	23478	37083	10.79	1.0E-103	AB789566.1	EST_HUMAN	EST1375749 MAGI2 resequences, MAGH Homo sapiens cDNA
10878	23963	37591	1.52	1.0E-103	BE549706.1	EST_HUMAN	au51904.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518326 5' similar to
10971	24051	37684	9.5	1.0E-103	AI762759.1	EST_HUMAN	TR:O15046 O15046 KIAA0338 ;
11072	24147	37785	2.45	1.0E-103	11424061	NT	7p41103.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230813 3' similar to gb:M69043 MAJOR
11072	24147	37786	2.45	1.0E-103	11424061	NT	HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN (HUMAN);
11083	24157	37794	2.4	1.0E-103	AF149773.1	NT	PHOSPHOLIPASE C NEIGHBORING ;
11083	24157	37795	2.4	1.0E-103	AF149773.1	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
11656	24735	38426	2.67	1.0E-103	AU136283.1	EST_HUMAN	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
11731	23917	37542	4.1	1.0E-103	L43610.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11986	24953		1.71	1.0E-103	AB024759.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
12044	25025	38730	2.26	1.0E-103	BE644611.1	EST_HUMAN	AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5'
12178	25138		3.4	1.0E-103	AF224669.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
12209	25162		1.22	1.0E-103	11526291	NT	Homo sapiens TSA305 gene, exon 16
12414	26203	32083	1.71	1.0E-103	AB011369.1	NT	766810.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to
243	13465	26494	2.46	1.0E-104	AL037549.3	EST_HUMAN	contains MER29.13 MER29 repetitive element ;
243	13465	26495	2.46	1.0E-104	AL037549.3	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
1937	15030	28182	1.92	1.0E-104	4502428	NT	(UBE2D3) genes, complete cds
							Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
							Homo sapiens gene for AF-6, complete cds
							DKFZp564H1072.1 564 (synonym: hbr2) Homo sapiens cDNA clone DKFZp564H1072 5'
							DKFZp564H1072.1 564 (synonym: hbr2) Homo sapiens cDNA clone DKFZp564H1072 5'
							Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3528	16691	29700	0.95	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3850	17010		5.46	1.0E-103	AF023881.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3884	17053	30053	0.9	1.0E-103	AA485683.1	EST_HUMAN	ab10d12.51 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element ;
3933	17092	30090	1.54	1.0E-103	11430876	NT	Homo sapiens neuropilin 1 (NRP1), mRNA
4110	17264	30264	4.83	1.0E-103	T23683.1	EST_HUMAN	seq340 b44IB3MA-Cd109+10-Bio Homo sapiens cDNA clone b44IB3MA-Cd109+10-Bio-7 3'
5325	18438		0.83	1.0E-103	AA451616.1	EST_HUMAN	z43b04.r1 Soares fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789199 5' similar to
6056	18238	32563	0.9	1.0E-103	BF569527.1	EST_HUMAN	TR-G292352 G292352 COLLAGEN CHAIN RH ;
6063	19245	32571	1.67	1.0E-103	AF179695.1	NT	602186023F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310573 5'
6397	19596	32926	0.8	1.0E-103	11435053	NT	Homo sapiens septin 2 (SEP2) mRNA, partial cds
6397	19596	32927	0.8	1.0E-103	11495053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6587	19748	33130	0.84	1.0E-103	AW954556.1	EST_HUMAN	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6887	19748	33131	0.84	1.0E-103	AW954556.1	EST_HUMAN	EST366636 MAGC resequences, MAGC Homo sapiens cDNA
6725	25831	33273	1.15	1.0E-103	AA781442.1	EST_HUMAN	al26e03.at Soares testis_NHT Homo sapiens cDNA clone 1391452 3'
6768	19924	33318	0.91	1.0E-103	AF053490.1	NT	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4
6859	20011	33422	1.66	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI CGAP Bim25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
6859	20011	33423	1.66	1.0E-103	AI590071.1	EST_HUMAN	Q13769 ANONYMOUS ;
6987	18506	31521	1.77	1.0E-103	5032282	NT	tm58b05.x1 NCI CGAP Bim25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
6987	18508	31522	1.77	1.0E-103	5032282	NT	Q13769 ANONYMOUS ;
7108	18535	31490	1.04	1.0E-103	11431100	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS184, DXS206, DXS230, DXS238, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7179	20310	33753	0.98	1.0E-103	AJ286980.1	NT	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA
7375	20454	33919	1.88	1.0E-103	AW965776.1	EST_HUMAN	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
7488	20563	34032	3.6	1.0E-103	BE748158.1	EST_HUMAN	EST377849 MAGC resequences, MAGC Homo sapiens cDNA
7951	21001	34511	4	1.0E-103	AI590071.1	EST_HUMAN	601571537F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838545 5'
7951	21001	34512	4	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI CGAP Bim25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10593	23828		0.64	1.0E-102	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
10647	23681	37291	0.87	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
10647	23681	37292	0.87	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
10687	23720	37325	3.26	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-260499-074 BT074 Homo sapiens cDNA
10687	23720	37326	3.26	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-260499-074 BT074 Homo sapiens cDNA
10748	23781	37394	1.5	1.0E-102	AA970766.1	EST_HUMAN	on57h04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1560823 3' similar to
11323	24386	38030	1.37	1.0E-102	BE97468.1	EST_HUMAN	SW-CAV2_HUMAN P51636 CAVEOLIN-2, [1];
11327	24390	38035	2.44	1.0E-102	4507822	NT	601439392F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924186 5'
11327	24390	38036	2.44	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11600	24653	38337	1.47	1.0E-102	AA868675.1	EST_HUMAN	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11690	24688	38378	2.47	1.0E-102	BF359243.1	EST_HUMAN	ak9h10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408347 3'
12008	24994	38699	2.83	1.0E-102	U41302.1	NT	RC8-ET0072-150600-071-F01 E10072 Homo sapiens cDNA
12182	25142		5.69	1.0E-102	AL183280.2	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
12775	25517	32000	5.67	1.0E-102	AW300862.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
12891	25553	32015	1.25	1.0E-102	11419159	NT	xk07c12.x1 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2666038 3'
71	13308	26331	0.85	1.0E-103	BE908158.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLL T4), mRNA
71	13308	26332	0.85	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
102	13338	26365	8.24	1.0E-103	D87078.2	NT	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
213	13436	26466	0.84	1.0E-103	5453763	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
1004	14175	27234	74.34	1.0E-103	AJ278348.1	NT	Homo sapiens nuclear protein (KKEID repeat) (NOP56) mRNA
1272	14429	27500	7.08	1.0E-103	BE877541.1	EST_HUMAN	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1626	14778	27683	3.51	1.0E-103	AF012872.1	NT	601485388F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:3887876 5'
1964	15107	28207	1.02	1.0E-103	7657692	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pik230) mRNA, complete cds
2031	15172	28280	0.95	1.0E-103	4502428	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2031	15172	28281	0.95	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2379	15510	28638	1.95	1.0E-103	AU134891.1	EST_HUMAN	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2523	16348	28772	1.84	1.0E-103	AF060568.1	NT	AU134991 PLACET1 Homo sapiens cDNA clone PLACE1000965 5'
2685	15805	28921	1	1.0E-103	N32770.1	EST_HUMAN	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3137	16313		2.76	1.0E-103	BE744722.1	EST_HUMAN	ww1d08.s1 Soares_placenta_8tp8weeks_2nbHP8cpw Homo sapiens cDNA clone IMAGE:266599 3'
3467	16634	29653	5.33	1.0E-103	AW298245.1	EST_HUMAN	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
							UI-H-BWO-gt4h-11-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2733185 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2383	15514	28942	1.91	1.0E-102	AI124689.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95 HUMAN Q08379 GOLGIN-96 ;
2383	16514	28943	1.91	1.0E-102	AI124689.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95 HUMAN Q08379 GOLGIN-96 ;
3090	16256		0.74	1.0E-102	Y13932.1	NT	Homo sapiens PRKY exon 7
3133	16309	29322	1.47	1.0E-102	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3203	16378	29387	3.73	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3203	16378	29388	3.73	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4347	17480	30472	1.74	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4533	17571	30655	2.57	1.0E-102	BE251310.1	EST_HUMAN	6071107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5'
5224	18346	31316	1.28	1.0E-102	R66488.1	EST_HUMAN	y3204.1 Soares placenta N2HP Homo sapiens cDNA clone IMAGE:140934 5'
5487	18986	31704	1.6	1.0E-102	AF067133.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
5887	19057		6.87	1.0E-102	AB034951.1	NT	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds
5905	19094	32408	3.25	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5905	19094	32409	3.25	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5912	19100	32414	0.81	1.0E-102	11433046	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
6422	19591	32968	2.81	1.0E-102	AI459825.1	EST_HUMAN	ar2109.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137 Q13137 NDP52 ;
7227	20090	33507	0.7	1.0E-102	AW451643.1	EST_HUMAN	UI-H-B13-aj-4-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736835 3'
7288	20369	33823	0.91	1.0E-102	BE729323.1	EST_HUMAN	607561505F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831241 5'
7314	20396	33858	1.02	1.0E-102	BE388108.1	EST_HUMAN	607277215F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618243 5'
7428	20506	33977	1.5	1.0E-102	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7510	20584	34057	8.03	1.0E-102	AJ236984.1	NT	Homo sapiens mRNA for Centaurin-alpha2 protein
7802	20858	34350	2.61	1.0E-102	AV710738.1	EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CuAAKD03 5'
8418	21499	35031	3.85	1.0E-102	BE763051.1	EST_HUMAN	QV3-NT0025-210800-236-H08 NT0025 Homo sapiens cDNA
8691	21771	35301	1.71	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKC Homo sapiens cDNA clone GKCCEE11 5'
8691	21771	35302	1.71	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKC Homo sapiens cDNA clone GKCCEE11 5'
8802	21881	35419	0.81	1.0E-102	AB007823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9131	22210	35754	1.2	1.0E-102	BE388083.1	EST_HUMAN	607283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
9131	22210	35755	1.2	1.0E-102	BE388083.1	EST_HUMAN	607283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
9481	22538	36102	0.84	1.0E-102	AV756842.1	EST_HUMAN	AV756842 BM Homo sapiens cDNA clone BMF-AUD06 5'
9522	22587	36165	2	1.0E-102	T70393.1	EST_HUMAN	yd13407.1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:67021 5'
9522	22587	36166	2	1.0E-102	T70393.1	EST_HUMAN	yd13407.1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:67021 5'
9611	22666	36237	3.11	1.0E-102	AU124629.1	EST_HUMAN	AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8517	21598	35132	0.71	1.0E-101	AW630070.1	EST_HUMAN	h174g10.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868578 5' similar to gb.J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
8517	21598	35133	0.71	1.0E-101	AW630070.1	EST_HUMAN	h174g10.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868578 5' similar to gb.J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
9212	22290	35832	1.1	1.0E-101	AA036800.1	EST_HUMAN	z129g08.r1 Soares_pregnant_uterus_NIHPU Homo sapiens cDNA clone IMAGE:471998 5' similar to PIR:S54640 S54640 YD9335.03c protein - yeast;
9301	22998	36167	0.99	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9331	22996	36168	0.99	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9661	21103	34619	17.36	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9661	21103	34620	17.36	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9676	22638	36209	19.41	1.0E-101	8845492	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
9659	22993	36593	3.36	1.0E-101	BE519667.1	EST_HUMAN	601472808T1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875953 3'
9959	22998	36594	3.36	1.0E-101	BE519667.1	EST_HUMAN	601472808T1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875953 3'
10098	23136	36737	0.68	1.0E-101	10863960	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
10620	23654	37284	1.94	1.0E-101	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10656	23690	37289	4.37	1.0E-101	AI570293.1	EST_HUMAN	b77d11.k1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb.M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10656	23690	37300	4.37	1.0E-101	AI570293.1	EST_HUMAN	b77d11.k1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb.M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10771	23804	37426	0.83	1.0E-101	BE973648.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
10771	23804	37427	0.83	1.0E-101	BE973648.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
11371	24432	38089	1.31	1.0E-101	AB020626.1	NT	Homo sapiens mRNA for KIAA0819 protein, partial cds
12059	25040	38748	1.85	1.0E-101	AI908168.1	EST_HUMAN	RC-BT163-290495-085 BT163 Homo sapiens cDNA
12059	25040	38749	1.85	1.0E-101	AI908168.1	EST_HUMAN	RC-BT163-290495-085 BT163 Homo sapiens cDNA
12738	25489		2.24	1.0E-101	BE163887.1	EST_HUMAN	QV3-HT0460-230200-101-403 HT0460 Homo sapiens cDNA
12793	25529		12.79	1.0E-101	AW939051.1	EST_HUMAN	QV1-DT0068-240200-085-a01 DT0068 Homo sapiens cDNA
40	13278	26284	0.61	1.0E-102	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
351	13562	26589	4.57	1.0E-102	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
635	13820	26844	0.61	1.0E-102	BE25470.1	EST_HUMAN	601108292F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
796	13875	27028	1.06	1.0E-102	4557534	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1141	14306	27362	1.9	1.0E-102	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1297	14453	27518	2.05	1.0E-102	11437148	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1297	14453	27519	2.05	1.0E-102	11437148	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1450	14603	27681	355.9	1.0E-102	BE408447.1	EST_HUMAN	601286982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629901 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1614	14787	27850	1.44	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1785	14934	28028	1.57	1.0E-101	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1785	14934	28029	1.57	1.0E-101	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1939	15140	28247	2.07	1.0E-101	4502998	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1), mRNA
2116	15254	28373	2.76	1.0E-101	BE843070.1	EST_HUMAN	RC3-3T0281-160600-016-109 ST0281 Homo sapiens cDNA
2425	16062	28680	1.2	1.0E-101	5729892	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2680	15800	28917	4.62	1.0E-101	X72993.1	NT	H. sapiens EWS gene, exon 5
2802	15916	29025	9.27	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
2802	15916	29026	9.27	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3020	16198		20.15	1.0E-101	AJ252312.1	NT	Homo sapiens genomic downstream Rhesus box
3273	16447	29467	2.97	1.0E-101	4885270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3313	16486		2.3	1.0E-101	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3488	16635	29654	1.82	1.0E-101	AW065556.1	EST_HUMAN	EST377628 MAGE resequences, MAGI Homo sapiens cDNA
3487	15916	29025	3.59	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3487	15916	29026	3.59	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3981	17138	30142	3.81	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
5147	18269	31239	1.14	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5147	18269	31240	1.14	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5248	18369	31336	0.6	1.0E-101	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
5248	18369	31337	0.6	1.0E-101	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
5433	18633	31611	1.94	1.0E-101	AW965139.1	EST_HUMAN	EST377212 MAGE resequences, MAGI Homo sapiens cDNA
6126	19305	32645	4.07	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6126	19305	32646	4.07	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6934	19987	33396	0.96	1.0E-101	11430734	NT	Homo sapiens carbonic anhydrase VII (CA7), mRNA
7423	20500		1.26	1.0E-101	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7473	20548	34019	4.22	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3), mRNA, alternative splice form 4, partial cds
7473	20548	34020	4.22	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3), mRNA, alternative splice form 4, partial cds
7645	20714	34182	7.65	1.0E-101	AW008475.1	EST_HUMAN	wv5512.x1 NCJ_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'
7749	20809		1.99	1.0E-101	BE27384.1	EST_HUMAN	60109217F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349901 5'
7900	20952	34459	6.54	1.0E-101	BF330759.1	EST_HUMAN	RC1-BT0313-220700-018-f12 BT0313 Homo sapiens cDNA
8097	21179	34886	0.74	1.0E-101	BE275821.1	EST_HUMAN	60112162F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3349869 5'
8097	21179	34697	0.74	1.0E-101	BE275821.1	EST_HUMAN	60112162F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3349869 5'
8245	21327	34943	1.6	1.0E-101	BF029174.1	EST_HUMAN	601764886F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996837 5'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9887	22736		0.84	1.0E-100	AU127720.1	EST_HUMAN	AU127720 NT ZRP2 Homo sapiens cDNA clone NT ZRP2001918 5'
9782	22822	36400	2.17	1.0E-100	AB045846.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
9782	22822	36401	2.17	1.0E-100	AB045846.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
10048	23086	36687	1.81	1.0E-100	AW630487.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:2969396 5'
10048	23086	36688	1.81	1.0E-100	AW630487.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:2969396 5'
10688	23721	37327	0.64	1.0E-100	BF347519.1	EST_HUMAN	Human endogenous retrovirus HERV-K, pol gene
10782	23815		1.35	1.0E-100	Y10391.1	NT	Human endogenous retrovirus HERV-K, pol gene
10996	24075	37708	6.64	1.0E-100	BF327292.1	EST_HUMAN	MRO-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA
11564	24619	38300	1.56	1.0E-100	X94633.1	NT	H. sapiens CD97 gene exon 4
11564	24619	38301	1.55	1.0E-100	X94633.1	NT	H. sapiens CD97 gene exon 4
11635	24715	38405	3.91	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11635	24715	38406	3.91	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11665	13241	26241	3.07	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
11977	24962		2.21	1.0E-100	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
12128	25108	38812	1.93	1.0E-100	AJ131034.1	NT	Homo sapiens class gene, exon 12
12177	25137	38832	7.59	1.0E-100	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12312	26037		1.78	1.0E-100	BF446549.1	EST_HUMAN	7q88h03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to TR-Q21997 Q21997
12493	25341	32063	4.97	1.0E-100	11545732	NT	COSMID R151. [2] TR-Q9UA08 ;
12754	25500	32033	1.31	1.0E-100	11418123	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
13195	25778	31935	6.91	1.0E-100	11417974	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
79	13315	26342	0.92	1.0E-101	7110714	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
79	13315	26343	0.92	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
704	13887	26919	1.4	1.0E-101	AB007915.2	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
722	13904	26945	6.12	1.0E-101	7110734	NT	Homo sapiens mRNA for KIAA0448 protein, partial cds
722	13904	26946	6.12	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
792	13971	27023	1.37	1.0E-101	7657454	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
876	14052	27117	1.35	1.0E-101	4503914	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
948	14121	27182	0.85	1.0E-101	Z20686.1	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
1009	14180	27243	6.07	1.0E-101	BF681218.1	EST_HUMAN	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
1077	14243	27259	1.39	1.0E-101	AI221878.1	EST_HUMAN	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase (GART) mRNA
1614	14767	27849	1.44	1.0E-101	5521480	NT	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase (GART) mRNA
							Homo sapiens of cardiac alpha-myosin heavy chain gene
							602156474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297291 5'
							gg99e09.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
							Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2315	15447		1.14	1.0E-100	D83349.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2507	15634	28754	1.41	1.0E-100	X62468.1	NT	H. sapiens mRNA for IFN-gamma (pKC-O)
2771	15896	28996	2.5	1.0E-100	11418976	NT	Homo sapiens KIAA0857 protein (KIAA0857), mRNA
3093	16259		6.55	1.0E-100	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4326	17469	30456	1.67	1.0E-100	AF057354.1	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
4351	17494	30474	2.28	1.0E-100	4503792	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5202	18323	31291	3.01	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5202	18323	31292	3.01	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5404	18606	31578	1.74	1.0E-100	BF244218.1	EST_HUMAN	601883164F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080999 5'
5625	18819	31893	0.76	1.0E-100	AW075983.1	EST_HUMAN	xa82f01.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573305 3' similar to gb.X12433
5818	19008	32314	1.45	1.0E-100	AW075983.1	EST_HUMAN	PROTEIN PHPS1-2 (HUMAN);
5864	19054	32361	1.78	1.0E-100	AU118182.1	EST_HUMAN	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
5860	19146	32461	0.85	1.0E-100	AF135116.1	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
6292	19465	32817	0.9	1.0E-100	X14690.1	NT	Human mRNA for plasma inter-alpha-trypsin inhibitor heavy chain H(3)
6292	19465	32818	0.9	1.0E-100	4557568	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6626	19786	33174	5.62	1.0E-100	AU140214.1	EST_HUMAN	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
6824	19977	33384	1.36	1.0E-100	R10887.1	EST_HUMAN	yf38c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'
6908	20223	33653	1.77	1.0E-100	7382478	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
6982	20210	33638	1.02	1.0E-100	AA496841.1	EST_HUMAN	ae33b06.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418
6982	20210	33639	1.02	1.0E-100	AA496841.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN ;
7026	20162	33663	1.18	1.0E-100	BF376478.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN ;
7026	20162	33684	1.18	1.0E-100	BF376478.1	EST_HUMAN	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
7033	20169	33591	6.2	1.0E-100	X04571.1	NT	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
8728	21809	35345	3.53	1.0E-100	BF103853.1	EST_HUMAN	Human mRNA for kidney epidermal growth factor (EGF) precursor
8766	21845		5.59	1.0E-100	AL163203.2	NT	601647357F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3931310 5'
9216	22294	35837	0.47	1.0E-100	AU116951.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
9216	22294	35838	0.47	1.0E-100	AU116951.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9433	22507	36073	3.88	1.0E-100	AB040918.1	NT	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9510	22776		1.65	1.0E-100	AB972388.1	EST_HUMAN	Homo sapiens mRNA for KIAA1488 protein, partial cds
9633	21076	34588	2.28	1.0E-100	AW599611.1	EST_HUMAN	wf37609.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2489920 3' similar to contains element
							MER22 repetitive element ;
							PM0-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1980	15123	28225	1.21	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (38kD) (FKBP6) mRNA, and translated products
3154	16329	29339	0.93	1.0E-99	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4499	17639	30621	2.64	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4499	17639	30622	2.64	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
6943	20266	33694	1.25	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
6943	20266	33695	1.25	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7289	25842	33827	0.81	1.0E-99	X98022.1	NT	H. sapiens E6-AP gene exon 2
9400	22474		0.75	1.0E-99	11419721	NT	Homo sapiens ALEX1 protein (LOC51309), mRNA
9720	22785	36356	1.7	1.0E-99	AW340174.1	EST_HUMAN	hd02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908374 3' similar to TR:002711
11403	24464	38128	2.56	1.0E-99	7427514	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN
11403	24464	38129	2.56	1.0E-99	7427514	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11462	24521	38191	1.88	1.0E-99	5901979	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11659	24738	38429	2.83	1.0E-99	AB023222.1	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
11996	24981	38687	2.45	1.0E-99	11417191	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
12257	25193		4.52	1.0E-99	AF240786.1	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
1	13241	26241	1.7	1.0E-100	AL163247.2	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2	13241	26241	2.91	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
70	13307	26329	1.92	1.0E-100	11418230	NT	Homo sapiens chromosome 21 segment HS21C047
70	13307	26330	1.92	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
89	13324	26353	0.82	1.0E-100	AW276237.1	EST_HUMAN	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
173	13397	26425	0.89	1.0E-100	AL163206.2	NT	xv78b11.x1 NC1_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2824605 3'
327	13541	26573	1.84	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C006
353	13584	26592	1.87	1.0E-100	T05087.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
450	13848		2.24	1.0E-100	AF003528.1	NT	EST02975 Fetal brain, Stragelene (cat#936206) Homo sapiens cDNA clone HFCR32
502	13697		5.88	1.0E-100	X89631.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
522	13715	26742	1.21	1.0E-100	BE180609.1	EST_HUMAN	G. gorilla DNA for ZNF80 gene homolog
1044	14210	27266	4.57	1.0E-100	7681685	NT	RC3-HT0625-040500-022-509 HT0625 Homo sapiens cDNA
1044	14210	27267	4.57	1.0E-100	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1577	14730		1.3	1.0E-100	AW207655.1	EST_HUMAN	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1581	14733	27814	1.66	1.0E-100	AI200857.1	EST_HUMAN	UHH-B11-afk-c-07-Q-U1.1 NC1_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
							qf62f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA
							P81061 CYSTATIN1

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6732	19888	33280	0.94	6.0E-99	7706138	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
6816	19889	33376	0.74	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
6816	19889	33377	0.74	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8298	21378	34899	1.85	6.0E-99	X99101.1	NT	H. sapiens mRNA for estrogen receptor
8314	21396	34921	0.59	6.0E-99	6801589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8964	22043	35886	2.67	6.0E-99	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
9084	22143	36688	7.6	6.0E-99	AF080255.1	NT	Homo sapiens iodester protein mRNA, complete cds
9084	22143	36689	7.6	6.0E-99	AF080255.1	NT	Homo sapiens iodester protein mRNA, complete cds
9123	22202	35744	0.59	6.0E-99	11431994	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 1 (ITPR1), mRNA
9123	22202	35745	0.59	6.0E-99	11431994	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 1 (ITPR1), mRNA
10958	24039	37674	3.15	6.0E-99	11526299	NT	Homo sapiens BH3 interacting domain death agonist (BID), mRNA
11742	23928	37563	2.02	6.0E-99	9910279	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
11742	23928	37554	2.02	6.0E-99	9910279	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
2022	15163	28268	1	5.0E-99	Y11365.1	NT	H. sapiens IMPA gene, exon 8
4686	17821	30809	1.81	5.0E-99	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7SSA2 to TCRBV12S2 region
12502	25346		2.49	5.0E-99	BE890177.1	EST_HUMAN	601513157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'
8516	21597		4.95	3.0E-99	M95566.1	NT	Human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds
1268	14426		7.26	2.0E-99	AW274792.1	EST_HUMAN	XP0906.X1 NCI CGAP HNG Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);
3331	16504	29522	1.4	2.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4665	17800	30787	1.82	2.0E-99	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7851	20906	34410	0.76	2.0E-99	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8904	21983	35523	10.79	2.0E-99	W23507.1	EST_HUMAN	2b46d06.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306635 5' similar to
9353	22428	35986	0.75	2.0E-99	R78254.1	EST_HUMAN	gb:M16182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
11367	24428	36085	3.16	2.0E-99	AF247457.2	NT	y81509.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145826 5'
12081	25061	38767	1.64	2.0E-99	10863980	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
325	13539	26571	1.49	1.0E-99	AF114487.1	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
390	13596	26632	1.75	1.0E-99	11626190	NT	Homo sapiens interectin long isoform (ITSN) mRNA, complete cds
1452	14605	27684	3.61	1.0E-99	M30938.1	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
1587	14739	27818	1.16	1.0E-99	AF192523.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1587	14739	27820	1.16	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1980	15123	28224	1.21	1.0E-99	4503730	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
							Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8889	21968	35503	0.8	2.0E-98	L76686.1	NT	Homo sapiens NKAT4b mRNA, complete cds
8889	21968	35504	0.8	2.0E-98	L76686.1	NT	Homo sapiens NKAT4b mRNA, complete cds
9737	22802	36376	1.56	2.0E-98	X12684.1	NT	H sapiens arginase gene exon 3 (EO 3.5.3.1)
10624	23658		1.65	2.0E-98	7705868	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
12136	25116		1.61	2.0E-98	AB046813.1	NT	Homo sapiens mRNA for KIAA1593 protein, partial cds
12492	25340	32052	2.23	2.0E-98	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
418	13613	26553	27.52	1.0E-98	AI862007.1	EST_HUMAN	P29318 60S RIBOSOMAL PROTEIN L23A. ;
457	13662	26598	3.27	1.0E-98	AW598311.1	EST_HUMAN	P1M0-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA
1840	14986	28086	28.16	1.0E-98	N49818.1	EST_HUMAN	Y23105.1 Sceres fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:243585 5' similar to PIR:S54204 S54204 ribosomal protein L28 - human ;
5432	18532	31610	3.3	1.0E-98	AA195854.1	EST_HUMAN	Zp88c09.1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:828240 5' similar to TR:G8086562 G808652 NEBULIN. ;
5687	18881	32172	0.97	1.0E-98	BE390627.1	EST_HUMAN	601284988F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606692 5'
5687	18881	32173	0.97	1.0E-98	BE390627.1	EST_HUMAN	601284988F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606692 5'
9199	22277	35815	0.59	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
9199	22277	35816	0.59	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
5539	19125	32438	1.05	9.0E-99	AI905004.1	EST_HUMAN	QV-BT073-191298-012 BT073 Homo sapiens cDNA
5539	19125	32439	1.05	9.0E-99	AI905004.1	EST_HUMAN	QV-BT073-191298-012 BT073 Homo sapiens cDNA
6165	19341	32588	4.01	9.0E-99	AW968635.1	EST_HUMAN	EST380711 MAGC resequences, MAGJ Homo sapiens cDNA
11384	24445	38105	1.85	9.0E-99	AI479829.1	EST_HUMAN	tm69h07.x1 NCJ CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BD_HUMAN
11384	24445	38106	1.85	9.0E-99	AI479829.1	EST_HUMAN	tm69h07.x1 NCJ CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BD_HUMAN
11700	24697	38389	1.72	9.0E-99	AA134604.1	EST_HUMAN	P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
8924	22003	35542	1.19	8.0E-99	9635487	NT	z990d02.L1 Stragene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565443 5' similar to
5956	19142	32458	9.25	7.0E-99	AF035808.1	NT	Human endogenous retrovirus, complete genome
11909	24896	38599	1.91	7.0E-99	AF001886.1	NT	Homo sapiens occllin (hln) gene, exon 5
484	13678	26713	0.72	6.0E-99	U10961.1	NT	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon
2196	15331	28456	6.2	6.0E-99	11430555	NT	Human G2 protein mRNA, partial cds
2196	15331	28457	6.2	6.0E-99	11430555	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
3995	17152	30160	2.8	6.0E-99	AW975394.1	EST_HUMAN	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
4870	18003	30986	1.42	6.0E-99	4502680	NT	EST388473 MAGC resequences, MAGN Homo sapiens cDNA
							Homo sapiens CD34 antigen (CD34) mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1403	14557	27831	0.93	8.0E-98	AB03768.1	NT	Homo sapiens HPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
1591	14743	27825	1.1	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1581	14743	27826	1.1	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1765	14914	28009	2.79	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1765	14914	28010	2.79	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3896	17055	30055	6.45	8.0E-98	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
6207	19382	32732	0.96	5.0E-98	BE885973.1	EST_HUMAN	601507503F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909097 5'
2247	15380	28508	1.35	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
2673	15793	28910	2.1	3.0E-98	AB014807.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2807	15921		5.04	3.0E-98	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
7085	20179	33602	1.99	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7085	20179	33603	1.99	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
8851	22030	35571	4.07	3.0E-98	H46698.1	EST_HUMAN	yot7g09.r1 Scores adult brain N255HB55Y Homo sapiens cDNA clone IMAGE:178240 5'
9497	22563	36115	0.54	3.0E-98	8922036	NT	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA
10087	23125	36726	1.82	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
10087	23125	36727	1.82	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
10691	23724	37330	0.89	3.0E-98	BE900454.1	EST_HUMAN	601673686F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956517 5'
11195	24284	37899	2.55	3.0E-98	U59309.1	NT	Human fumarate precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
11819	24808	38504	2.22	3.0E-98	A1159975.1	EST_HUMAN	qb80h02.x1 Scores_fetal_heart NBHH10W Homo sapiens cDNA clone IMAGE:1708451 3'
13138	25739		3.01	3.0E-98	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
754	13935	28880	0.87	2.0E-98	BE261694.1	EST_HUMAN	601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'
2141	15277	28399	4.06	2.0E-98	BE264281.1	EST_HUMAN	601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2311	15443	28578	2.21	2.0E-98	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4411	17553	30538	0.82	2.0E-98	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4459	17599	30577	4.23	2.0E-98	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4948	18078	31052	1.39	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
4948	18078	31053	1.39	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
5492	18691	31708	4.76	2.0E-98	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6763	19948	33247	1.7	2.0E-98	4506788	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
7801	20857	34348	1.25	2.0E-98	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
7801	20857	34349	1.25	2.0E-98	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
8807	21866	35426	4.44	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8807	21866	35427	4.44	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
897	14073	27139	7.16	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1473	15039	27712	1.94	3.0E-97	4758813	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2508	15998	28755	2.4	3.0E-97	U36255.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 7
3333	16506	29523	0.96	3.0E-97	5174478	NT	Homo sapiens pericentriin (PCNT) mRNA
4902	18032	31021	22.23	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
5557	19719	33095	2.72	1.0E-97	BE596486.1	EST_HUMAN	601339520F1 NIH_MGC 63 Homo sapiens cDNA clone IMAGE:3681821 5'
7039	20092	33509	0.69	1.0E-97	5453881	NT	Homo sapiens phosphotyrosine kinase, gamma 1 (muscle) (PHKG1) mRNA
9956	23005	36600	1.02	1.0E-97	R10887.1	EST_HUMAN	y38c08.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:129134 3'
10945	24027	37663	2.84	1.0E-97	11427757	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
10945	24027	37684	2.84	1.0E-97	11427757	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
11589	24642	38324	1.38	1.0E-97	AA563761.1	EST_HUMAN	nk29g02.st NCI_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:1014962 3'
11756	23942	37568	8.3	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
11756	23942	37569	8.3	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
924	14099	27163	2.34	1.0E-98	BE030973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
1305	14481	27528	1.32	9.0E-98	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
6432	19600		0.79	9.0E-98	AJ250713.1	NT	Homo sapiens CLDN12 gene for claudin-12
8020	21072	34583	4.13	9.0E-98	AB046956.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
8020	21072	34584	4.13	9.0E-98	AB046956.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
8109	21191	34711	5.62	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
8109	21191	34712	5.62	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
9316	22392	35943	1.78	9.0E-98	X05989.1	NT	Human mRNA for amyloid A4(751) protein
9425	22499	36064	1.12	9.0E-98	11821580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9492	22549	36112	1.6	9.0E-98	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
9540	22605		0.81	9.0E-98	AF057726.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 8
9567	22709	36276	1.28	9.0E-98	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
9567	22709	36277	1.28	9.0E-98	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
10467	23502	37115	0.67	9.0E-98	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
10575	23610	37215	0.5	9.0E-98	11431544	NT	Homo sapiens protease-activated receptor 3 (PAR3), mRNA
11253	24322	37962	2.62	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11253	24322	37963	2.62	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
12487	14099	27163	4.97	9.0E-98	BE030973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9134	22213	35757	0.75	6.0E-97	BE898012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
9134	22213	35758	0.75	6.0E-97	BE898012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
10821	23854	37475	0.65	6.0E-97	AA320332.1	EST_HUMAN	EST22872 Adipose tissue, white II Homo sapiens cDNA 5' end
10821	23854	37476	0.65	6.0E-97	AA320332.1	EST_HUMAN	EST22872 Adipose tissue, white II Homo sapiens cDNA 5' end
11592	24690	38381	2.42	6.0E-97	X18804.1	NT	Human mRNA for alpha-actinin
8204	21286	34809	1.73	5.0E-97	AL043314.2	EST_HUMAN	DKFZp434N0323.1 434 (synonym: hta3) Homo sapiens cDNA clone DKFZp434N0323 5'
8336	21417	34943	11.21	6.0E-97	AA418026.1	EST_HUMAN	z07012.s1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:767788 3' similar to TR:G1304125
9877	22917	36502	3.12	5.0E-97	BF154912.1	EST_HUMAN	G1304125 PMS4 MRNA
11840	24829	38519	1.68	5.0E-97	BE148597.1	EST_HUMAN	RCO-BT0812-250900-032-409 BT0812 Homo sapiens cDNA
11840	24829	38520	1.68	5.0E-97	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-502 HT0241 Homo sapiens cDNA
962	14135	27196	2.13	4.0E-97	BE004436.1	EST_HUMAN	MRO-HT0241-150500-010-502 HT0241 Homo sapiens cDNA
1059	15102	28202	1.41	4.0E-97	5463572	NT	CMA-BN0108-170300-293-406 BN0106 Homo sapiens cDNA
5683	18877	32166	0.92	4.0E-97	4557326	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
6902	20190	33615	8.47	4.0E-97	Y11339.2	NT	Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (APOH) mRNA
6962	20190	33616	8.47	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
7161	20294	33737	1.09	4.0E-97	7710125	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
7214	20079	33492	0.92	4.0E-97	11422155	NT	Homo sapiens ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA
8329	21411	34937	1.06	4.0E-97	4557708	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8553	21634	35171	1.43	4.0E-97	11421783	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2) mRNA
8779	21858	35401	0.51	4.0E-97	11431050	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
8820	21899	35438	0.82	4.0E-97	11423233	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
9449	22565	36128	1.06	4.0E-97	AB011166.1	NT	Homo sapiens cytochrome P450, subfamily VB, polypeptide 1 (CYP4B1), mRNA
9449	22565	36129	1.06	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
10652	23686	37296	0.55	4.0E-97	11431050	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
11435	24496	38162	1.99	4.0E-97	11863122	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
11435	24496	38163	1.99	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11719	23905	37528	4.51	4.0E-97	AB042557.1	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
12472	25325	37528	5.28	4.0E-97	11418318	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
253	13473	26504	1.59	3.0E-97	AB032998.1	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
897	14073	27138	7.16	3.0E-97	4502166	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
							Homo sapiens amyloid beta (A4) precursor protein (protease nexin-I, Alzheimer disease) (APP), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7163	20296	33740	0.91	5.0E-96	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7684	20749	34231	0.76	5.0E-96	AB024334.1	NT	Homo sapiens mRNA for 14-3-3gamma, complete cds
8297	21379	34900	1.87	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
8297	21379	34901	1.87	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 6
12063	25063	38769	1.33	5.0E-96	7661973	NT	Homo sapiens KIAA0175 gene product (KIAA0175), mRNA
4308	17451		15.95	3.0E-96	H68656.1	EST_HUMAN	Y87H12.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:212327 5'
426	13623		5.76	2.0E-96	4503098	NT	Homo sapiens chondroin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
766	13947	26994	1.1	2.0E-96	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1834	14981	28079	1.03	2.0E-96	7706205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
4890	18011	30995	1.56	2.0E-96	BE148074.1	EST_HUMAN	RC3-H10230-040500-110-g02 HT0230 Homo sapiens cDNA
7620	20690	34165	0.59	2.0E-96	BF369731.1	EST_HUMAN	QV4-GN0120-250800-427-512 GN0120 Homo sapiens cDNA
7620	20690	34166	0.59	2.0E-96	BF369731.1	EST_HUMAN	QV4-GN0120-250800-427-512 GN0120 Homo sapiens cDNA
9181	22259		4.9	2.0E-96	AV689461.1	EST_HUMAN	AV689461 GKC Homo sapiens cDNA clone GKC/FMD07 5'
12298	25214		2.54	2.0E-96	AW249440.1	EST_HUMAN	2819351.Sprime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2819351 5'
638	13823	26845	0.86	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
638	13823	26846	0.96	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
688	13872	26805	3.08	1.0E-96	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1822	14971	28063	9.97	1.0E-96	AW95054.1	EST_HUMAN	EST367124 MAGE resequences, MAGEC Homo sapiens cDNA
1822	14971	28064	9.97	1.0E-96	AW95054.1	EST_HUMAN	EST367124 MAGE resequences, MAGEC Homo sapiens cDNA
5331	18444		1.59	1.0E-96	5453913	NT	Homo sapiens phospholipid transfer protein (PLTP) mRNA
7105	18532	31487	1.19	1.0E-96	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7194	20059	33470	0.71	1.0E-96	6912455	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
8407	21488	35017	0.9	1.0E-96	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8407	21488	35018	0.9	1.0E-96	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8913	21592	35531	21.44	1.0E-96	11419429	NT	Homo sapiens similar to ecdonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
9051	22130	35674	2.22	1.0E-96	AF274893.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10362	23397	37007	0.68	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
10362	23397	37008	0.68	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
12274	13823	26845	3.29	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
12274	13823	26846	3.29	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
3405	16575	29590	0.72	6.0E-97	BF245240.1	EST_HUMAN	601863712F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4081202 5'
7730	20792		3.4	6.0E-97	BE141849.1	EST_HUMAN	IL6-HT0117-011098-004-D07 HT0117 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12721	25480		1.3	2.0E-95	11417860	NT	Homo sapiens hypothetical protein (HS32281A), mRNA
13067	26698	31066	7.4	2.0E-95	11418184	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
							TR: G1067084 G1067084 F59H2.6 :
						EST_HUMAN	TR: G1067084 G1067084 F59H2.6 :
5732	18925	32219	8.08	1.0E-96	AA284651.1		TR: G1067084 G1067084 F59H2.6 :
						EST_HUMAN	TR: G1067084 G1067084 F59H2.6 :
5732	18925	32220	8.06	1.0E-96	AA284651.1		TR: G1067084 G1067084 F59H2.6 :
7883	20748	34229	4.11	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-290800-011-G11 FN0019 Homo sapiens cDNA
7883	20748	34230	4.11	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-290800-011-G11 FN0019 Homo sapiens cDNA clone IMAGE:31763 5'
7883	20748	34231	4.11	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-290800-011-G11 FN0019 Homo sapiens cDNA clone IMAGE:3922423 5'
9683	22625	36197	0.45	1.0E-96	R17806.1	EST_HUMAN	Y098506.1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:3899761 5'
9683	22625	36197	0.45	1.0E-96	R17806.1	EST_HUMAN	Y098506.1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:3899761 5'
8388	21469	34996	1.56	9.0E-96	BE897259.1	EST_HUMAN	601437232F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3899761 5'
455	16012	26687	0.88	8.0E-96	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3899761 5'
455	16012	26688	0.88	8.0E-96	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3899761 5'
5628	18822	30183	2.8	8.0E-96	AW836047.1	EST_HUMAN	PMO-LT0019-090300-002-409 LT0019 Homo sapiens cDNA
4018	17175	28600	1.25	7.0E-96	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
2394	16465	29579	2.48	6.0E-96	BE111984.1	EST_HUMAN	MR0-HT0559-250200-002-407 HT0559 Homo sapiens cDNA
3394	16564	29579	0.71	6.0E-96	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3571	16736	29751	10.25	6.0E-96	M26873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3'end
11839	24828	38517	2.41	6.0E-96	7662289	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
11839	24828	38517	2.41	6.0E-96	7662289	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
11891	24879	38576	1.94	6.0E-96	8923939	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12064	25045	38753	1.32	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12064	25045	38754	1.32	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
330	13544	28574	3.55	5.0E-96	AB032998.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
865	14041	27104	3.4	5.0E-96	AB032998.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
865	14041	27105	3.4	5.0E-96	AB032998.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
2684	16804	29284	1.72	5.0E-96	11416767	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
3092	16268	31381	0.71	5.0E-96	X60812.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
5024	18153	31381	1.69	5.0E-96	AF284750.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
5296	18414	33341	0.79	5.0E-96	AF149773.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
6788	19943	33341	1.1	5.0E-96	AF149773.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
6851	20004	33413	0.58	5.0E-96	AJ277557.1	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
6921	20236	33669	3.68	5.0E-96	11424399	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
6921	20236	33670	3.68	5.0E-96	11424399	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2536	15661	28784	3.62	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2582	15707	28826	1.34	2.0E-95	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
2662	15784		0.99	2.0E-95	R16245.1	EST_HUMAN	ya49d08.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53383 3'
3228	16400	29412	2.1	2.0E-95	AF015452.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3555	16818	29829	3.6	2.0E-95	7709900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3655	16818	29830	3.6	2.0E-95	7709900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3706	16867	29870	0.81	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
3844	17004	30006	0.62	2.0E-95	A1290264.1	EST_HUMAN	qim01c02.x1 Soares_NhrMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:723G7.4 CE03705;
4481	17621	30602	1.38	2.0E-95	7657185	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
5151	18273	31242	3.5	2.0E-95	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5230	18352	31321	0.99	2.0E-95	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5597	18792	31840	4.12	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA
5597	18792	31841	4.12	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA
5815	19005	32310	1.24	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5815	19005	32311	1.24	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5855	19046	32352	0.63	2.0E-95	11525883	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
6270	19444	32793	3.86	2.0E-95	M59724.1	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7
6579	19741	33122	0.9	2.0E-95	11427182	NT	Homo sapiens Transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6579	19741	33123	0.9	2.0E-95	11427182	NT	Homo sapiens Transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6700	19858	33248	3.25	2.0E-95	AF237737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6903	20218	33647	1.47	2.0E-95	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
9343	22419	35973	1.48	2.0E-95	11421795	NT	Homo sapiens ribophorin II (RPN2), mRNA
10592	23627	37236	0.56	2.0E-95	11434330	NT	Homo sapiens KIAA1065 protein (KIAA1065), mRNA
10962	24043	37678	1.98	2.0E-95	4757853	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRI1A) mRNA
11138	24210	37836	1.35	2.0E-95	7661993	NT	Homo sapiens Ste20-related serine/threonine kinase (KIAA0204), mRNA
12002	24987	38691	1.69	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12002	24987	38692	1.69	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12103	25083		1.57	2.0E-95	AF161420.1	NT	Homo sapiens HSPC302 mRNA, partial cds
12608	25407	32047	2.31	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9565	22707	36274	1.98	8.0E-95	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
10053	23091	36693	2.45	8.0E-95	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH), mRNA
10083	23121		2.92	8.0E-95	AB037816.1	NT	Homo sapiens mRNA for KIAA1995 protein, partial cds
10440	23475	37079	0.81	8.0E-95	9845523	NT	Homo sapiens early growth response 2 (Krex-20 (Drosophila) homolog) (EGR2), mRNA
10953	24035	37670	1.59	8.0E-95	AF112152.1	NT	Homo sapiens HCF-binding transcription factor Zhangfei (ZF), mRNA
11773	24765	38461	1.72	8.0E-95	10864024	NT	Homo sapiens zincin (ZIN), mRNA
11982	24957	38669	1.32	8.0E-95	7019572	NT	Homo sapiens zincin (ZIN), mRNA
11982	24957	38670	1.32	8.0E-95	7019572	NT	Homo sapiens zincin (ZIN), mRNA
12887	25598		17.21	8.0E-95	AA629056.1	EST_HUMAN	zu84b01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.1 L1 repetitive element ;
286	13504	28537	6.07	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
286	13504	28538	6.07	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
2519	15645	28767	1.37	7.0E-95	M75973.1	NT	Human hepatocyte growth factor gene, exon 8
2519	15645	28768	1.37	7.0E-95	M75973.1	NT	Human hepatocyte growth factor gene, exon 8
4486	17628	30608	15.92	7.0E-95	M95708.1	NT	Homo sapiens Ly6-like protein (CD59) mRNA, complete cds
4535	17673		1.09	7.0E-95	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9418	22492	36058	0.62	4.0E-95	BE438625.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
215	13438	28468	0.82	3.0E-95	AV648361.1	EST_HUMAN	AV648361 GLC Homo sapiens cDNA clone GLC01F01 3'
5558	18756	31794	1.52	3.0E-95	BF528041.1	EST_HUMAN	602071146F1 NC1 CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214147 5'
5791	25811	32285	0.94	3.0E-95	4503354	NT	Homo sapiens dedicator of cyto-kinesis 1 (DOCK1) mRNA
7315	20397	33859	0.73	3.0E-95	AA412321.1	EST_HUMAN	z87d01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730273 5'
7315	20397	33860	0.73	3.0E-95	AA412321.1	EST_HUMAN	z87d01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730273 5'
7525	20598	34071	2.01	3.0E-95	AW958121.1	EST_HUMAN	EST370191 IMAGE resequences, IMAGE Homo sapiens cDNA
7525	20598	34072	2.01	3.0E-95	AW958121.1	EST_HUMAN	EST370191 IMAGE resequences, IMAGE Homo sapiens cDNA
9555	22620	36190	1.62	3.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9555	22620	36191	1.62	3.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9948	22987	36581	0.86	3.0E-95	BF213446.1	EST_HUMAN	601846212F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4070451 5'
1676	14828	27911	3.52	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1676	14828	27912	3.52	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1996	15136	28242	73.27	2.0E-95	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
1998	15139	28246	3.97	2.0E-95	BE393873.1	EST_HUMAN	601312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5'
2497	15624	28743	1.5	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2497	15624	28744	1.5	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3158	16333	29342	2.05	1.0E-94	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3158	16333	29343	2.05	1.0E-94	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4478	17618	30500	1.11	1.0E-94	9506692	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
6198	16373	32724	0.69	1.0E-94	AE000269.1	NT	Escherichia coli K-12 MG1685 section 159 of 400 of the complete genome
6395	19555	32925	1.91	1.0E-94	AL040518.1	EST_HUMAN	DKFZp434G0314.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G0314 5'
6405	19574	32936	0.82	1.0E-94	H08270.1	EST_HUMAN	y8702.1 Scores infant brain INIB Homo sapiens cDNA clone IMAGE:45053 5'
6648	19507	33194	0.66	1.0E-94	AV725992.1	EST_HUMAN	AV725992 HTC Homo sapiens cDNA clone HTCBF05 5'
8304	21386	34908	0.8	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8304	21386	34909	0.8	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9456	22572	36138	2.17	1.0E-94	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
9950	23029	36620	1.35	1.0E-94	BE780478.1	EST_HUMAN	601468748F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872099 5'
11321	24384	38028	3.11	1.0E-94	U65590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
11597	24550	38334	1.88	1.0E-94	AI272244.1	EST_HUMAN	ap22e02x1 Schiller cell adherens junction protein (AJAP1) cDNA clone IMAGE:1956122 3' similar to TR:Q62845
12051	25032	38738	1.34	1.0E-94	11418871	NT	Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR, ;
12639	13378	26410	2.02	1.0E-94	BE295714.1	EST_HUMAN	Homo sapiens KIAA0164 gene product (KIAA0164), mRNA
12988	13378	26410	1.73	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
1506	14659	27741	6.05	9.0E-95	AF027302.1	NT	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3224	16398	29409	1.09	9.0E-95	7662027	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3224	16398	29410	1.09	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5521	18718	31733	1.46	9.0E-95	X82569.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5521	18718	31734	1.46	9.0E-95	X82569.1	NT	Homo sapiens glyT1 gene (exons 1c and 2)
8446	21527	35054	1.58	9.0E-95	AF274753.1	NT	Mmusculus glyT1 gene (exons 1c and 2)
149	13374	26407	2.9	8.0E-95	AF154830.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
4658	17794	30779	1.68	8.0E-95	AI700998.1	EST_HUMAN	Homo sapiens carbamyl phosphate synthetase 1 mRNA, complete cds
4658	17794	30780	1.68	8.0E-95	AI700998.1	EST_HUMAN	wa09e04.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340506 3' similar to gb:K00558
7087	20181	33605	0.73	8.0E-95	11416376	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
7390	20468	33934	1.4	8.0E-95	11426529	NT	wa09e04.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340600 3' similar to gb:K00558
7390	20468	33935	1.4	8.0E-95	11426529	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
8391	21472	34998	2.08	8.0E-95	AF032897.1	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
9565	22707	36273	1.98	8.0E-95	11420944	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
							Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
							Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
							Homo sapiens KIAA0255 gene product (KIAA0255), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8840	21919	35457	0.85	5.0E-94	BF529115.1	EST_HUMAN	602042163F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180023 5'
11215	24284	37922	1.43	5.0E-94	11423962	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
11215	24284	37923	1.43	5.0E-94	11423962	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
12503	26177	31558	3.8	5.0E-94	T83398.1	EST_HUMAN	U98504.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:118239 3'
1890	18034	26177	16.49	4.0E-94	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2723	18841	28952	0.99	4.0E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3762	18923	28926	1.12	4.0E-94	AW197851.1	EST_HUMAN	U98504.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3762	18923	28926	1.12	4.0E-94	AW197851.1	EST_HUMAN	U98504.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
4840	17973	30683	3.06	4.0E-94	U591312.1	EST_HUMAN	U98504.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE:
6597	19757	33144	1.48	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6597	19757	33145	1.48	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
7052	20105	26833	0.9	4.0E-94	L27386.1	NT	Homo sapiens huntingtin (HD) gene, exon 37
626	13811	26833	1.76	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
739	13921	26961	1.13	3.0E-94	4502506	NT	Homo sapiens complement component 5 (C5) mRNA
1779	14928	28021	12.9	3.0E-94	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1779	14928	28022	12.9	3.0E-94	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1813	14962	28055	3.18	3.0E-94	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
4308	17449	30435	0.67	3.0E-94	AA484505.1	EST_HUMAN	U98504.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:774782 5'
4437	17577	30557	0.72	3.0E-94	AA781836.1	EST_HUMAN	U98504.s1 Soares testis_NH-T Homo sapiens cDNA clone 1375163 3'
5798	18888	32292	3.21	3.0E-94	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6279	19453	32801	1.13	3.0E-94	AB011536.1	NT	Homo sapiens mRNA for MEGF2, partial cds
6581	19743	33125	3.84	3.0E-94	11526228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
7978	21027	34541	0.63	3.0E-94	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
8393	21474	35001	0.96	3.0E-94	AF152309.1	NT	Homo sapiens protocadherin alpha 13 (PCDH-alpha13) mRNA, complete cds
8787	21866	35408	4.41	3.0E-94	AB014579.1	NT	Homo sapiens mRNA for KIAA0679 protein, partial cds
9791	22831	38410	7.29	3.0E-94	AF087942.1	NT	Homo sapiens glycogenin-1L mRNA, complete cds
11362	24423	38079	1.94	3.0E-94	4757821	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
11976	24960	38662	2.11	3.0E-94	U26711.1	NT	Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete cds
9854	22993	36587	0.67	2.0E-94	A1910393.1	EST_HUMAN	U98504.s1 Soares C016 Homo sapiens cDNA clone IMAGE:2391813 3'
9854	22993	36588	0.67	2.0E-94	A1910393.1	EST_HUMAN	U98504.s1 Soares C016 Homo sapiens cDNA clone IMAGE:2391813 3'
153	13378	26410	3.07	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631038 5'

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3000	16176	29197	5.88	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3287	16451		1.23	1.0E-93	AF231981.1	NT	Homo sapiens long chain polynunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4549	17637	30668	3.28	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5348	18481	31426	0.92	1.0E-93	AF123488.1	NT	Homo sapiens estrogen receptor alpha (ESR1) gene, exon 6
5348	18481	31427	0.92	1.0E-93	AF123488.1	NT	Homo sapiens estrogen receptor alpha (ESR1) gene, exon 6
5684	18678	32167	2.39	1.0E-93	U78508.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5684	18878	32168	2.39	1.0E-93	U78508.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5885	19074	32383	1.2	1.0E-93	AF227138.1	NT	Homo sapiens candidate taste receptor T2R14 gene, complete cds
6037	19220	32543	10.78	1.0E-93	4557792	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
6326	19498	32855	4.8	1.0E-93	7662241	NT	Homo sapiens KIAA0672 gene product (KIAA0672), mRNA
6931	20246	33679	1.94	1.0E-93	11431580	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7400	20478	33946	3.24	1.0E-93	D42072.1	NT	Human mRNA for NF1 N-isoform-exon11, complete cds
8455	21536	35066	2.29	1.0E-93	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
8740	21819	35353	1.15	1.0E-93	Y10183.1	NT	H. sapiens mRNA for MEMD protein
8850	21929	35468	1.14	1.0E-93	AF182032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
9651	21094	34608	2.03	1.0E-93	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
9655	21098	34612	1.14	1.0E-93	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9787	22827	36403	3.9	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9787	22827	36404	3.9	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9926	22966	36555	1.24	1.0E-93	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10349	23394	36594	0.59	1.0E-93	11433846	NT	Homo sapiens ryanodine receptor 3 (RYR3), mRNA
12820	25647		1.62	1.0E-93	AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
12923	25608		3.71	1.0E-93	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
13108	25723	31941	1.36	1.0E-93	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
13123	26173		1.42	1.0E-93	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
10819	23852		1.13	8.0E-94	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4070	17226	30233	1.94	8.0E-94	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
5483	18682	31698	3.51	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5483	18682	31699	3.51	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
6173	19349	32695	2.24	5.0E-94	AA722434.1	EST_HUMAN	z987g06.st Soares_fetal_heart_NH1H19W Homo sapiens cDNA clone IMAGE:409594 3'
7150	20285	33726	1.45	5.0E-94	AJ015800.1	EST_HUMAN	cl83405.s1 Soares_total_fetus_Nb21F8_9w Homo sapiens cDNA clone IMAGE:1623389 3'

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195	13418	26448	5.69	2.0E-93	AB015610.1	NT	Chlorocephus aethiops mRNA for ribosomal protein S4X, complete cds
333	13547	26578	13.77	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
334	13547	26578	6.74	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1946	14799	27884	3.9	2.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
2199	16334	28461	2.23	2.0E-93	U40763.1	NT	Human Cdk-associated RS cyclophilin CARS-Cyp mRNA, complete cds
2555	16680	28805	1.02	2.0E-93	BE252882.1	EST_HUMAN	601117589F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3558220 5'
5254	18374	31340	1.19	2.0E-93	BE253201.1	EST_HUMAN	601117589F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3557243 5'
5533	18730	31746	5.08	2.0E-93	AW964385.1	EST_HUMAN	EST378458 MAGE resequencing, MAGH Homo sapiens cDNA
5544	18741	31775	0.7	2.0E-93	4768153	NT	Homo sapiens deafness, autosomal dominant 5 (DFNA5), mRNA
5660	18854		0.84	2.0E-93	BF351469.1	EST_HUMAN	QV3-HT0513-280300-128-h04 HT0513 Homo sapiens cDNA
5754	18946	32248	1.08	2.0E-93	11430039	NT	Homo sapiens hypothetical protein (LOC51316), mRNA
5768	18960	32281	0.76	2.0E-93	U74313.1	EST_HUMAN	HSU74313 Human chromosome 14 Homo sapiens cDNA clone 1-88
6822	19975		1.2	2.0E-93	AW502002.1	EST_HUMAN	UHF-BNO-aks-g-09-O-U.11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078329 5'
11333	24396	38044	1.39	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
11333	24396	38045	1.39	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
12525	25358		1.78	2.0E-93	AA128735.1	EST_HUMAN	228c10.s1 Soares_pregnant_uterus_NBHPU Homo sapiens cDNA clone IMAGE:503346 3'
12824	25420		3.25	2.0E-93	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
12930	25613		6.34	2.0E-93	BF03527.1	EST_HUMAN	601488531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
105	13341	26369	1.38	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
105	13341	26369	1.38	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
531	13724	28750	7.76	1.0E-93	7657016	NT	Homo sapiens hypothetical protein (D328E19.C1.1), mRNA
813	13802	28822	3.32	1.0E-93	AI146755.1	EST_HUMAN	076408.x1 NCI_QGAP_QLL1 Homo sapiens cDNA clone IMAGE:1872503 3' similar to TR-Q62384 Q62384
896	14071	27136	3.43	1.0E-93	D87876.1	NT	ZINC FINGER PROTEIN.1
1194	14366	27414	0.6	1.0E-93	4503872	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1265	14422	27487	7.22	1.0E-93	8923270	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67KD) (GAD1), transcript variant GAD67, mRNA
1265	14422	27488	7.22	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1376	14531	27604	9.7	1.0E-93	AF167706.1	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
2414	15544	28672	1.08	1.0E-93	AF231981.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2634	15659	28783	3.06	1.0E-93	AF055086.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2576	15702		1.29	1.0E-93	AL137200.1	NT	Homo sapiens MHC class 1 region
2883	14480	27546	1.32	1.0E-93	BE297369.1	EST_HUMAN	Novel human gene mapping to chromosome 1
2883	14480	27547	1.32	1.0E-93	BE297369.1	EST_HUMAN	601177866F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2883	14480	27547	1.32	1.0E-93	BE297369.1	EST_HUMAN	601177866F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7892	20944	34450	3.52	6.0E-93	AF067136.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
8804	21883	35422	0.73	5.0E-93	4557626	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8804	21883	35423	0.73	5.0E-93	4557626	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9822	22852	36443	2.02	5.0E-93	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10012	23030	36844	1.35	5.0E-93	5032186	NT	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
10275	23310	36906	1.78	5.0E-93	AF069313.2	NT	Homo sapiens WSB1 protein (WSB1) mRNA, complete cds
11064	24140	37775	1.92	5.0E-93	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12651	25791	31921	2.31	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
90	13325		5.63	4.0E-93	AA459933.1	EST_HUMAN	z60e09.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:795688 3' similar to SW:CLPA_RAT
458	13653	26690	2.38	4.0E-93	4557879	NT	P37397 CALPONIN, ACIDIC ISOFORM 1
458	13653	26691	2.38	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
793	13972	27024	1.16	4.0E-93	7657454	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
793	13972	27025	1.16	4.0E-93	7657454	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
1210	14371	27431	2.12	4.0E-93	8923658	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2033	15174	28284	4.37	4.0E-93	AF047677.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
2318	15450	28582	1.19	4.0E-93	AF157476.1	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
2672	15792	28909	1.16	4.0E-93	7656972	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
3656	16819	29831	0.73	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
4159	17310	30306	1.51	4.0E-93	4504654	NT	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA
5136	16819	29831	0.75	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
5760	18952	32255	5.01	4.0E-93	T46864.1	EST_HUMAN	y994c12.r1 Stratagene liver (H937224) Homo sapiens cDNA clone IMAGE:78638 5' similar to similar to SP:A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN
11398	24459	38123	10.47	4.0E-93	AV692051.1	EST_HUMAN	AV692051 GKc Homo sapiens cDNA clone GKGDPR07 5'
3742	16903	29906	12.26	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
3742	16903	29907	12.26	3.0E-93	BF690633.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
4350	17493		2.6	3.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
6893	19851	33242	1.31	3.0E-93	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast homolog)-like 2 (GCN5L2), mRNA
11040	24119	37752	2.86	3.0E-93	AB24829.1	EST_HUMAN	w602405.x1 NCI_CGAP_G05 Homo sapiens cDNA clone IMAGE:2304489 3'
195	13418	26447	5.59	2.0E-93	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds

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12782	25524	32005	1.36	2.0E-92	AF106356.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
13066	15843	28954	73.58	2.0E-92	5912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1897	15040	28150	2.95	1.0E-92	R78078.1	EST_HUMAN	y80c08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
1897	15040	28151	2.95	1.0E-92	R78078.1	EST_HUMAN	y80c08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
2135	16271	28392	35.12	1.0E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
8441	21522	35051	0.82	1.0E-92	BE439625.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
							ig01b02.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107487 3' similar to SW:PTNF_HUMAN
9365	22440	35999	3.24	1.0E-92	A1360356.1	EST_HUMAN	Q16825 PROTEIN-TYROSINE PHOSPHATASE D1, contains Alu repetitive element; contains element MER17 repetitive element;
9365	22440	36000	3.24	1.0E-92	A1360356.1	EST_HUMAN	ig01b02.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107487 3' similar to SW:PTNF_HUMAN
2085	15225	28347	3.53	9.0E-93	AU121681.1	EST_HUMAN	Q16825 PROTEIN-TYROSINE PHOSPHATASE D1, contains Alu repetitive element; contains element MER17 repetitive element;
							AUT121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
2100	15240		20.41	9.0E-93	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) H Homo sapiens cDNA 5' end similar to ribosomal protein L29
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2712	15830		1.69	9.0E-93	AF223391.1	NT	601281867F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3603832 5'
3703	16894	28867	1.35	9.0E-93	BE388571.1	EST_HUMAN	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
11947	24893		7.79	9.0E-93	11418526	NT	601460521F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3863908 5'
6723	19880	33271	2.4	8.0E-93	BF036364.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
256	13475	26506	7.25	7.0E-93	AF231919.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
3144	16320	29332	0.74	6.0E-93	11526176	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6819	19972	33360	0.97	6.0E-93	AB033093.1	NT	Homo sapiens PTH-responsive osteosarcoma B1 protein (B1) mRNA, complete cds
7056	20109	33525	7.64	6.0E-93	AF095771.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1412	14566	27640	0.99	5.0E-93	AB014511.1	NT	wc09c08.x1 NCL_CGAP_Py28 Homo sapiens cDNA clone IMAGE:2314670 3'
1439	14592	27666	4.61	5.0E-93	AI674184.1	EST_HUMAN	wc09c08.x1 NCL_CGAP_Py28 Homo sapiens cDNA clone IMAGE:2314670 3'
1439	14592	27667	4.61	5.0E-93	AI674184.1	EST_HUMAN	wc09c08.x1 NCL_CGAP_Py28 Homo sapiens cDNA clone IMAGE:2314670 3'
1504	14657		4.17	5.0E-93	AL163201.2	NT	Homo sapiens chromosome 21 segment HS27C001
1869	16049	28123	1.03	5.0E-93	AJ297710.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 2
3305	16479	29600	3.73	5.0E-93	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin
5920	19107	32420	1.09	5.0E-93	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
							Homo sapiens wbcst1 (WBSCR1) and wbcst5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
6235	18410		1.75	5.0E-93	AF045555.1	NT	

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12878	26198		1.67	3.0E-92	BF367138.1	EST_HUMAN	RC1-GN0021-240800-012-a11 GN0021 Homo sapiens cDNA
26	13264	26266	1.54	2.0E-92	4501898	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
183	13405	26433	4.28	2.0E-92	11422948	NT	Homo sapiens hypothetical protein d1462023.2 (D1462023.2), mRNA
183	13405	26434	4.28	2.0E-92	11422946	NT	Homo sapiens hypothetical protein d1462023.2 (D1462023.2), mRNA
768	13949	26997	5.49	2.0E-92	BE298190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
768	13949	26998	5.49	2.0E-92	BE298190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1752	14901		1.62	2.0E-92	S78653.1	NT	mitg=mas-related [Human, Genomic, 2418 nt]
1980	15132	28236	2.53	2.0E-92	AB181119.1	EST_HUMAN	Wk27407.X1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
1980	15132	28237	2.53	2.0E-92	AB181119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2020	15161	28265	1.01	2.0E-92	4507464	NT	Wk27407.X1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
2020	15161	28266	1.01	2.0E-92	4507464	NT	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2106	15245	28368	5.35	2.0E-92	4506860	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
2725	15843	28554	22.36	2.0E-92	6912457	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
3701	16862	29864	1.02	2.0E-92	AF231619.1	NT	Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA
3701	16862	29865	1.02	2.0E-92	AF231619.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
3777	16938	29944	7.02	2.0E-92	5903180	NT	Homo sapiens chromosome 21 unknown mRNA
4403	17546	30530	1.17	2.0E-92	M10978.1	NT	Homo sapiens chromosome 21 unknown mRNA
5108	18236		4.1	2.0E-92	AL040437.1	EST_HUMAN	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
5879	19069	32377	0.64	2.0E-92	AF016535.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6491	19599		7.19	2.0E-92	4504756	NT	DKFZp434C0414.1 r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0414 5'
6748	19904	33297	2.6	2.0E-92	AB028991.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
7627	20697		0.61	2.0E-92	U67780.1	NT	Homo sapiens Integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL) mRNA
7657	20697		0.64	2.0E-92	U67780.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
8058	22135	35680	1.28	2.0E-92	AW340174.1	EST_HUMAN	Human NPY Y1-like receptor pseudogene mRNA, complete cds
10997	24076	37709	4.68	2.0E-92	11434900	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
11257	24328	37965	3.22	2.0E-92	11434759	NT	h02h02.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808371 3' similar to TR:O02711
11409	24470	38134	5.71	2.0E-92	AW836290.1	EST_HUMAN	O02711 PRO-POLYUTASE POLYPROTEIN ;
11409	24470	38135	5.71	2.0E-92	AW836290.1	EST_HUMAN	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
12758	25502	32035	8.46	2.0E-92	AB029016.1	NT	Homo sapiens zinc finger protein 198 (ZNF198), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8620	21700	35238	5.05	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8721	21801	35337	0.71	8.0E-92	11426569	NT	Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA
9262	22339	35889	2.53	8.0E-92	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10232	23257	36857	0.91	8.0E-92	Y13829.1	NT	Homo sapiens mRNA for MBNL protein
11043	24121	37795	2.86	8.0E-92	AF074393.1	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
11942	24722	38415	1.93	8.0E-92	4503340	NT	Homo sapiens dihydrodipicamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
12740	25491	32028	1.59	8.0E-92	1143470.4	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
68	13305	28328	1.91	7.0E-92	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
246	16008	28498	1.71	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0768 protein, partial cds
246	16008	28498	1.71	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0768 protein, partial cds
604	13793	27533	1.68	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Sepsis truncated isoform mRNA, complete cds
1309	14465	27533	1.94	7.0E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2260	15393	28519	3.85	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2260	15393	28520	3.85	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2630	15753	28868	6.13	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2787	15903	28010	6.84	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (D1S165E), mRNA
3426	18466	28603	0.7	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3426	18466	28610	0.7	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4710	17845	30828	1.19	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2980 nt]
4710	17845	30829	1.19	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2980 nt]
5284	18403	31371	0.98	7.0E-92	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
5376	18578	31448	5.51	7.0E-92	AA446206.1	EST_HUMAN	z666d12.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781175 5'
2178	15313	28441	0.96	3.0E-92	11434814	NT	Homo sapiens Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MJD), mRNA
2178	15313	28442	0.96	3.0E-92	11434814	NT	Homo sapiens Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MJD), mRNA
2824	15938	28048	2.74	3.0E-92	BE900714.1	EST_HUMAN	601501242F NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902839 5'
5997	18182	32504	3.96	3.0E-92	AA378336.1	EST_HUMAN	ES191020 Synovial sarcoma Homo sapiens cDNA 5' and similar to ribosomal protein S13
11002	24081	37716	3.26	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
11002	24081	37717	3.26	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9488	22546	36108	0.73	3.0E-91	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
11480	24539	38207	1.49	3.0E-91	AB029003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
11480	24539	38208	1.49	3.0E-91	AB029003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
13037	18486	31430	8.54	3.0E-91	AF169553.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
13037	18486	31431	8.54	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
49	13288	26300	2.94	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1274	14431	27502	2.74	1.0E-91	AW449746.1	EST_HUMAN	UHL-B13-aks-d-01-QJL.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
5529	18726	31742	0.78	1.0E-91	11434402	NT	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA
6983	20211	33640	1.96	1.0E-91	BF348182.1	EST_HUMAN	60202088F1 NCI CGAP Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
6983	20211	33641	1.96	1.0E-91	BF348182.1	EST_HUMAN	60202088F1 NCI CGAP Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
12130	25110	38814	1.48	1.0E-91	AV763053.1	EST_HUMAN	AV763053 MDS Homo sapiens cDNA clone MDSBCC05 5'
12540	28114		1.5	1.0E-91	H15121.1	EST_HUMAN	ym30e03.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:49587 5'
1270	14428	27496	5.77	9.0E-92	AJ001689.1	NT	Homo sapiens NKX2D gene, exon 10
1270	14428	27497	5.77	9.0E-92	AJ001689.1	NT	Homo sapiens NKX2D gene, exon 10
5309	18426	31396	0.66	9.0E-92	AB020940.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
5579	18774	31820	5.86	9.0E-92	U03007.1	NT	Human Na ⁺ /K ⁺ ATPase alpha-subunit mRNA, partial cds
5722	18915	32210	2.62	9.0E-92	11427149	NT	Homo sapiens NALP1 mRNA, complete cds
6583	19745	33127	3.77	9.0E-92	AF310105.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8041	21124	34644	0.55	9.0E-92	AJ250568.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8041	21124	34845	0.55	9.0E-92	AJ250568.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
8569	21850	35191	1.53	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
8569	21850	35192	1.53	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9474	22531	36095	1.83	9.0E-92	11422088	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
95	13330	26357	6.63	8.0E-92	W26367.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
286	13513	26547	3.09	8.0E-92	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
1866	15012	28119	1.43	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90KD) (DGKG), mRNA
1866	15012	28120	1.43	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90KD) (DGKG), mRNA
5508	18707	31722	0.68	8.0E-92	AB046820.1	NT	Homo sapiens mRNA for KIAA1600 protein, partial cds
5615	18809	31877	0.8	8.0E-92	AF264717.1	NT	Homo sapiens FVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6677	19836	33225	1.28	8.0E-92	AJ000976.1	NT	Homo sapiens MCP-4 gene
6680	19839	33228	0.91	8.0E-92	AF179428.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit variant 1 (REV3L) mRNA, complete cds
8283	21365		0.55	8.0E-92	11416961	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
8620	21700	35235	5.05	8.0E-92	U04193.1	NT	Human lens membrane protein (mp18) gene, exon 11

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8960	22038	35582	1.47	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLOBYF08.3'
12871	26831		1.61	5.0E-91	AI169566.1	EST_HUMAN	qet0111 x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744365 3' similar to contains MIR b2 MIR MIR repetitive element:
3272	18448	29465	1.58	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3272	18448	29465	1.58	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
11171	24242	37875	3.22	4.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
12376	25267	32074	3.27	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
12376	25267	32119	3.27	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
12685	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
12685	25457	32020	1.16	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
1647	14800	27885	2.17	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1847	14800	27885	2.17	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1832	15983	28077	1.1	3.0E-91	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
3420	16589	29605	1.29	3.0E-91	AL183283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3551	16716	29729	4.85	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3551	16716	29730	4.85	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3888	17047	30047	0.93	3.0E-91	AF084530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4714	17849	30832	4.41	3.0E-91	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5094	18222	31193	1.48	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5094	18222	31194	1.48	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5803	18993	32296	3.55	3.0E-91	11434964	NT	Homo sapiens epidermal secretory protein (19.5KD) (HE1), mRNA
6434	19602		2.56	3.0E-91	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6713	19871	33262	2.98	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
6713	19871	33263	2.98	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
7816	20871	34368	4.48	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
7816	20871	34368	4.48	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
8132	21214	34735	0.69	3.0E-91	6601589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8970	22048	35592	2.73	3.0E-91	D19494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds

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748	13929	26971	17.93	1.0E-90	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
748	13929	26972	17.93	1.0E-90	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1134	14299		2.25	1.0E-90	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1334	14491	27560	3.46	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1334	14491	27561	3.46	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1701	14853		2.61	1.0E-90	BE379884.1	EST_HUMAN	601159583F2 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3511118 5'
1951	15094	28195	3.73	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila))-like (LOC57167), mRNA
2915	16093	29106	6.46	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3054	17112	30112	0.59	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3954	17112	30113	0.59	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
4543	17681	30663	1.68	1.0E-90	AF167340.1	NT	Homo sapiens soluble intertein 1 receptor accessory protein (L1TRAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
5792	18983	32286	2.08	1.0E-90	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
5959	19145	32480	0.9	1.0E-90	11428910	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7220	20065	33500	0.73	1.0E-90	U91934.1	NT	Human retina-derived POU-domain factor-1 mRNA, complete cds
7849	20804	34408	2.31	1.0E-90	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
9021	22100	35640	3	1.0E-90	11422089	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
9493	22550		0.92	1.0E-90	AF163854.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9516	22581	36148	1.4	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9516	22581	36149	1.4	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
4313	17458	30444	8.29	8.0E-91	D12234.1	EST_HUMAN	HUM0005381 Liver HepG2 cell line. Homo sapiens cDNA clone s381 3'
8501	21582	35118	1.14	7.0E-91	11419234	NT	Homo sapiens makorin, fing finger protein, 1 (MKRN1), mRNA
10507	23542	37153	0.65	7.0E-91	AI904151.1	EST_HUMAN	GM-BT043-090289-075 BT043 Homo sapiens cDNA
3563	16728	29744	1.85	5.0E-91	AA702794.1	EST_HUMAN	z80b04.s1 Soares fetal_liver_spleen_1NF1.S_51 Homo sapiens cDNA clone IMAGE:448015 3'
4639	17775	30755	1.14	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4639	17775	30756	1.14	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4830	18060	31042	0.67	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4930	18060	31043	0.67	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
6750	19908	33300	1.25	5.0E-91	AI879995.1	EST_HUMAN	eu49709.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518121 3' similar to SW:ASPG_FLAME Q47896 N4-(BETA-N-ACETYL-GLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR
8400	21481	35009	1.33	5.0E-91	BF314882.1	EST_HUMAN	601901624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130933 5'
8960	22039	35581	1.47	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLO Homo sapiens cDNA clone GLOCBYF08 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3088	16284	29281	0.93	4.0E-90	6906918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3088	16284	29282	0.93	4.0E-90	6906918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4779	17914	30800	3.63	4.0E-90	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4919	18049	31037	2.1	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4839	18039	31047	1.91	4.0E-90	M95967.1	NT	Human prothrombin converting enzyme (NEC2) gene, exon 8
12885	16101	29114	1.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12885	16101	29115	1.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8036	21119	34638	0.91	3.0E-90	BF516168.1	EST_HUMAN	UIH-BW1-any-b-04-Q-U1.s1 NC1 CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
8036	21119	34639	0.91	3.0E-90	BF516168.1	EST_HUMAN	UIH-BW1-any-b-04-Q-U1.s1 NC1 CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
11830	24916	38619	28.7	3.0E-90	BE563833.1	EST_HUMAN	601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 5'
220	13442	26473	4.5	2.0E-90	BE567913.1	EST_HUMAN	601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1200	14362	27421	6.48	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1200	14362	27422	6.48	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3048	17106	30103	2.95	2.0E-90	AI138213.1	EST_HUMAN	qc54c02.x1 Soares, placenta, 8d69weeks, 2NblHPrct9W Homo sapiens cDNA clone IMAGE:1713410 3'
4811	17944	30930	1.05	2.0E-90	AB006627.1	NT	similar to SW:OLF3_MOUSE P29276 OLFACTORY RECEPTOR OR3. ;
5029	18158	31135	10.16	2.0E-90	5729855	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
5896	19084	32395	0.6	2.0E-90	11525901	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
5896	19084	32396	0.6	2.0E-90	11525901	NT	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
5903	19092	32406	3.89	2.0E-90	AW672686.1	EST_HUMAN	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
9993	23032	36623	0.99	2.0E-90	11427320	NT	ba49d05.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2899881 5' similar to TR:O75208 O75208 HYPOTHETICAL 35.5 KD PROTEIN. ;
9993	23032	36624	0.99	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
10165	23022	36795	1.46	2.0E-90	AU118985.1	EST_HUMAN	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
10165	23022	36796	1.46	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
11758	23944	37571	3.06	2.0E-90	11024711	NT	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
287	13505	26539	4.1	1.0E-90	4502168	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
385	15963	26628	2.28	1.0E-90	AF231920.1	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-I, Alzheimer disease) (APP), mRNA
386	15963	26628	1.56	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
713	13895	26932	1.92	1.0E-90	AJ237598.1	NT	Homo sapiens chromosome 21 unknown mRNA
713	13895	26933	1.92	1.0E-90	AJ237598.1	NT	Homo sapiens mRNA for T-box transcription factor (T-box gene), partial
713	13895	26933	1.92	1.0E-90	AJ237598.1	NT	Homo sapiens mRNA for T-box transcription factor (T-box gene), partial

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1864	15010	28116	1.07	5.0E-60	AI222095.1	EST_HUMAN	cg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
1864	15010	28117	1.07	5.0E-60	AI222095.1	EST_HUMAN	cg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
2622	15745	28858	2.37	5.0E-90	AF114487.1	NT	Homo sapiens interseitin long isoform (ITSN) mRNA, complete cds
4882	17977	30784	4.51	5.0E-90	4506354	NT	Homo sapiens pregnancy zone protein (PZP) mRNA
4683	17818	30806	0.78	5.0E-60	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5708	18901	32196	2.85	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5726	18919		0.72	5.0E-90	AF008915.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
5810	19000	32307	1.32	5.0E-90	AB015617.1	NT	Homo sapiens ELKS mRNA, complete cds
5886	18901	32196	1.88	6.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
6869	20021	33430	0.95	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
6869	20021	33431	0.95	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7364	20443	33905	2.04	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7364	20443	33906	2.04	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7736	20797	34286	7.98	5.0E-90	4557288	NT	Homo sapiens adenylylase cyclase 9 (ADCY9) mRNA
8488	21569	35107	4.89	5.0E-90	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
9882	22922	36506	1.17	5.0E-90	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
10488	23523	37133	0.71	5.0E-90	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10663	23697	37306	9.66	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
10723	23756	37362	0.53	5.0E-90	7662051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10723	23756	37363	0.53	5.0E-90	7662051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
12948	25659		1.77	5.0E-90	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
13000	25649		4.54	5.0E-90	AI523368.1	EST_HUMAN	ar78n05.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2128761 3'
313	13529	26562	2.04	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
313	13529	26563	2.04	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1110	14275	27332	4.36	4.0E-90	4505316	NT	H. sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1724	14874	27906	13.42	4.0E-90	X99033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
2823	16101	28114	0.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2823	16101	28115	0.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8422	21603	36035	1.07	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8422	21603	36036	1.07	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1088	14254	27309	4.38	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1089	14254	27309	2.91	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1361	16035	27591	3.26	8.0E-90	BE670561.1	EST_HUMAN	7c36f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284683 3'
1361	16035	27592	3.26	8.0E-90	BE670561.1	EST_HUMAN	7c36f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284683 3'
8757	21836	35377	0.6	8.0E-90	BE177830.1	EST_HUMAN	RC1-HT0598-120400-022-b08 HT0598 Homo sapiens cDNA
10939	24021	37654	1.38	8.0E-90	A1222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
10939	24021	37655	1.38	8.0E-90	A1222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
859	14036		6.81	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8619	21639		2.14	7.0E-90	AA782977.1	EST_HUMAN	af63d08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375503 3'
9166	22244	35787	2.13	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
9166	22244	35788	2.13	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
10220	23256	36844	0.46	7.0E-90	AW273794.1	EST_HUMAN	xx24a02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814026 3'
10340	23375	36985	4.2	7.0E-90	H68840.1	EST_HUMAN	y86a04.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:212180 3' similar to SP:C1TC_HUMAN P11566 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;
10340	23375	36986	4.2	7.0E-90	H68840.1	EST_HUMAN	y86a04.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:212180 3' similar to SP:C1TC_HUMAN P11566 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;
10872	23706	37314	0.62	7.0E-90	BF526089.1	EST_HUMAN	602071208F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214257 5'
3136	16312	29324	1.16	6.0E-90	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
3136	16312	29325	1.16	6.0E-90	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
4342	17485	30467	11.21	6.0E-90	89223398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
6105	16285	32618	2.84	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
6105	16285	32619	2.84	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
8522	21603	35140	4.01	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
8522	21603	35141	4.01	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
159	13384		27.59	5.0E-90	AB035344.1	NT	Homo sapiens TOL6 gene, exon 1-10b
1219	14380	27439	6.22	5.0E-90	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
120	13616	26656	0.73	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
128	13616	26657	0.73	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
421	13616	26656	0.89	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
421	13616	26657	0.89	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
543	13736	26760	0.63	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2945	16122	29135	1.53	2.0E-89	AI222095.1	EST_HUMAN	q99608.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
4263	17408	30394	1.18	2.0E-89	AF089897.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4269	17414	30402	5.14	2.0E-89	X58742.1	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4269	17414	30403	5.14	2.0E-89	X58742.1	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4469	17609	30587	1.13	2.0E-89	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4619	17756	30736	1	2.0E-89	AJ007378.1	NT	Homo sapiens GGT gene, exon 5
5459	18783	31842	1.39	2.0E-89	BE541744.1	EST_HUMAN	60106599F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452423 5'
5598	18783	31842	3.55	2.0E-89	AB007646.1	NT	Homo sapiens gene for LECT2, complete cds
5909	19098	32412	1.5	2.0E-89	U03385.1	NT	Homo sapiens gene for LECT2, complete cds
6339	19509	32865	0.79	2.0E-89	AL163285.2	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
7847	20902	34405	5.28	2.0E-89	U81004.1	NT	Homo sapiens chromosome 21 segment HS21C085
8119	21201	34722	3.11	2.0E-89	11428801	NT	Human GT24 (GT24) mRNA, partial cds
8612	21692	35229	0.9	2.0E-89	AJ245503.1	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
9453	22659	36136	0.72	2.0E-89	AB037754.1	NT	Homo sapiens partial mRNA for PEX5 related protein
10015	23053	36647	1.22	2.0E-89	AF170814.1	NT	Homo sapiens mRNA for KIAA1333 protein, partial cds
10015	23053	36648	1.22	2.0E-89	AF170814.1	NT	Homo sapiens CaBP5 (CAEP5) gene, exon 5
11655	24734	38425	2.63	2.0E-89	11434411	NT	Homo sapiens CaBP5 (CAEP5) gene, exon 5
11871	24859	38554	3.52	2.0E-89	11433673	NT	Homo sapiens Integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
12017	25001	38703	1.64	2.0E-89	U10692.1	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
12877	25584	38561	4.25	2.0E-89	AF156981.1	NT	Human IMAGE-7 antigen (IMAGE7) pseudogene, complete cds
11877	24865	38561	6.88	1.0E-89	BF196052.1	EST_HUMAN	Human IMAGE-7 antigen (IMAGE7) pseudogene, complete cds
11877	24885	38562	6.88	1.0E-89	BF196052.1	EST_HUMAN	Homo sapiens human endogenous retrovirus W gag(C3.37 G gag (gag) gene, complete cds
							h181d09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778
							SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN ;
							h181d09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778
							SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN ;

Table 4

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